

SEQ 102543

Access DB#

SEARCH REQUEST FORM

TEXT 102949

Scientific and Technical Information Center

CRFE

Requester's Full Name: BAD-THUY NGUYEN Examiner #: 73403 Date: 8/27/03
 Art Unit: 1041 Phone Number 308-4243 Serial Number: 09/830,876
 Mail Box and Bldg/Room Location: 7E05 Results Format Preferred (circle): PAPER DISK E-MAIL

If more than one search is submitted, please prioritize searches in order of need.

 Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc, if known. Please attach a copy of the cover sheet, pertinent claims, and abstract.

Title of Invention: _____

Inventors (please provide full names): JOHN H. SKERRITT

Earliest Priority Filing Date: 11/11/1998

**For Sequence Searches Only* Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.*

please search antibody that bind to SEQ ID 1-3
 of alpha-amylase

Inventor

AA
 1-15
 2-10
 3-10

thank you

66
 61
 02

STAFF USE ONLY

Searcher: <u>Hansky</u>	Type of Search	Vendors and cost where applicable
Searcher Phone #: _____	NA Sequence (#) _____	STN <u>P238</u>
Searcher Location: _____	AA Sequence (#) <u>3</u>	Dialog _____
Date Searcher Picked Up: _____	Structure (#) _____	Questel/Orbit _____
Date Completed: <u>9/3</u>	Bibliographic _____	Dr.Link _____
Searcher Prep & Review Time: <u>SEQ:8 STN:25</u>	Litigation _____	Lexis/Nexis _____
Clerical Prep Time: _____	Fulltext _____	Sequence Systems <u>02</u>
Online Time: <u>Seq:8 STN:17</u>	Patent Family _____	WWW/Internet _____
	Other <u>11</u>	Other (specify) _____

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STIC SEARCH RESULTS FEEDBACK FORM

Biotech-Chem Library

Questions about the scope or the results of the search? Contact *the searcher* or *contact:*

Mary Hale, Information Branch Supervisor
308-4258, CM1-1E01

Voluntary Results Feedback Form

➤ I am an examiner in Workgroup: Example: 1610

➤ Relevant prior art **found**, search results used as follows:

- ☐ 102 rejection
- ☐ 103 rejection
- ☐ Cited as being of interest.
- ☐ Helped examiner better understand the invention.
- ☐ Helped examiner better understand the state of the art in their technology.

Types of relevant prior art found:

- ☐ Foreign Patent(s)
- ☐ Non-Patent Literature
(journal articles, conference proceedings, new product announcements etc.)

➤ Relevant prior art **not found**:

- ☐ Results verified the lack of relevant prior art (helped determine patentability).
- ☐ Results were not useful in determining patentability or understanding the invention.

Comments:

Drop off or send completed forms to STIC/Biotech-Chem Library CM1 - Circ. Desk



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(FILE 'HOME' ENTERED AT 11:12:37 ON 03 SEP 2003)

FILE 'CAPLUS' ENTERED AT 11:12:46 ON 03 SEP 2003

L1 207 S SKERRITT J?/AU

L2 69 S L1 AND (CEREAL OR GRAIN)

L3 17614 S ALPHA-AMYLASE OR .ALPHA.AMYLASE OR .ALPHA. AMYLASE

L4 3 S L2 AND L3 *← related to instant application*

L5 53 S L2 AND ANTIBOD? *→ includes L4 cites*

SELECT RN L4 1-3

FILE 'REGISTRY' ENTERED AT 11:17:41 ON 03 SEP 2003

L6 6 S E1-6 *6 cpds from L4 cites* - *inventor search*

FILE 'CAPLUS' ENTERED AT 11:18:52 ON 03 SEP 2003

FILE 'REGISTRY' ENTERED AT 11:19:24 ON 03 SEP 2003

L7 4 S L6 NOT CL/ELS *← getting rid of calc salts*

FILE 'CAPLUS' ENTERED AT 11:19:53 ON 03 SEP 2003

L8 3 S L7 AND L4 *3 cites w/ 4 cpds displayed*

L9 51 S L5 NOT L4 *51 cites*

FILE 'REGISTRY' ENTERED AT 11:21:39 ON 03 SEP 2003

L10 1 S IDALVSIRTRGQIHS/SQSP *← Seq ID 1*

L11 35 S CRDDRPYADG/SQSP *← Seq ID 2*

L12 7 S VNWNKVGGG/SQSP *← Seq ID 3*

} searched as exact & embedded sequences

FILE 'CAPLUS' ENTERED AT 11:24:50 ON 03 SEP 2003

L13 1 S L10

L14 5 S L11

L15 3 S L12

L16 1 S L13-15 AND ANTIBOD? *1 cite mentions antibodies*

FILE 'USPATFULL' ENTERED AT 11:25:44 ON 03 SEP 2003

L17 0 S L10

L18 0 S L11

L19 0 S L12

FILE 'CAPLUS' ENTERED AT 11:26:03 ON 03 SEP 2003

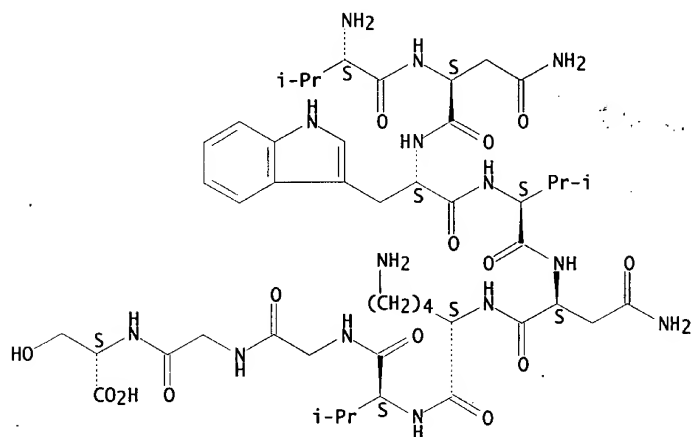
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=> d sqide 17

L7 ANSWER 1 OF 4 REGISTRY COPYRIGHT 2003 ACS on STN
 RN 268202-96-6 REGISTRY
 CN L-Serine, L-valyl-L-asparaginy1-L-tryptophyl-L-valyl-L-asparaginy1-L-lysyl-L-valylglycylglycyl- (9CI) (CA INDEX NAME)
 FS PROTEIN SEQUENCE; STEREOSEARCH
 SQL 10

SEQ 1 VNVVNVKVGGS
 MF C47 H74 N14 O14
 SR CA
 LC STN Files: CA, CAPLUS

Absolute stereochemistry.



1 REFERENCES IN FILE CA (1937 TO DATE)
 1 REFERENCES IN FILE CAPLUS (1937 TO DATE)

=> d sqide 17 2

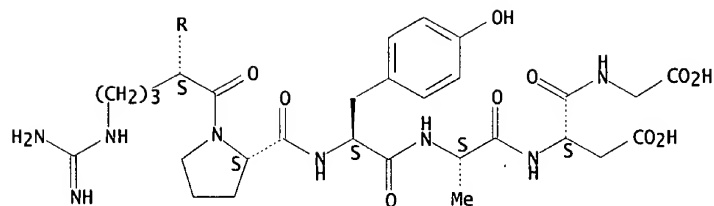
L7 ANSWER 2 OF 4 REGISTRY COPYRIGHT 2003 ACS on STN
 RN 268202-95-5 REGISTRY
 CN Glycine, L-cysteinyl-L-arginyl-L-.alpha.-aspartyl-L-.alpha.-aspartyl-L-arginyl-L-prolyl-L-tyrosyl-L-alanyl-L-.alpha.-aspartyl- (9CI) (CA INDEX NAME)
 FS PROTEIN SEQUENCE; STEREOSEARCH
 SQL 10

SEQ 1 CRDDRPYADG
 MF C46 H70 N16 O18 S
 SR CA
 LC STN Files: CA, CAPLUS

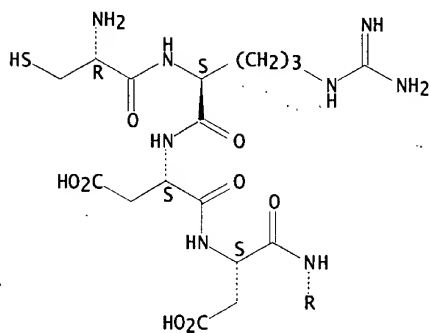
Absolute stereochemistry.

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PAGE 1-A



PAGE 2-A



1 REFERENCES IN FILE CA (1937 TO DATE)
1 REFERENCES IN FILE CAPLUS (1937 TO DATE)

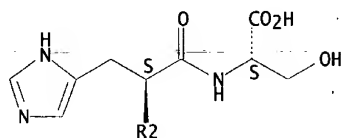
=> d sqide 17 3

L7 ANSWER 3 OF 4 REGISTRY COPYRIGHT 2003 ACS on STN
RN 268202-94-4 REGISTRY
CN L-Serine, L-isoleucyl-L-.alpha.-aspartyl-L-alanyl-L-leucyl-L-valyl-L-seryl-
L-isoleucyl-L-arginyl-L-threonyl-L-arginylglycyl-L-glutaminy-L-isoleucyl-
L-histidyl- (9CI) (CA INDEX NAME)
FS PROTEIN SEQUENCE; STEREOSEARCH
SQL 15

SEQ 1 IDALVSIRTR GQIHS
MF C71 H124 N24 O22
SR CA
LC STN Files: CA, CAPLUS

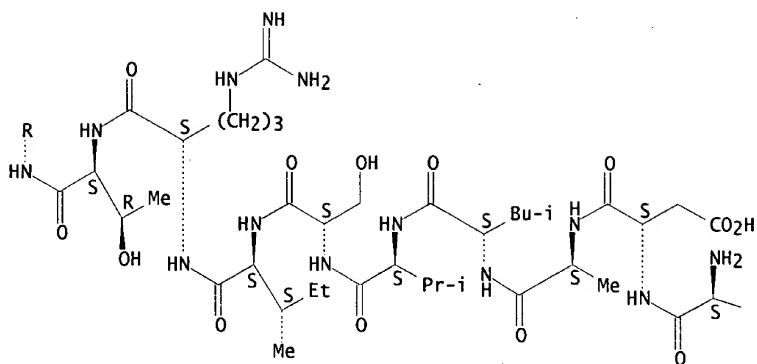
Absolute stereochemistry.

PAGE 1-A



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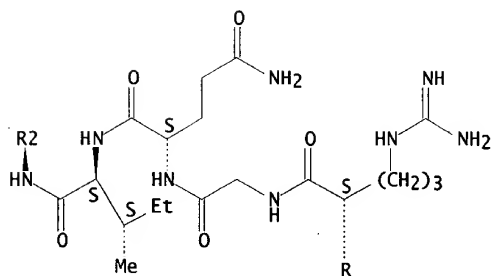
PAGE 2-A



PAGE 2-B



PAGE 3-A



1 REFERENCES IN FILE CA (1937 TO DATE)
1 REFERENCES IN FILE CAPLUS (1937 TO DATE)

=> d 17 4

L7 ANSWER 4 OF 4 REGISTRY COPYRIGHT 2003 ACS on STN
RN 9000-90-2 REGISTRY
CN Amylase, .alpha.- (9CI) (CA INDEX NAME)

Searched by Susan Hanley 305-4053

Page 3

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OTHER NAMES:

CN .alpha.-Amylase
 CN 1,4-.alpha.-D-Glucan glucanohydrolase
 CN 1,4-.alpha.-D-Glucanase
 CN 1,4-.alpha.-Glucanase
 CN Amano AD 1
 CN Amylase AD
 CN Amylase THC 250
 CN Amylogal CS
 CN Amylolisin 5
 CN Amylopsin
 CN Amylosubtilin
 CN Aquazym 120L
 CN Aquazyme 240
 CN Bactosol TK
 CN Ban
 CN Ban (enzyme)
 CN BAN 120L
 CN BAN 240
 CN Ban 480L
 CN Beisol T 2090
 CN Biobake 40000
 CN Bioferm
 CN Bioferm P
 CN Bioprep TBS
 CN Biotex GT
 CN Biozyme A
 CN Biozyme F
 CN Brewers Amylique TS
 CN Buclamase
 CN Canalpha 1000P
 CN Canalpha 600L
 CN Canalpha 60P
 CN Clarase
 CN Denazyme SA 7
 CN Desize 160
 CN E.C. 3.2.1.1
 CN Ekikakoso 6T
 CN EMCEmaltex 1000
 CN Endoamylase
 CN FD Super
 CN Fortizyme
 CN Fungamyl
 CN Fungamyl 2500BG
 CN Fungamyl 300L
 CN Fungamyl 800L
 CN G 995
 CN G-zyme G 995
 CN G6-Amylase
 CN Gamalpha HT 120L
 CN Gemsize 4A

ADDITIONAL NAMES NOT AVAILABLE IN THIS FORMAT - Use FCN, FIDE, or ALL for
 DISPLAY

AR 9000-85-5, 152923-47-2, 152923-48-3, 152923-49-4
 DR 9001-95-0, 9036-05-9, 9077-78-5, 135319-50-5, 106009-10-3, 70356-39-7,
 144133-13-1

MF Unspecified

CI COM, MAN

LC STN Files: ADISNEWS, AGRICOLA, ANABSTR, BIOBUSINESS, BIOSIS, BIOTECHNO,
 CA, CABA, CAPLUS, CASREACT, CBNB, CEN, CHEMCATS, CHEMLIST, CIN, CSCHEM,
 CSNB, DDFU, DIOGENES, DRUGU, EMBASE, IFICDB, IFIPAT, IFIUDB, IPA, MRCK*,
 MSDS-OHS, NAPRALERT, NIOSHTIC, PHARMASEARCH, PIRA, PROMT, RTECS*,
 TOXCENTER, USAN, USPAT2, USPATFULL

(*File contains numerically searchable property data)

Other Sources: DSL**, EINECS**, TSCA**

(**Enter CHEMLIST File for up-to-date regulatory information)

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NGUYEN 09/830,876

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***

13729 REFERENCES IN FILE CA (1937 TO DATE)

207 REFERENCES TO NON-SPECIFIC DERIVATIVES IN FILE CA

13740 REFERENCES IN FILE CAPLUS (1937 TO DATE)

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=> d ibib abs hitrn 18 1-3

L8 ANSWER 1 OF 3 CAPLUS COPYRIGHT 2003 ACS on STN

ACCESSION NUMBER: 2002:53744 CAPLUS

DOCUMENT NUMBER: 137:120380

TITLE: Albumin polymorphism and mapping of a dimeric .
alpha.-amylase inhibitor in wheatAUTHOR(S): Singh, J.; Appels, R.; Sharp, P. J.; Skerritt, J.
H.CORPORATE SOURCE: Cooperative Research Centre for Quality Wheat Products
and Processes, North Ryde, NSW 2113, AustraliaSOURCE: Australian Journal of Agricultural Research (2001),
52(11&12), 1173-1179

CODEN: AJAE9; ISSN: 0004-9409

PUBLISHER: CSIRO Publishing

DOCUMENT TYPE: Journal

LANGUAGE: English

AB Any new protein or DNA marker is potentially useful to add detail to already constructed genetic chromosome maps and may be valuable in breeding programs wherever polymorphism exists. Non-gluten proteins represent 15-20% of total wheat grain proteins. Isoelec. focusing of wheat (*Triticum aestivum* L. em Thell.) proteins on ultrathin gels showed high resolu. and was found to be a useful tool in the differentiation of wheat varieties. Seventeen hexaploid wheat varieties were screened to investigate polymorphism of albumin proteins using isoelec. focusing. Polymorphism was obsd. for albumin polypeptides of pI 5.20, 5.85, 6.25, and 7.1, and 8.0. The polymorphic protein of pI 7.1 was mapped by analyzing doubled haploid populations from the intervarietal crosses, Cranbrook Halberd and Synthetic Opata 85. This protein locus was designated as Iha-B1.2, and is located on the short arm of chromosome 3B.

IT 9000-90-2, .alpha.-Amylase

RL: BSU (Biological study, unclassified); BIOL (Biological study)
(inhibitor WDA1-3; albumin polymorphisms and mapping of dimeric
.alpha.-amylase inhibitor WDA1-3 in wheat using
isoelec. focusing)

REFERENCE COUNT: 21 THERE ARE 21 CITED REFERENCES AVAILABLE FOR THIS
RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L8 ANSWER 2 OF 3 CAPLUS COPYRIGHT 2003 ACS on STN

ACCESSION NUMBER: 2000:335649 CAPLUS

DOCUMENT NUMBER: 132:333681

TITLE: Detection of preharvest sprouting in cereal
grains by immunoassay of .alpha.-
amylase

INVENTOR(S): Skerritt, John Howard

PATENT ASSIGNEE(S): Quality Wheat CRC Limited, Australia

SOURCE: PCT Int. Appl., 51 pp.

CODEN: PIXXD2

DOCUMENT TYPE: Patent

LANGUAGE: English

FAMILY ACC. NUM. COUNT: 1

PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2000028319	A1	20000518	WO 1999-AU995	19991111
W: AU, CA, JP, US				
RW: AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE				
CA 2345403	AA	20000518	CA 1999-2345403	19991111
EP 1137935	A1	20011004	EP 1999-957719	19991111
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, FI				
JP 2002529735	T2	20020910	JP 2000-581446	19991111
AU 757926	B2	20030313	AU 2000-15341	19991111
PRIORITY APPLN. INFO.:			AU 1998-7058	A 19981111

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WO 1999-AU995 W 19991111

AB A two-site immunoassay for the qual. or quant. detection of .alpha.-amylase in a test sample comprises: (i) exposing the test sample to a first ("capture") antibody or antibody fragment which specifically or preferentially binds to a first epitope on the .alpha.-amylase under conditions permitting binding; (ii) subsequently exposing bound .alpha.-amylase to a second ("detection") antibody or antibody fragment which specifically or preferentially binds to a second epitope on the .alpha.-amylase that is distinct from the first epitope, under conditions permitting binding of the second antibody or its fragment to the bound .alpha.-amylase; and (iii) detecting any binding of the second antibody or its fragment to the bound .alpha.-amylase, wherein either of the first or second epitopes is an epitope comprising one or more of the amino acid sequences: IDRLVSIRTRGQIHS, CRDDRYPYADG, or VNWNKVGGS and variants thereof showing .gtoreq.80% (preferably .gtoreq.90%) sequence identity. The immunoassay is useful for detecting weather damage (i.e., preharvest sprouting) in cereal grain. Thus, a rapid tube sandwich ELISA detected .alpha.-amylase in preharvest-sprouted wheat exts. at .apprx.4 ng/mL.

IT 9000-90-2, .alpha.-Amylase 268202-94-4
268202-95-5 268202-96-6

RL: ANT (Analyte); ANST (Analytical study)
(detection of preharvest sprouting in cereal grains
by immunoassay of .alpha.-amylase)

REFERENCE COUNT: 3 THERE ARE 3 CITED REFERENCES AVAILABLE FOR THIS
RECORD; ALL CITATIONS AVAILABLE IN THE RE FORMAT

L8 ANSWER 3 OF 3 CAPLUS COPYRIGHT 2003 ACS on STN

ACCESSION NUMBER: 1999:636830 CAPLUS

DOCUMENT NUMBER: 131:335982

TITLE: Development of a field enzyme-linked immunosorbent
assay (ELISA) for detection of .alpha.-
amylase in preharvest-sprouted wheat

AUTHOR(S): Verity, J. Christiana K.; Hac, Luch; Skerritt,
John H.

CORPORATE SOURCE: Quality Wheat CRC Ltd. and CSIRO Plant Industry,
Canberra, ACT 2601, Australia

SOURCE: Cereal Chemistry (1999), 76(5), 673-681
CODEN: CECHAF; ISSN: 0009-0352

PUBLISHER: American Association of Cereal Chemists

DOCUMENT TYPE: Journal

LANGUAGE: English

AB A sandwich ELISA was developed for detection of .alpha.-amylase in preharvest sprouted wheat and adapted to rapid field-use formats requiring 15-20 min to perform. Polyclonal and monoclonal antibodies were prepd. to detect a mixt. of high and low pI isoenzymes of .alpha.-amylase and high pI isoenzymes only. All antibodies detected .alpha.-amylase on immunoblots of either a crude wheat ext. or of purified enzyme, but only the polyclonal antibodies functioned in a sandwich ELISA. Depending on the antibody combination, the tube ELISA detected either the high and low pI isoenzymes of .alpha.-amylase or the high pI isoenzymes only with a detection limit of .apprxeq.0.5-1.0 ng/mL of amylase. Wheats with falling nos. (FN) of <350 s could be discriminated from sound wheats, with decreasing FN producing increasing assay color. Using 130 wheat grain samples, ELISA absorbances for detection of both high and low pI isoenzymes and of high pI isoenzymes only were highly pos. correlated with amylase enzyme activity and neg. correlated with FN. The correlations were similar for detection of both isoenzyme families and for detection of high pI isoenzymes only. Analyses of three sets of wheat samples from different environments demonstrated that the relationship between ELISA absorbance and FN had little dependence on wheat cultivar. The precision of sample anal. using the field ELISA was similar to the precision of FN test app.

IT 9000-90-2, .alpha.-Amylase

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NGUYEN 09/830,876

RL: ANT (Analyte); ANST (Analytical study)
(field ELISA for detection of α -amylase in
preharvest-sprouted wheat)

REFERENCE COUNT: 45 THERE ARE 45 CITED REFERENCES AVAILABLE FOR THIS
RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

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=> d ibib abs 19 1-51

L9 ANSWER 1 OF 51 CAPLUS COPYRIGHT 2003 ACS on STN

ACCESSION NUMBER: 2002:397370 CAPLUS
DOCUMENT NUMBER: 138:38254
TITLE: Simple ELISA Detection of a New Polymorphic Ha Locus
Encoded Protein
AUTHOR(S): Partridge, M. A. K.; Appels, R.; Skerritt, J.
H.
CORPORATE SOURCE: CSIRO Plant Industry and Quality Wheat CRC Ltd,
Canberra, 2601, Australia
SOURCE: Journal of Cereal Science (2002), 35(2), 189-200
CODEN: JCSCDA; ISSN: 0733-5210
PUBLISHER: Elsevier Science Ltd.
DOCUMENT TYPE: Journal
LANGUAGE: English

AB A rapid two-site sandwich ELISA was developed for detection of a previously uncharacterized protein encoded at the Ha locus on chromosome 5DS of wheat (*Triticum aestivum*). The assay used the combined specificity of two antibodies to detect a protein that was sol. in aq. alc., salt solns. and water. It was expressed in the endosperm of all soft wheats and *Triticum tauschii* accessions tested. The ELISA was highly specific, with no signal obtained with varieties that did not express the protein. The presence of the 5DS-encoded protein correlated with a significant change in both water absorption and av. hardness and particle size indexes in a doubled haploid population derived from a cross between cvs. Cranbrook.times.Halberd. Only some hard varieties expressed this protein indicating that the protein is not predictive for hardness. However, it may be a new factor, or a marker for a new factor, affecting kernel texture. A polypeptide of Mr 66 000 was purified from an ext. of Halberd flour by immunoaffinity chromatog. Its N-terminal amino acid sequence identified it as an albumin with high homol. to both mammalian serum albumins and sucrose synthase from a range of cereals. The assay may be valuable in wheat breeding programs for assessing kernel texture where the parents are of different ELISA phenotype, or for varietal identification, as the expression of the polypeptide is variable in hard wheat varieties.

REFERENCE COUNT: 40 THERE ARE 40 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L9 ANSWER 2 OF 51 CAPLUS COPYRIGHT 2003 ACS on STN

ACCESSION NUMBER: 2001:76313 CAPLUS
DOCUMENT NUMBER: 134:251498
TITLE: A new candidate protein for high lysine content in wheat grain
AUTHOR(S): Singh, Jaswinder; Sharp, Peter J.; Skerritt, John
H.
CORPORATE SOURCE: CSIRO Plant Industry and Quality Wheat CRC Ltd,
Canberra, 2601, Australia
SOURCE: Journal of the Science of Food and Agriculture (2001),
81(2), 216-226
CODEN: JSFAAE; ISSN: 0022-5142
PUBLISHER: John Wiley & Sons Ltd.
DOCUMENT TYPE: Journal
LANGUAGE: English

AB Translation elongation factor 1.alpha. (EF-1.alpha.) from cereal embryo was recently reported to be rich in lysine, and the possibility of using this protein as a marker for feed quality was explored in maize. In this study we used immunochem. methods to investigate the relationship between the content of EF-1.alpha. and other proteins from wheat germ and lysine content in both hexaploid (bread) wheats and diploid wheat progenitors to the wheat A-genome. The levels of grain lysine, as well as their variation between lines or cultivars, were greater for the diploid wheats. While there was a significant correlation between the levels of EF-1.alpha. and grain lysine content, the binding of antibodies to a protein of Mr 37000 showed a higher correlation. This protein was characterized by amino acid sequencing as fructose

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1,6-bisphosphate aldolase. The possibility of using fructose
1,6-bisphosphate aldolase as a marker for feed quality and development of
a simple ELISA for quantification of lysine in wheat is demonstrated.
REFERENCE COUNT: 30 THERE ARE 30 CITED REFERENCES AVAILABLE FOR THIS
RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L9 ANSWER 3 OF 51 CAPLUS COPYRIGHT 2003 ACS on STN
ACCESSION NUMBER: 2000:161331 CAPLUS
DOCUMENT NUMBER: 132:206946
TITLE: Discrimination of glutenin subunits of wheat
INVENTOR(S): Giersch, Thomas Mario; Skerritt, John Howard
; Hill, Amanda Susanne
PATENT ASSIGNEE(S): Quality Wheat Crc Limited, Australia
SOURCE: PCT Int. Appl., 58 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2000012557	A1	20000309	WO 1999-AU690	19990827
W: AU, CA, JP, US				
RW: AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE				
AU 9956116	A1	20000321	AU 1999-56116	19990827
PRIORITY APPLN. INFO.:			AU 1998-5548	A 19980828
			WO 1999-AU690	W 19990827

AB **Antibodies** and immunoassays are disclosed for discriminating
different high mol. wt. glutenin subunits (HMW-GS) in wheat. The
antibodies and immunoassays allow for the identification of
preferred cultivars in plant breeding and for detn. of HMW-GS in wheat
grain sample such as meal, flour and wheat grain ext.

REFERENCE COUNT: 5 THERE ARE 5 CITED REFERENCES AVAILABLE FOR THIS
RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L9 ANSWER 4 OF 51 CAPLUS COPYRIGHT 2003 ACS on STN
ACCESSION NUMBER: 1998:80631 CAPLUS
DOCUMENT NUMBER: 128:165067
TITLE: Identification and characterization of U.S. wheats
carrying null alleles at the wx loci
AUTHOR(S): Graybosch, R. A.; Peterson, C. J.; Hansen, L. E.;
Rahman, S.; Hill, A.; Skerritt, J. H.
CORPORATE SOURCE: USDA-ARS, University of Nebraska, Lincoln, NE, 68583,
USA
SOURCE: Cereal Chemistry (1998), 75(1), 162-165
CODEN: CECHAF; ISSN: 0009-0352
PUBLISHER: American Association of Cereal Chemists
DOCUMENT TYPE: Journal
LANGUAGE: English

AB Granule-bound starch synthase (GBSS) is the primary enzyme responsible for
the synthesis of amylose in amyloplasts of cereal endosperm
cells. Bread wheats, due to their hexaploid genetic system, carry three
genes (wx loci) encoding GBSS. Purifn. and sepn. of GBSS from more than
200 North American hexaploid wheats allowed the indentification of
genotypes that carry null alleles at either the wx-A1 and wx-B1 loci. In
addn., the cultivar Ike carried both wx-A1 and wx-B1 null alleles. No
wx-D1 nulls were detected. Null alleles were found in 10% of the hard
winter wheats tested, but in only 2% of the samples soft winter wheats.
Amylose contents of wheats carrying single null alleles at either the
wx-A1 or wx-B1 loci often were lower than those of wild type wheats, but
greater redn. in amylose content was obsd. in Ike. Monoclonal
antibodies were used to quantify water-extractable GBSS in both
wild-type and null genotypes. Gene dosage compensation was evident,
although GBSS content, as measured by ELISA, was significantly lower in
Ike than in all other wheats. The indentification of null alleles in

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adapted genotypes suggests the development of wheats with a wide range of amylose contents will be possible by simple genetic crossing and selection.

REFERENCE COUNT: 12 THERE ARE 12 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L9 ANSWER 5 OF 51 CAPLUS COPYRIGHT 2003 ACS on STN

ACCESSION NUMBER: 1997:703350 CAPLUS

DOCUMENT NUMBER: 127:356397

TITLE: Measurement of beta-amylase in malting barley (*Hordeum vulgare* L.). I. Development of a quantitative ELISA for beta-amylase

AUTHOR(S): Evans, D. E.; MacLeod, L. C.; Eglinton, J. K.; Gibson, C. E.; Zhang, X.; Wallace, W.; Skerrett, J. H.; Lance, R. C. M.

CORPORATE SOURCE: Dep. Plant Sci., Univ. Adelaide, Glen Osmond, SA 5064, Australia

SOURCE: Journal of Cereal Science (1997), 26(2), 229-239

CODEN: JCSCDA; ISSN: 0733-5210

PUBLISHER: Academic

DOCUMENT TYPE: Journal

LANGUAGE: English

AB A double antibody, sandwich ELISA (ELISA) was developed using polyclonal antibodies specific to beta-amylase to est. the amt. of 'free' (sol. in aq. saline soln.) or 'combined' (extd. with saline soln. including reducing agent) beta-amylase protein in barley grain and malt. This ELISA was used to quantify the amt. of beta-amylase in barley grain and malt from four varieties grown at nine sites in South Australia in 1993. The antibody used to develop the ELISA reacted differently with beta-amylase dependent on whether the source was barley grain or malt, and on the beta-amylase band pattern in isoelec. focussing (IEF) of the barley variety. On the basis of their IEF band patterns barley varieties were divided into two types, designated Bmy1-Sd1 and Bmy1-Sd2. Malting resulted in proteolytic cleavage of the beta-amylase peptide with a redn. in the apparent mol. wt. of up to Mr 4000 and the appearance of new malt beta-amylase IEF bands that were more basic. The new malt beta-amylase IEF band patterns still allowed the identification of the Bmy1-Sd1 and Bmy1-Sd2 IEF types despite the change in mol. wt. and pI. The data obtained using the beta-amylase ELISA were highly correlated with beta-amylase activity for both the free and combined fractions when the IEF band pattern and its source, barley grain or malt, were taken into account.

L9 ANSWER 6 OF 51 CAPLUS COPYRIGHT 2003 ACS on STN

ACCESSION NUMBER: 1996:324233 CAPLUS

DOCUMENT NUMBER: 125:8895

TITLE: Rapid testing for insecticide residues in stored products using immuno- and enzyme- assays

AUTHOR(S): Skerrett, J. H.; Hill, A. S.; Edward, S. L.; Beasley, H. L.; Lee, N.; McAdam, D. P.; Rigg, A. J.

CORPORATE SOURCE: Division Plant Industry, CSIRO, Canberra, 2601, Australia

SOURCE: Stored Product Protection, Proceedings of the International Working Conference on Stored-Product Protection, 6th, Canberra, Aust., Apr. 17-23, 1994 (1994), Volume 2, 843-847. Editor(s): Highley, Ed. CAB International: Wallingford, UK.

CODEN: 62WJAN

DOCUMENT TYPE: Conference

LANGUAGE: English

AB Accurate knowledge of the presence and levels of protectant residues in stored products is important for several reasons: for adequate control of possible infestation, to ensure that levels do not exceed legal Maximum Residue Limits, and to police specifications in sale/export contracts. While residue levels can be accurately detd. by gas-chromatog., the large no. of samples and sampling times required for thorough monitoring led us

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to develop an alternative method, suitable for on-site testing. Specific antibodies have been employed for the major grain protectants used in Australia and overseas: organophosphates (fenitrothion, chlorpyrifos-Me, pirimiphos-methyl), cabaryl, methoprene and synthetic pyrethroids (bioresmethrin, permethrin, phenothrin). Tests for deltamethrin and some other pyrethroids are under development. In addn., other grain protectant compds. such as malathion, methacrifos, dichlorvos, bromophos and etrimfos can be detected using a novel cholinesterase inhibition test. The reagents needed to perform the tests have been packaged into compact test kits, some of which are now com. available. All the immunoassay tests are performed in the same manner: grain or other commodity is extd. by blending in methanol, drops of the ext. added to an antibody-coated microwell or tube followed by drops of an enzyme conjugate soln. After a few minutes, the microwell or tube is washed in water to remove unbound components, then a color developer added. Different levels of protectant in the sample produce graded differences in yellow color. The cholinesterase test is performed similarly. Tests have been tuned for detection in the 0.05/ 0.1-10 ppm residue range in the commodity. Kits designed for simultaneous testing of a large no. of samples under lab. conditions have also been developed and are suitable for anal. of malted, baked or noodle end-products as well as raw grain. Insecticidal protectants are also important in developing countries. In a new collaboration with Indian scientists, we are extending this work to some other plant-based commodities and organochlorines, fungicides and other organophosphates. Advantages of immunoassay kits here will be the low capital and per-test costs.

L9 ANSWER 7 OF 51 CAPLUS COPYRIGHT 2003 ACS on STN

ACCESSION NUMBER: 1996:172786 CAPLUS
DOCUMENT NUMBER: 124:255671
TITLE: Cereal seed storage proteins
AUTHOR(S): Skerriitt, John H.; Tatham, Arthur S.
CORPORATE SOURCE: Division Plant Industry, CSIRO, Canberra, Australia
SOURCE: Structure of Antigens (1996), Volume 3, 349-86.
Editor(s): Van Regenmortel, M. H. V. CRC: Boca Raton, Fla.
CODEN: 57YWAS
DOCUMENT TYPE: Conference; General Review
LANGUAGE: English

AB A review with approx. 225 refs. Topics discussed include prolamins, evolutionary relationships of prolamins, methods of anal. of prolamins as antigens, epitope mapping approaches, structure of gluten polymers, and structure in relation to celiac toxicity and allergenicity.

L9 ANSWER 8 OF 51 CAPLUS COPYRIGHT 2003 ACS on STN

ACCESSION NUMBER: 1995:929212 CAPLUS
DOCUMENT NUMBER: 124:4892
TITLE: The major proteins of wheat endosperm starch granules
AUTHOR(S): Rahman, Sadequr; Kosar-Hashemi, Behjat; Samuel, Michael S.; Hill, Amanda; Abbott, David C.; Skerriitt, John H.; Preiss, Jack; Appels, Rudi; Morell, Matthew K.
CORPORATE SOURCE: Cooperative Research Centre for Plant Science, Canberra, 0200, Australia
SOURCE: Australian Journal of Plant Physiology (1995), 22(5), 793-803
CODEN: AJPPCH; ISSN: 0310-7841
PUBLISHER: Commonwealth Scientific and Industrial Research Organization
DOCUMENT TYPE: Journal
LANGUAGE: English

AB Wheat starch contains two classes of assocd. proteins: proteins which are embedded within the granule and loosely assocd. surface proteins. The characterization of the major proteins that are embedded in the granule are described. Gel electrophoresis on the basis of size resolved these proteins into five bands of mol. wts. 60, 75, 85, 100 and 105 kDa. These

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polypeptides were demonstrated to be within the granule by their resistance to proteinase K digestion when granules were ungelatinized. The N-terminal sequences of these polypeptides are reported. The most prominent polypeptide is the 60 kDa granule-bound starch synthase. The N-terminal sequence obtained from the 75 kDa polypeptide shows homol. to rice sol. starch synthase. The 85 kDa band was resolved into at least two types of polypeptides, one of which reacted with polyclonal antiserum to the maize branching enzyme IIB. The 100 and 105 kDa polypeptides were located only in the granule and are related, on the basis of N-terminal sequence similarity and cross-reactivity to monoclonal **antibodies**. SDS-PAGE and monoclonal **antibody** cross-reactivity expts. suggest that the 100 and 105 kDa polypeptides are absent from starch granules from all other species examd., including other **cereals**. Thus, all the major granule proteins are involved in starch biosynthesis.

L9 ANSWER 9 OF 51 CAPLUS COPYRIGHT 2003 ACS on STN

ACCESSION NUMBER: 1995:58091 CAPLUS

DOCUMENT NUMBER: 122:8232

TITLE: Applications and limitations of immunochemical analysis of biopolymer quality in **cereals**

AUTHOR(S): Skerrett, J. H.; Andrews, J. L.; Blundell, M.; Beasley, H. L.; Bekes, F.

CORPORATE SOURCE: Div. Plant Ind., CSIRO, Canberra, 2601, Australia
SOURCE: Food and Agricultural Immunology (1994), 6(2), 173-84
CODEN: FAIMEZ; ISSN: 0954-0105

PUBLISHER: Carfax

DOCUMENT TYPE: Journal; General Review

LANGUAGE: English

AB A review with 37 refs. The mixing and baking properties of wheaten doughs are detd. largely by the content, compn. and interactions of the major groups of flour proteins, the disulfide-bonded glutenin subunits and monomeric gliadins. Prediction of dough and bread quality is currently based on medium-scale rheol. and baking tests, but the slow throughput of such tests limits their use both by millers and baking companies and in early-generation screening by plant breeders. Thus identification and quantification of sp. flour proteins by immunoassay has the potential advantages of speed, simplicity and applicability to small samples in breeding. Tech. problems can arise from the low solubilities of these proteins and their high degrees of sequence homol. (which often give rise to extensive **antibody** cross-reaction). These problems can be minimized by modifications to methods and combining monoclonal **antibodies** with selected extn. conditions to enhance the functional specificity of the assay. Limitations also arise from attempting to predict the behavior of a complex system, in which mol. interactions and processing changes have been important, purely from flour polypeptide compn. The authors have used quant. immunoassays for sp. groups of glutenins and gliadins to predict aspects of dough strength and extensibility, while 'yes-no' direct enzyme-linked immunosorbent assays can be used to screen for products of particular wheat or translocated rye genes assocd. with sp. dough qualities. Monoclonal **antibodies** are also being employed to purify sp. flour proteins under non-denaturing conditions and in conjunction with novel very small scale dough testing equipment to directly assess functionality in doughs.

L9 ANSWER 10 OF 51 CAPLUS COPYRIGHT 2003 ACS on STN

ACCESSION NUMBER: 1995:34291 CAPLUS

DOCUMENT NUMBER: 122:104453

TITLE: Quality-related epitopes of high Mr subunits of wheat glutenin

AUTHOR(S): Andrews, J. L.; Skerrett, J. H.

CORPORATE SOURCE: Div. Plant Ind., CSIRO, North Ryde, 2113, Australia
SOURCE: Journal of Cereal Science (1994), 19(3), 219-29
CODEN: JCSCDA; ISSN: 0733-5210

DOCUMENT TYPE: Journal

LANGUAGE: English

AB Three hundred and eighty-four immobilized overlapping nonapeptides, corresponding to the full amino acid sequences of three high Mr subunits

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of glutenin from bread wheat (*Triticum aestivum*) **grain**, were used to det. the linear epitopes recognized by four monoclonal **antibodies**. These **antibodies** were selected on the basis of significant and pos. correlations between their binding to wheat flour exts. in a two-site (sandwich) enzyme immunoassay and rheol. measures of dough strength, an important aspect of bread wheat quality. The **antibodies** did not bind to a single, specific sequence but bound a series of related peptides in each high Mr glutenin subunit examd. The sequences recognized were not identical for the four **antibodies**, but in each case were in the central repeating domain of the high Mr glutenin subunits, and usually comprised regions that overlapped the degenerate repeat nonamer and hexamer sequences. High Mr glutenin subunits that have been assocd. with greater dough strength, such as the D-genome allelic products 10x5 and 10y10, displayed an increased no. of the epitope sequences. The location of the epitopes in sequences of overlapping .beta.-turns in the repetitive region supports the hypothesis that dough elasticity arises partly from .beta.-turn-forming secondary structure in the repeat regions of the Mr glutenin subunits. Addnl. .beta.-turns within high Mr subunits may extend their structure to allow increased interaction between the glutenin subunits and with the other proteins of the gluten complex, thus improving dough strength.

L9 ANSWER 11 OF 51 CAPLUS COPYRIGHT 2003 ACS on STN

ACCESSION NUMBER: 1994:268438 CAPLUS
DOCUMENT NUMBER: 120:268438
TITLE: Improved immunoassay for chlorpyrifos-methyl (Reldan) in **grain**.
AUTHOR(S): Edward, Simone L.; Skerritt, John H.; Hill, Amanda S.; McAdam, David P.
CORPORATE SOURCE: Div. Plant Ind., CSIRO, North Ryde, 2113, Australia
SOURCE: Food and Agricultural Immunology (1993), 5(3), 129-44
CODEN: FAIMEZ; ISSN: 0954-0105
DOCUMENT TYPE: Journal
LANGUAGE: English

AB An improved immunoassay for Reldan in **grain** was developed, based on an immobilized polyclonal **antibody**. This assay had greater sensitivity (limit of detection of 0.cntdot.02 ppm in **grain**, or 0.cntdot.05-0.cntdot.1 ppb in buffer), was less susceptible to interference from methanol (used to ext. the residue from **grain**) and had greater precision than the earlier monoclonal **antibody** assay (Skerritt, J.H., et al, 1992). The polyclonal **antibody** exhibited greater cross-reaction with chlorpyrifos-Et (not used as a **grain** protectant), but less with fenitrothion and bromophos (used occasionally as **grain** protectants), and employed a more stable peroxidase conjugate than the monoclonal **antibody** assay. Good correlations were obtained between Reldan residue levels in wheat **grain** detd. by the improved immunoassay and by gas chromatog. The properties of the polyclonal **antibody** should also allow its use in a rapid field assay.

L9 ANSWER 12 OF 51 CAPLUS COPYRIGHT 2003 ACS on STN

ACCESSION NUMBER: 1994:268419 CAPLUS
DOCUMENT NUMBER: 120:268419
TITLE: Rapid field tests for the organophosphorus pesticides, fenitrothion and pirimiphos-methyl--reliable estimates of residues in stored **grain**
AUTHOR(S): Beasley, H. L.; Skerritt, J. H.; Hill, A. S.; Desmarchelier, J. M.
CORPORATE SOURCE: Div. Plant Ind., CSIRO, North Ryde, 2113, Australia
SOURCE: Journal of Stored Products Research (1993), 29(4), 357-69
CODEN: JSTPAR; ISSN: 0022-474X
DOCUMENT TYPE: Journal
LANGUAGE: English

AB In order for **grain** handlers and traders to reliably est. residues of **grain** protectants in the field, **antibody**-based tests were developed for the organophosphorus pesticides,

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fenitrothion and pirimiphos-Me. To complement the rapid anal., rapid but efficient extn. techniques were developed. In these tests, a pesticide-contg. methanol ext. of the grain sample and an enzyme-labeled component are added dropwise to precoated tubes contg. buffer. After a brief incubation, the tubes are rinsed out in tap water and a substrate/chromogen for the enzyme is added. The color developed is stabilized by acidification and the test result read either by eye or in a portable field photometer. Significant levels of the particular pesticide result in a pale color compared to a dark green pesticide-free control. No calcs. were required to provide a quant. est. of residue as this could be read directly from a graph of color yield (absorbance) vs logarithm of pesticide concn., using std. solns. of pesticide. For fenitrothion, the test had a limit of detection of 4 ng/mL (0.1 ppm in grain) and gave quant. ests. in the range 0.5-15 ppm (in the grain), while the pirimiphos-Me test had a limit of detection of 1 ng/mL (0.03 ppm in grain) and gave quant. ests. over the range 0.1-15 ppm. Thus both tests can be used to segregate "pesticide-free" grain, with residues below 0.1 ppm. Data obtained using the field test correlated well with those obtained using lab. methods, including both gas-liq. chromatog. and immunoassay using microwell plates. The field immunoassay reagents were formatted into a small prototype test kit, and the components stabilized for field use.

L9 ANSWER 13 OF 51 CAPLUS COPYRIGHT 2003 ACS on STN

ACCESSION NUMBER: 1994:268414 CAPLUS

DOCUMENT NUMBER: 120:268414

TITLE: Analysis of the grain-protectant pesticides chlorpyrifos-methyl and methoprene with a 15-min immunoassay for field or elevator use

AUTHOR(S): Edward, Simone L.; Hill, Amanda S.; Ashworth, Paul; Matt, Jonathan; Skerritt, John H.

CORPORATE SOURCE: Div. Plant Ind., CSIRO, North Ryde, Australia

SOURCE: Cereal Chemistry (1993), 70(6), 748-52

CODEN: CECHAF; ISSN: 0009-0352

DOCUMENT TYPE: Journal

LANGUAGE: English

AB Antibody-based tests for field use have been developed to enable semiquant. anal. of two grain protectants, chlorpyrifos-Me and methoprene. In these tests, a pesticide-contg. methanol ext. of the pment.

L9 ANSWER 15 OF 51 CAPLUS COPYRIGHT 2003 ACS on STN

ACCESSION NUMBER: 1993:664564 CAPLUS

DOCUMENT NUMBER: 119:264564

TITLE: Quantitation of bioresmethrin, a synthetic pyrethroid grain protectant, by enzyme immunoassay

AUTHOR(S): Hill, Amanda S.; McAdam, David P.; Edward, Simone L.; Skerritt, John H.

CORPORATE SOURCE: Div. Plant Ind., CSIRO, North Ryde, NSW 2113, UK

SOURCE: Journal of Agricultural and Food Chemistry (1993), 41(11), 2011-18

CODEN: JAFCAU; ISSN: 0021-8561

DOCUMENT TYPE: Journal

LANGUAGE: English

AB An enzyme immunoassay was developed for the synthetic pyrethroid, bioresmethrin, by use of a novel approach for synthesis of the pyrethroid-protein hapten conjugate for antibody prepn. Bioresmethrin was hydrolyzed at the ester linkage, and following protection of the chrysanthemic acid-group, the 2-methylprop-1-ene substituent was oxidatively cleaved. The newly formed and unprotected acid group was reesterified to the other bioresmethrin hydrolysis product [[2-(phenylmethyl)-4-furyl]-methanol], and following substitution of the protecting group, the hapten was coupled to either protein for antibody prodn. or peroxidase for use in the immunoassay. The most sensitive assay employed an antibody prepd. to a deriv. with a 4-carbon spacer arm between bioresmethrin and carrier protein, but used a bioresmethrin-enzyme reporter prepd. using a 4-

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(aminomethyl)cyclohexane-carboxylic acid spacer arm (limit of detection 2 ppb in buffer, 50 ppb in whole wheat or barley grain). Good correlations between HPLC and ELISA detns. of bioresmethrin in whole or ground barley grain were obtained. The sensitivity of the assay was slightly lower in ground grain or flour milling fractions due to interference from coextractives in methanol exts. Apart from resmethrin, of which bioresmethrin is the 1R,3R-trans-isomer, the assay did not detect a variety of other pyrethroids in com. use.

L9 ANSWER 16 OF 51 CAPLUS COPYRIGHT 2003 ACS on STN

ACCESSION NUMBER: 1993:537750 CAPLUS

DOCUMENT NUMBER: 119:137750

TITLE: A simple **antibody**-based test for dough strength. III. Further simplification and collaborative evaluation for wheat quality screening
AUTHOR(S): Andrews, John L.; Blundell, Malcolm J.; Skerritt, John H.

CORPORATE SOURCE: Div. Plant Ind., CSIRO, North Ryde, 2113, Australia

SOURCE: Cereal Chemistry (1993), 70(3), 241-6

CODEN: CECHAF; ISSN: 0009-0352

DOCUMENT TYPE: Journal

LANGUAGE: English

AB An **antibody**-based method for discrimination of wheat flours or whole meals on the basis of differences in dough strength (Skerritt 1991b), as measured by extensigraph max. resistance for example, was simplified for use in large-scale screening to predict dough quality. The major modification was the addn. of unlabeled **antibody** to the dild. grain ext. being analyzed, which simplified sample handling. It reduced the diln. of the grain exts. being tested and improved the differentiation between flours of different strengths. A method was also developed for simultaneous extn. and testing of sets of 96 unweighed whole meal samples. The method was tested in a collaboration trial in eight labs. (none with significant prior immunoassay experience) using two sep. analyses of a set of 16 flours, including three blind duplicates. Each lab. reported highly significant correlations between color developed in the assay and rheol. measurements of dough strength, such as farinograph development time and extensigraph max. resistance. Good ests. of within- and between-lab. precision were also obtained, indicating that the method was suitable for quality assessment in wheat breeding.

L9 ANSWER 17 OF 51 CAPLUS COPYRIGHT 2003 ACS on STN

ACCESSION NUMBER: 1992:488842 CAPLUS

DOCUMENT NUMBER: 117:88842

TITLE: Mono- and polyclonal **antibodies** to the organophosphate fenitrothion. 1. Approaches to hapten-protein conjugation

AUTHOR(S): McAdam, David P.; Hill, Amanda S.; Beasley, Helen L.; Skerritt, John H.

CORPORATE SOURCE: Div. Plant Ind., CSIRO, Canberra, 2601, Australia

SOURCE: Journal of Agricultural and Food Chemistry (1992), 40(8), 1466-70

CODEN: JAFCAU; ISSN: 0021-8561

DOCUMENT TYPE: Journal

LANGUAGE: English

AB Three different chem. approaches were used to couple the organophosphorus pesticide fenitrothion to carrier proteins for prodn. of polyclonal and monoclonal **antibodies**. Hapten conjugates coupled through the pesticide phosphate group yielded the most specific and highest affinity **antibodies**, although **antibodies** of moderate affinity were obtained by derivatization and coupling through the arom. nitro group following its redn. and amide formation with an adipic acid spacer arm. Assay formats using either immobilized **antibody** or immobilized hapten-protein conjugate could be used to det. free fenitrothion. The most sensitive assay could detect 1 ng of fenitrothion. It is recommended for the detection of residues of fenitrothion used for the protection of stored cereals.

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L9 ANSWER 18 OF 51 CAPLUS COPYRIGHT 2003 ACS on STN

ACCESSION NUMBER: 1992:488841 CAPLUS

DOCUMENT NUMBER: 117:88841

TITLE: Mono- and polyclonal antibodies to the organophosphate fenitrothion. 2. Antibody specificity and assay performance

AUTHOR(S): Hill, Amanda S.; Beasley, Helen L.; McAdam, David P.; Skerritt, John H.

CORPORATE SOURCE: Div. Plant Ind., CSIRO, North Ryde, 2113, Australia

SOURCE: Journal of Agricultural and Food Chemistry (1992), 40(8), 1471-4

CODEN: JAFCAU; ISSN: 0021-8561

DOCUMENT TYPE: Journal

LANGUAGE: English

AB The performance and specificities of antibody-based assays for fenitrothion (I) were studied. I could be detected in grain in assays with either polyclonal or monoclonal antibodies using either immobilized antibody or immobilized hapten-protein conjugates. Most assay formats and antibodies distinguished I from structurally similar organophosphates, and variable extents of cross-reaction with metabolites were obsd. The concn. of I in wheat grain samples was measured in 3 assay formats with 2 antibodies, and in each case good correlations were obtained with the results obtained by gas-liq. chromatog. For routine use, a format detecting 3 ng and suitable for anal. over the range 100 ppb-20 ppm in grain was preferred.

L9 ANSWER 19 OF 51 CAPLUS COPYRIGHT 2003 ACS on STN

ACCESSION NUMBER: 1992:446860 CAPLUS

DOCUMENT NUMBER: 117:46860

TITLE: Enzyme-linked immunosorbent assay for quantitation of organophosphate pesticides: fenitrothion, chlorpyrifos-methyl, and pirimiphos-methyl in wheat grain and flour-milling fractions

AUTHOR(S): Skerritt, John H.; Hill, Amanda S.; Beasley, Helen L.; Edward, Simone L.; McAdam, David P.

CORPORATE SOURCE: Div. Plant Ind., CSIRO, North Ryde, 2113, Australia

SOURCE: Journal of AOAC International (1992), 75(3), 519-28

CODEN: JAINEE; ISSN: 1060-3271

DOCUMENT TYPE: Journal

LANGUAGE: English

AB Simple, competitive enzyme-linked immunosorbent assays (ELISAs) were developed for the quantitation of each of 3 major organophosphate insecticides: fenitrothion (FN), chlorpyrifos-Me (CPM), and pirimiphos-Me (PIRM). The performance of these assays on wheat grain and (for FN and CPM) on milling fractions such as flour, wheat germ, and bran was assessed. Each assay was specific for the particular compd., i.e., no significant cross-reaction with the other 2 pesticides was obsd. Only limited reactions were noted with major metabolites or analogs of these pesticides. Assay limits of detection of 0.3 ng FN, 0.2 ng CPM, and 0.02 ng PIRM were recorded, corresponding to limits of detection in whole grain of 0.08 ppm FN, 0.2 ppm CPM, and 0.03 ppm PIRM. Each compd. in grain and milling fractions could be extd. quant. by shaking in MeOH. Multiresidue anal. of the 3 insecticides was performed by simultaneously adding the cereal ext. (dild. in phosphate buffer) to sep. duplicate microwells coated with antibodies to FN, CPM, and PIRM and adding appropriate pesticide-horseradish peroxidase conjugates. High correlations between gas chromatog. and the ELISA methods were obtained for insecticide levels in whole wheat and in milling fractions. The ELISA assays had precision similar to those of instrumental pesticide analyses.

L9 ANSWER 20 OF 51 CAPLUS COPYRIGHT 2003 ACS on STN

ACCESSION NUMBER: 1992:446838 CAPLUS

DOCUMENT NUMBER: 117:46838

TITLE: Analysis of the synthetic pyrethroids, permethrin and

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1(R)-phenothrin, in grain using a monoclonal antibody-based test
 AUTHOR(S): Skerritt, John H.; Hill, Amanda S.; McAdam, David P.; Stanker, Larry H.
 CORPORATE SOURCE: Div. Plant Ind., CSIRO, North Ryde, 2113, Australia
 SOURCE: Journal of Agricultural and Food Chemistry (1992), 40(7), 1287-92
 CODEN: JAFCAU; ISSN: 0021-8561
 DOCUMENT TYPE: Journal
 LANGUAGE: English
 AB A monoclonal antibody generated to the synthetic pyrethroid-related hapten, (3-phenoxybenzyl)-2,2-dimethylcyclopropane-1,3-dicarboxylate-protein conjugate, was used to develop assays for detg. permethrin and 1(R)-phenothrin in wheat grain and flour milling fractions. The earlier 3-h assay was simplified by using 2 approaches. The antibody was directly conjugated to the enzyme horseradish peroxidase (HRP), which eliminated a sep. incubation and washing step from the assay. Also, an assay was developed with microwell-bound monoclonal antibody and a HRP-labeled 3-phenoxybenzoic acid deriv. These assay formats have advantages in increased sensitivity and, in the case of the latter assay, accuracy with grain and flour samples. The most sensitive assay format could detect 1.5 ng/mL permethrin; 50% inhibition of antibody binding occurred at 10 ng/mL. These values corresponded to 75 ppb and 500 ppb, resp., in the original wheat sample. MeOH was the most effective pyrethroid extractant. Use of a simple cleanup procedure for ground grain exts. improved ELISA accuracy but could be omitted for screening purposes.

L9 ANSWER 21 OF 51 CAPLUS COPYRIGHT 2003 ACS on STN
 ACCESSION NUMBER: 1992:127228 CAPLUS
 DOCUMENT NUMBER: 116:127228
 TITLE: Cellular and humoral responses in celiac disease. 2. Protein extracts from different cereals
 AUTHOR(S): Skerritt, John H.; Devery, Jannine M.; Penttila, Imme A.; LaBrooy, Justin T.
 CORPORATE SOURCE: Div. Plant Ind., CSIRO, North Ryde, 2113, Australia
 SOURCE: Clinica Chimica Acta (1991), 204(1-3), 109-22
 CODEN: CCATAR; ISSN: 0009-8981
 DOCUMENT TYPE: Journal
 LANGUAGE: English
 AB The humoral and cellular immune responses to grain protein exts. from celiac-toxic and non-toxic cereals were compared by use of a no. of ELISA and immunoblotting methods and the indirect leukocyte migration inhibition factor (LMIF) assay. Both adult and child celiacs had elevated levels of serum antibody to proteins from the celiac-toxic cereals, namely bread wheat, durum wheat, rye and barley and low levels of proteins from other cereals. Using protein-blotting techniques, antibody binding was greatest to gliadins/low-mol.-mass glutenin subunits and homologous prolamins from rye and barley, consistent with the ELISA findings. Competition ELISA and preabsorption tests indicated that antibody reaction to maize storage proteins did not simply result from cross-reaction of antigliadin antibodies. In LMIF assays, only the wheat exts. had activity in celiac patients. This is most likely partly due to loss of some T-cell epitopes from the extn. technique required for these proteins, as well as the relatively small effects seen for even very active fractions in the LMIF assay.

L9 ANSWER 22 OF 51 CAPLUS COPYRIGHT 2003 ACS on STN
 ACCESSION NUMBER: 1992:55602 CAPLUS
 DOCUMENT NUMBER: 116:55602
 TITLE: Immunocytochemical localization of wheat storage proteins in endosperm cells 30 days after anthesis
 AUTHOR(S): Stenram, Unna; Heneen, Waheeb K.; Skerritt, John H.
 CORPORATE SOURCE: Dep. Crop Genet. Breed., Swed. Univ. Agric. Sci., Svaloev, S-268 00, Swed.

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SOURCE: Journal of Experimental Botany (1991), 42(244),
1347-55
CODEN: JEBOA6; ISSN: 0022-0957

DOCUMENT TYPE: Journal

LANGUAGE: English

AB Antisera against seven different wheat (*Triticum aestivum*) storage protein subfractions were characterized using (1) ELISA with gliadins and low- and high-mol. wt. glutenin subunits and (2) electrophoresis (SDS-PAGE and acidic buffer PAGE) and immunoblotting. The specificities of these antisera (polyclonal antibodies) and 13 monoclonal antibodies covered various patterns of reactivity with alpha-, beta-, gamma- and omega-gliadins and low- and high-mol. wt. glutenins. The antisera and antibodies were applied to ultrathin sections of wheat endosperm tissue, from kernels fixed 30 days after anthesis, and were detected by secondary antibodies tagged with either 5 or 15 nm gold particles using transmission electron microscopy. Labeling was denser when the small gold particles were used but irresp. of gold particle size, labeling of polyclonal antisera predominated when the endosperm cells were subjected to both mono- and polyclonal antibodies. Each of the antisera and monoclonal antibodies that labeled the protein bodies, labeled them more or less uniformly. This indicates that only one kind of protein body, contg. all gliadin and glutenin subfractions, exists during this stage of grain development. Electron-dense globular inclusions found in many protein bodies were not labeled. Label was also found on protein-like material present in the lumen of the rough endoplasmic reticulum and on vesicles of the Golgi app. Thus, concn. of storage proteins takes place both at the site of synthesis, the lumen of the rough endoplasmic reticulum, and at the site of processing and transport, the vesicles of the Golgi app. Fusions between these proteinaceous materials give rise to larger protein bodies and ultimately to the protein matrix.

L9 ANSWER 23 OF 51 CAPLUS COPYRIGHT 2003 ACS on STN

ACCESSION NUMBER: 1991:605926 CAPLUS

DOCUMENT NUMBER: 115:205926

TITLE: Monoclonal and polyclonal antibodies and test method for determination of fenitrothion and closely related organophosphates

INVENTOR(S): Skerritt, John Howard; Hill, Amanda Susanne; McAdam, David Peter

PATENT ASSIGNEE(S): Commonwealth Scientific and Industrial Research Organization, Australia

SOURCE: PCT Int. Appl., 30 pp.
CODEN: PIXXD2

DOCUMENT TYPE: Patent

LANGUAGE: English

FAMILY ACC. NUM. COUNT: 1

PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 9100294	A1	19910110	WO 1990-AU278	19900629
W: AU, CA, GB, JP, US				
RW: AT, BE, CH, DE, DK, ES, FR, GB, IT, LU, NL, SE				
CA 2062820	AA	19901231	CA 1990-2062820	19900629
CA 2062820	C	20021112		
AU 9058550	A1	19910117	AU 1990-58550	19900629
AU 633113	B2	19930121		
ZA 9005132	A	19911030	ZA 1990-5132	19900629
EP 479834	A1	19920415	EP 1990-909585	19900629
EP 479834	B1	19991110		
R: AT, BE, CH, DE, DK, ES, FR, GB, IT, LI, LU, NL, SE				
JP 04503760	T2	19920709	JP 1990-509255	19900629
JP 08008874	B4	19960131		
AT 186553	E	19991115	AT 1990-909585	19900629
US 5541079	A	19960730	US 1994-300931	19940906
PRIORITY APPLN. INFO.:			AU 1989-5018	A 19890630

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WO 1990-AU278 A 19900629
US 1991-784389 B1 19911230

OTHER SOURCE(S): MARPAT 115:205926

AB Monoclonal and polyclonal **antibodies** and fragments thereof are described which are capable of binding to specific members or groups of O,O-dialkyl-O-(X) phosphorothioate compds. [X = (substituted) arom. or (substituted) heterocyclic group]. Hybridoma cell lines, methods for making **antibodies** and immunogens, and assays and kits including the **antibodies** are also disclosed. Thus, fenitrothion was converted to the diazonium salt and then conjugated with ovalbumin for prodn. of **antibodies**. The **antibodies** were used in a competitive enzyme immunoassay for fenitrothion in wheat.

L9 ANSWER 24 OF 51 CAPLUS COPYRIGHT 2003 ACS on STN

ACCESSION NUMBER: 1991:603551 CAPLUS

DOCUMENT NUMBER: 115:203551

TITLE: Chromosomal control of wheat gliadin protein epitopes: analysis with specific monoclonal **antibodies**

AUTHOR(S): Skerriitt, J. H.; Martinuzzi, O.;

Metakovskii, E. V.

CORPORATE SOURCE: Div. Plant Ind., CSIRO, North Ryde, 2113, Australia

SOURCE: Theoretical and Applied Genetics (1991), 82(1), 44-53

CODEN: THAGA6; ISSN: 0040-5752

DOCUMENT TYPE: Journal

LANGUAGE: English

AB The genetic relationships between small clusters of monomeric alc.-sol. wheat (*Triticum aestivum* L.) grain storage proteins (gliadins) were studied using a panel of monoclonal **antibodies** and immunoblotting, ELISA, and RIA methods. Use of Chinese Spring nullisomic-tetrasomic lines showed that several narrow-specificity **antibodies** bound specifically to gliadins encoded by genes located on a single chromosome. In at least one case, **antibodies** bound to genetic blocks of gliadins, indicating that these block members have structural homol. However, often not all gliadins of a block were recognized by an **antibody**. For broad-specificity **antibodies** and some narrow-specificity **antibodies** structural genes on several chromosomes were important. Studies with several primitive wheat species indicated that, while **antibodies** usually bound gliadins from the same genome in bread and primitive wheats, **antibodies** sometimes bound proteins of quite differing mobilities in the two wheat types. Use of **antibodies** to identify gliadin blocks is simpler than block anal. based on performing crosses, and should be of value in monitoring genotype/end-use quality relationships.

L9 ANSWER 25 OF 51 CAPLUS COPYRIGHT 2003 ACS on STN

ACCESSION NUMBER: 1991:581642 CAPLUS

DOCUMENT NUMBER: 115:181642

TITLE: Determination of the insect growth regulator methoprene in wheat grain and milling fractions using an enzyme immunoassay

AUTHOR(S): Hill, Amanda S.; Mei, Joanne V.; Yin, Chih Ming;

Ferguson, Bruce S.; Skerriitt, John H.

CORPORATE SOURCE: Div. Plant Ind., CSIRO, North Ryde, 2113, Australia

SOURCE: Journal of Agricultural and Food Chemistry (1991),

39(10), 1882-6

CODEN: JAFCAU; ISSN: 0021-8561

DOCUMENT TYPE: Journal

LANGUAGE: English

AB The enzyme immunoassay of J. V. Mei, et al. (1990) was improved for the insect growth regulator methoprene, and the assay was used to det. methoprene in whole wheat grain and milling fractions, including flours, whole meal, bran, and wheat germ. Either MeOH or MeCN could be used to ext. methoprene from grain, flours, and bran; no cleanup of exts. was required. MeOH produced less matrix effects and could be tolerated at higher concns. in the assay. MeCN gave more reliable results in the extn. of methoprene from wheat germ. The improved assay had a sensitivity of 250 pg/mL, and 50% inhibition of **antibody** binding

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occurred at 3 ng/mL, corresponding to a max. sensitivity of 60 ppb and 50% inhibition of antibody binding at 0.75 ppm in the wheat sample when the routine assay method was used. The latter value is in keeping with residue levels typically found in methoprene-treated stored grain. Good correlations were found between methoprene detd. in wheat and grain fractions by the enzyme immunoassay and by conventional HPLC anal.

L9 ANSWER 26 OF 51 CAPLUS COPYRIGHT 2003 ACS on STN

ACCESSION NUMBER: 1991:557244 CAPLUS

DOCUMENT NUMBER: 115:157244

TITLE: Testing cereal products and samples by immunoassay. Test for organophosphate, carbamate, and pyrethroid grain protectants

AUTHOR(S): Skerritt, John H.; Robson, Lisa G.; McAdam, David P.; Hill, Amanda S.

CORPORATE SOURCE: Div. Plant Ind., Commonw. Sci. and Ind. Res. Organ., North Ryde, 2113, Australia

SOURCE: ACS Symposium Series (1990), 451(Immunoassays Trace Chem. Anal.), 124-38

CODEN: ACSMC8; ISSN: 0097-6156

DOCUMENT TYPE: Journal

LANGUAGE: English

AB Organophosphates, synthetic pyrethroids and/or carbaryl are applied to stored grain and grain storage facilities to minimize insect infestation. Local industry deregulation coupled with increasingly stringent export residue tolerances and consumer demand for chem.-free foods have markedly increased demand for pesticide residue testing. Monoclonal and polyclonal antibodies have been prep'd. and test methods developed for fenitrothion, the major organophosphate pesticide used on grain. Some antibodies were specific for fenitrothion and sensitive to 0.1-0.5 ng; other antibodies bound to closely related organophosphates as well. A simple cholinesterase inhibition test for general screening for organophosphates and carbamates is being adapted for use in field situations or high-throughput labs. Antibodies to certain pyrethroids (phenothrin, permethrin) are being assessed for use in simple test kits.

L9 ANSWER 27 OF 51 CAPLUS COPYRIGHT 2003 ACS on STN

ACCESSION NUMBER: 1991:534290 CAPLUS

DOCUMENT NUMBER: 115:134290

TITLE: Determination of gluten in foods using a monoclonal antibody-based competition enzyme immunoassay

AUTHOR(S): Hill, Amanda S.; Skerritt, John H.

CORPORATE SOURCE: Div. Plant Ind., CSIRO, North Ryde, 2113, Australia

SOURCE: Food and Agricultural Immunology (1990), 2(1), 21-35

CODEN: FAIMEZ; ISSN: 0954-0105

DOCUMENT TYPE: Journal

LANGUAGE: English

AB A sensitive competition enzyme-immunoassay for quantification of gluten in foods was developed, using horseradish peroxidase-labeled monoclonal antibodies. Selected antibodies specific for wheat .omega.-gliadin components were used, and these antibodies bound proteins from the related cereals, rye and barley, which are also toxic to individuals with gluten-intolerance (coeliac disease). Binding of these antibodies was not inhibited by heating of gluten during cooking or baking and the assay did not detect cereals not toxic in coeliac disease, such as maize or rice. Gluten could be quantified at higher levels in meat products or in cereal products such as flours or baked goods. Results were not affected by wheat variety. Quant. results could be obtained using simple extn. techniques and solvents (40% or 70% ethanol). Detection of gluten was quant. in a wide range of foods, except for certain products contg. gluten proteins that had been subjected to severe heat, enzymic, or chem. treatment. In these products overestimates rather than underestimates were usually obtained.

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L9 ANSWER 28 OF 51 CAPLUS COPYRIGHT 2003 ACS on STN

ACCESSION NUMBER: 1991:469981 CAPLUS
DOCUMENT NUMBER: 115:69981
TITLE: Immunology invades chemistry: testing cereals with antibodies
AUTHOR(S): Skerritt, John H.; Hill, Amanda S.; McAdam, David P.
CORPORATE SOURCE: Div. Plant Ind., CSIRO, North Ryde, 2113, Australia
SOURCE: Chemistry in Australia (1990), 57(9), 297-300
CODEN: CHAUDY; ISSN: 0312-8180
DOCUMENT TYPE: Journal; General Review
LANGUAGE: English

AB A review with 11 refs. of immunochem. assays used in cereal prodn. and processing, including detection of toxic, illegal, or quality component evaluating wheat gluten strength, dough extensibility, grain hardness, flour protein content and lipid and starch compn., variety identification, detection of pesticide residues, detection and detn. of gluten in foods, and detection of chill-proofing enzymes in beer.

L9 ANSWER 29 OF 51 CAPLUS COPYRIGHT 2003 ACS on STN

ACCESSION NUMBER: 1991:183936 CAPLUS
DOCUMENT NUMBER: 114:183936
TITLE: Enzyme immunoassay for determination of gluten in foods: collaborative study
AUTHOR(S): Skerritt, John H.; Hill, Amanda S.
CORPORATE SOURCE: Div. Plant Ind., CSIRO, North Ryde, 2113, Australia
SOURCE: Journal - Association of Official Analytical Chemists (1991), 74(2), 257-64
CODEN: JANCA2; ISSN: 0004-5756
DOCUMENT TYPE: Journal
LANGUAGE: English

AB A collaborative study was performed in 15 labs. to validate a monoclonal antibody-based enzyme immunoassay (EIA) for detn. of gluten in foods. The study included 13 samples: corn starch, gluten-free baking mixes, wheat flours, cookies, cooked meats, and a soup. Gluten was present in these samples at either zero or 0.02 to 10% by wt., i.e., over almost 3 orders of magnitude. The mean assay values for the foods varied from 88 to 105% of the actual amts. The assay was quant. for cereal products and the soup with repeatability (RSDr, relative std. deviation) and reproducibility (RSDR) of 16-22% and 24-33%, resp. The assay was semiquant. for the processed meat products (RSDr 14 and 26% and RSDR 46 and 56%), probably because gluten was unevenly distributed in the small (1 g) samples that were analyzed. The ELISA method produced no false pos. results, and false negatives obtained with tannin-contg. foods could be avoided by use of a modified sample extractant. None of the collaborators reported problems in following the protocol. The method has been adopted official first action by AOAC for detn. of wheat gluten in foods.

L9 ANSWER 30 OF 51 CAPLUS COPYRIGHT 2003 ACS on STN

ACCESSION NUMBER: 1991:78626 CAPLUS
DOCUMENT NUMBER: 114:78626
TITLE: Immunological homologies between wheat gluten and starch granule proteins
AUTHOR(S): Skerritt, J. H.; Frend, A. J.; Robson, L. G.; Greenwell, P.
CORPORATE SOURCE: Div. Plant Ind., CSIRO, North Ryde, 2113, Australia
SOURCE: Journal of Cereal Science (1990), 12(2), 123-36
CODEN: JCSCDA; ISSN: 0733-5210
DOCUMENT TYPE: Journal
LANGUAGE: English

AB Structural homologies between wheat (Triticum aestivum) gluten proteins and proteins present in well-washed starch granules were examd. with a panel of mouse monoclonal and mouse and rabbit polyclonal antibodies, using immunoblotting, ELISA, and immunocytochem. methods. Many antibodies raised against gluten protein fractions cross-reacted with starch granule proteins (SGP), but often

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weakly. **Antibodies** with similar gliadin and glutenin subunit specificities had similar SGP specificities. **Antibodies** to high-mobility (.alpha.-, .beta.-, .gamma.-) gliadins cross-reacted weakly with low-mol.-wt. SGP (Mr 8000, 19,000 and 30,000) on immunoblots, and very weakly in indirect ELISAs. Some of these **antibodies** labeled both protein bodies and the periphery of starch granules in sections of immature grain, consistent with low-mol.-wt. SGP, deemed to be surface SGP on the basis of extractability studies, indeed being present on the granule surface. Monoclonal **antibodies** that bound .gamma.- or .omega.-gliadins and glutenin subunits bound to higher mol. wt. SGP, esp. a protein of Mr 77,000, at concns. only slightly above those which labeled gluten proteins. As the interior of the starch granule section was labeled, these proteins are likely to be integral to the granule. **Antibodies** binding broadly to all major gluten protein classes also bound most high and low-mol.-wt. SGPs. Some starch proteins of Mr 15,000, which have been assocd. with endosperm softness, appeared to be immunol. distinct.

L9 ANSWER 31 OF 51 CAPLUS COPYRIGHT 2003 ACS on STN

ACCESSION NUMBER: 1990:629824 CAPLUS

DOCUMENT NUMBER: 113:229824

TITLE: Wheat low-molecular-weight glutenin subunits - structural relationship to other gluten proteins analyzed using specific **antibodies**

AUTHOR(S): Skerriitt, John H.; Robson, Lisa G.

CORPORATE SOURCE: Div. Plant Ind., CSIRO Wheat Res. Unit, North Ryde, 2113, Australia

SOURCE: Cereal Chemistry (1990), 67(3), 250-7

CODEN: CECHAF; ISSN: 0009-0352

DOCUMENT TYPE: Journal

LANGUAGE: English

AB The immunol. homol. of low-mol. wt. glutenin subunits (LMW-GS) were compared with the other major wheat gluten polypeptides, high-mol.-wt. glutenin subunits (HMW-GS), and gliadins. Conventional 1-dimensional polyacrylamide gel electrophoretic (PAGE) methods were used as well as a 2-step, 1-dimensional sodium dodecyl sulfate-page technique, together with immunoblotting and enzyme-immunoassay methods. Many **antibodies** raised to gliadins and HMW-GS bound well to LMW-GS. **Antibodies** with specificities for similar groups of gliadins bound to similar groups of glutenins; and HMW-GS but not to other grain proteins, suggesting the existence of "common gluten" amino acid sequences or conformations. The soly. and immunochem. similarities as well as the known linkage between the genes for LMW-GS and certain gliadins mean that LMW-GS may be responsible for many biochem. properties and quality effects usually attributed to gliadins.

L9 ANSWER 32 OF 51 CAPLUS COPYRIGHT 2003 ACS on STN

ACCESSION NUMBER: 1990:512017 CAPLUS

DOCUMENT NUMBER: 113:112017

TITLE: Cereal identification using **antibodies** to characteristic protein, and kits containing the **antibodies**

INVENTOR(S): Skerriitt, John Howawrd; Wrigley, Colin

Walter; Underwood, Patricia Anne

PATENT ASSIGNEE(S): Commonwealth Scientific and Industrial Research Organization, Australia

SOURCE: Pat. Specif. (Aust.), 12 pp.

CODEN: ALXXAP

DOCUMENT TYPE: Patent

LANGUAGE: English

FAMILY ACC. NUM. COUNT: 1

PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
AU 592987	B2	19900201	AU 1986-57023	19850502
AU 8657023	A1	19861106		

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PRIORITY APPLN. INFO.: AU 1985-401 19850502

AB A cereal variety or quality type is identified by applying a cereal grain ext. or grain germination product to a suitable support, treating the support with a (monoclonal) antibody to a specific protein, and detg. the amt. of bound antibody. In an EIA for barley using antibodies to B- and C-hordeins, varieties more suitable for beer malting showed greater rates of destruction of antibody binding sites than poorer quality varieties. Assays using immobilized capture antibodies are also described.

L9 ANSWER 33 OF 51 CAPLUS COPYRIGHT 2003 ACS on STN

ACCESSION NUMBER: 1990:404802 CAPLUS

DOCUMENT NUMBER: 113:4802

TITLE: Homologies between grain storage proteins of different cereal species. 2. Effects of assay format and grain extractant on antibody cross-reactivity

AUTHOR(S): Skerrett, John H.; Hill, Amanda S.

CORPORATE SOURCE: Div. Plant Ind., CSIRO, North Ryde, 2113, Australia

SOURCE: Journal of Cereal Science (1990), 11(2), 123-41

CODEN: JCSCDA; ISSN: 0733-5210

DOCUMENT TYPE: Journal

LANGUAGE: English

AB A variety of monoclonal antibodies with specificities for different wheat grain storage proteins has been shown to exhibit a no. of differing cross-reaction patterns with grain storage proteins from related cereal species (Skerrett and Lew, 1990). This antibody library provides an opportunity to measure the effects of a range of immunoassay methodol. variables on the cross-reactivity of these antibodies. Variation of the extractant used for grain proteins from different cereals altered both the amt. and compn. of protein extd. and thus the cross-reaction of the antibodies. Antibody cross-reactivity was greater when nitrocellulose membrane solid phases compared with polystyrene microwells were used for indirect ELISA. Quite differing cross-reactivity results were obtained when the same grain protein exts. were used in indirect, antigen-competition and sandwich-type assay formats. In the sandwich assay format, alteration of either the solid phase-bound or labeled antibody altered apparent antibody specificity. Thus, it is important when reporting immunol. homol. data, to define cross-reaction of antibodies with respect to the assay format used. Antibody specificity (or cross-reactivity) can be manipulated by variation of sample extractant, solid phase and the format of the assay.

L9 ANSWER 34 OF 51 CAPLUS COPYRIGHT 2003 ACS on STN

ACCESSION NUMBER: 1990:404801 CAPLUS

DOCUMENT NUMBER: 113:4801

TITLE: Homologies between grain storage proteins of different cereal species. 1. Monoclonal antibody reaction with total protein extracts

AUTHOR(S): Skerrett, John H.; Lew, Patricia Y.

CORPORATE SOURCE: Div. Plant Ind., CSIRO, North Ryde, 2113, Australia

SOURCE: Journal of Cereal Science (1990), 11(2), 103-21

CODEN: JCSCDA; ISSN: 0733-5210

DOCUMENT TYPE: Journal

LANGUAGE: English

AB The interactions of a library of monoclonal antibodies, prepd. to wheat (Triticum aestivus L.) gluten proteins, with exts. of total seed storage protein from a no. of related cereals was studied qual. using SDS-PAGE and immunoblotting techniques and studied quant. using indirect enzyme-immunoassay. Antibodies were of four cross-reaction types: (1) some antibodies, such as many of those binding .alpha.- and .beta.-gliadins, bound selectively to wheat grain proteins, (2) others with similar gliadin specificities, bound to prolamins from other Festucoid species (rye, barley and oats),

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(3) other **antibodies** specific for certain .gamma.- and .omega.-gliadins and high-mol.-wt. glutenins, bound very well to proteins from wheat, rye and barley grain, while (4) some **antibodies** showed anomalous cross-reactivities, binding well to wheat and maize prolamins but very weakly to rye or barley grain proteins. These homologies were generally in keeping with structural homologies of proteins from various cereal grains obtained from DNA sequencing and cross-hybridization studies. In some cases, new homologies were identified.

L9 ANSWER 35 OF 51 CAPLUS COPYRIGHT 2003 ACS on STN

ACCESSION NUMBER: 1990:156891 CAPLUS

DOCUMENT NUMBER: 112:156891

TITLE: **Antibody** responses reveal differences in oral tolerance to wheat and maize grain protein fractions

AUTHOR(S): Johnson, R. B.; Labrooy, J. T.; Skerritt, J. H.

CORPORATE SOURCE: Dep. Med., Univ. Adelaide, Adelaide, Australia

SOURCE: Clinical and Experimental Immunology (1990), 79(1), 135-40

CODEN: CEXIAL; ISSN: 0009-9104

DOCUMENT TYPE: Journal

LANGUAGE: English

AB The influence of diet on humoral immune responses to gluten- and corn-derived proteins was examd. by ELISA and protein blotting techniques. Mice raised on the corn-based (gluten-free) diet responded well to parenteral immunization with each of 6 gluten-derived protein preps. (whole gliadin, 2 omega-gliadin fractions, wheat salt-sol. proteins, a peptic-tryptic digest, and a subtilisin digest of gluten); serum **antibody** levels increased at least 300-fold in each case. In contrast, mice raised on the wheat-based diet responded poorly to immunization with either whole gliadin or omega-gliadin and were virtually nonresponsive to enzymic digest of gluten. Diet had little effect on the magnitude of the **antibody** response to wheat salt-sol. proteins, with both groups showing a 300-fold increase in titer. Similarly, tolerance to .alpha.-zeins, the alc.-sol. proteins of corn did not occur on either diet. Some oral tolerance was obsd. to corn glutelin. The specificity of the various **antibody** responses was then analyzed by immunoblotting. Following immunization with gluten proteins or digests, **antibodies** from the corn-fed mice bound more or less equally to each of the main gliadin bands and to the glutenins, whereas the mice on the wheat-based diet had **antibody** specific for omega-gliadin proteins. Serum **antibodies** from the corn-fed mice, immunized with either .alpha.-zein or corn glutelin, showed even labeling of the major corn endosperm proteins whereas **antibodies** from mice on the wheat diet showed strong labeling of the mol. wt. 27,000 and 58,000 bands. Diet influenced the specificity, as well as the magnitude, of serum **antibody** responses to cereal proteins. In addn., oral tolerance appeared to affect the humoral response to some cereal proteins more than others. Both of these findings have important implications for the understanding of celiac disease.

L9 ANSWER 36 OF 51 CAPLUS COPYRIGHT 2003 ACS on STN

ACCESSION NUMBER: 1989:572723 CAPLUS

DOCUMENT NUMBER: 111:172723

TITLE: Detection of glutens with monoclonal **antibody** -producing hybridoma cells

INVENTOR(S): Skerritt, John Howard; Hill, Amanda Susanne

PATENT ASSIGNEE(S): Commonwealth Scientific and Industrial Research Organization, UK

SOURCE: Brit. UK Pat. Appl., 21 pp.

CODEN: BAXXDU

DOCUMENT TYPE: Patent

LANGUAGE: English

FAMILY ACC. NUM. COUNT: 1

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PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
GB 2207921	A1	19890215	GB 1988-16366	19880708
GB 2207921	B2	19910529		
AU 8818917	A1	19890112	AU 1988-18917	19880708
AU 611921	B2	19910627		
CA 1294903	A1	19920128	CA 1988-571492	19880708
PRIORITY APPLN. INFO.:			AU 1987-2985	19870708

AB Hybridoma cell line ATCC HB9798 producing monoclonal antibodies (Mabs) against .omega.-gliadin of wheat and related proteins in rye and barley is prepd. The Mabs can be used for quant. and qual. detn. of gluten in samples. Balb/c mice were grown on a gluten-free diet till parturition and mated. After weaning, the female progeny were reared for one month on the gluten-free diet and immunized with .omega.-gliadin. Spleens were removed from mice and the cells were fused with mouse myeloma cell line sp 2/0. After selection, hybridoma 401/21 subclones were screened and further grown as ascites tumors to obtain antibody 401/21. The antibody 401/21 was immobilized on flat-bottom 96-well polystyrene microwell plates or strips for ELISA of food samples. The method could detect 0.01 and 0.001% (wt./wt.) gluten in food samples depending upon the diln. of the gluten ext.: lower levels were detectable in more concd. exts.

L9 ANSWER 37 OF 51 CAPLUS COPYRIGHT 2003 ACS on STN

ACCESSION NUMBER: 1989:491681 CAPLUS

DOCUMENT NUMBER: 111:91681

TITLE: Monoclonal antibodies used to characterize cDNA clones expressing specific wheat endosperm proteins

AUTHOR(S): Donovan, G. R.; Skerritt, J. H.; Castle, S. L.

CORPORATE SOURCE: Div. Plant Ind., CSIRO Wheat Res. Unit, North Ryde, Australia

SOURCE: Journal of Cereal Science (1989), 9(2), 97-111
CODEN: JCSCDA; ISSN: 0733-5210

DOCUMENT TYPE: Journal

LANGUAGE: English

AB A wheat cDNA library, prepd. from grain endosperm poly A+ mRNA and cloned into the Escherichia coli expression vector lambda gt11, has been screened with 9 monoclonal antibodies having specificities for different wheat endosperm proteins. At least 1 pos. cDNA clone was isolated and purified from those selected with each antibody. Each purified cDNA clone was induced to express fusion proteins, and the nitrocellulose membranes to which the proteins were transferred were incubated with each of the other antibodies at .gtoreq.2 concns. to investigate the extent of homologies between expression fusion proteins. The specificities of the antibodies were detd. using immunoblotting under the same conditions used for binding to the fusion proteins from the expressed cDNA clones. Denatured DNA from each antibody-selected cDNA clone was also characterized by hybridization to .alpha.-/.beta.-genomic gliadin and genomic high-mol.-wt. glutenin subunit DNA probes. Northern hybridizations using the isolated cDNA as probes for endosperm mRNA were also used to assist clone identification. Some monoclonal antibodies with overlapping specificities (identified from blotting and ELISA expts.) crossreacted with several expressed cDNA clones. However, in other instances, pos. identifications were made of the proteins coded for by single families of the cDNA clones. Monoclonal antibody screening of a wheat cDNA library is useful in identifying families of cDNA clones corresponding to different wheat polypeptides at the primary screening stage, obviating the need in many instances for the application of more tedious methods of clone identification.

L9 ANSWER 38 OF 51 CAPLUS COPYRIGHT 2003 ACS on STN

ACCESSION NUMBER: 1989:230112 CAPLUS

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DOCUMENT NUMBER: 110:230112
 TITLE: Protein modification during malting and brewing: some new analytical methods
 AUTHOR(S): Skerritt, J. H.; Collings, D.
 CORPORATE SOURCE: Div. Plant Ind., CSIRO, North Ryde, Australia
 SOURCE: Proceedings of the Convention - Institute of Brewing (Asia Pacific Section) (1988), 20th, 87-93
 CODEN: IBAZA2; ISSN: 0367-6897

DOCUMENT TYPE: Journal
 LANGUAGE: English

AB Modern protein anal. methods, including size-exclusion and reversed-phase HPLC, PAGE, and monoclonal antibody tests were used to examine protein modification in grain during malting and in mash exts. and wort in brewing. Size-exclusion HPLC and electrophoresis are useful for providing qual. anal. of malt modification and proteolysis and protein pptn. during mashing; hydrolysis of specific proteins can also be quantified by HPLC or by immunoassay. Other antibody tests to measure residual protein from malt and cereal adjuncts in finished beers and to det. whether proteolytic enzymes were used in chillproofing of beers are also described.

L9 ANSWER 39 OF 51 CAPLUS COPYRIGHT 2003 ACS on STN

ACCESSION NUMBER: 1989:191088 CAPLUS
 DOCUMENT NUMBER: 110:191088
 TITLE: Monoclonal antibody specific to gliadin protein of wheat, its production and use in kits and methods for detection of gliadin in food
 INVENTOR(S): Skerritt, John Howard; Wrigley, Colin
 PATENT ASSIGNEE(S): Walter; Underwood, Patricia Anne
 SOURCE: Commonwealth Scientific and Industrial Research Organization, Australia
 Pat. Specif. (Aust.), 16 pp.
 CODEN: ALXXAP
 DOCUMENT TYPE: Patent
 LANGUAGE: English
 FAMILY ACC. NUM. COUNT: 1
 PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
AU 572955	B2	19880519	AU 1985-38501	19840206
AU 8538501	A1	19850815		

PRIORITY APPLN. INFO.: AU 1984-3475 19840206

AB A hybridoma is manufd. which produces antibody specific for heat-stable and low-mobility gliadin(s). The antibody is used in a kit and immunoassay method for detecting gliadin in food. Mice were immunized with purified bread wheat gliadin and the spleen cells were fused with mouse myeloma Sp2/0 using PEG. The resultant hybrid cells were cloned and screened with wheat grain proteins. Of 386 clones examd., 2 secreted antibodies interacting with certain discrete bands in the .gamma.- and .omega.-gliadin regions of gradient gel electrophoresis-sepd. proteins. Neither rye pollen proteins nor a variety of other proteins (bovine milk .alpha.-lactalbumin, soybean trypsin inhibitor, etc.) bound these antibodies.

L9 ANSWER 40 OF 51 CAPLUS COPYRIGHT 2003 ACS on STN

ACCESSION NUMBER: 1988:525977 CAPLUS
 DOCUMENT NUMBER: 109:125977
 TITLE: Accumulation of gliadin and glutenin polypeptides during development of normal and sulfur-deficient wheat seed: analysis using specific monoclonal antibodies
 AUTHOR(S): Skerritt, J. H.; Lew, P. Y.; Castle, S. L.
 CORPORATE SOURCE: Div. Plant Ind., CSIRO, North Ryde, 2113, Australia
 SOURCE: Journal of Experimental Botany (1988), 39(203), 723-37
 CODEN: JEBOA6; ISSN: 0022-0957
 DOCUMENT TYPE: Journal

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LANGUAGE: English

AB A panel of monoclonal **antibodies** with various specificities for wheat (*Triticum aestivum*) gluten polypeptides has been used to analyze the accumulation of these polypeptides in the endosperm of developing wheat seeds grown under normal and S-deficient conditions. Immunoblots of polypeptides fractionated by SDS-PAGE allowed a qual. anal. of gliadin and high-mol.-wt. (HMW) glutenin accumulation for high- and low-S seeds 8-30 days after anthesis (d.a.a.). In addn., quant. anal. of the deposition of various gluten polypeptides was performed, with a solid-phase RIA on exts. of seeds harvested 4-36 d.a.a. The initial accumulation of HMW glutenin subunits was detectable at an earlier stage of development than that of gliadins for both normal and S-deficient seeds. The initiation of detectable gliadin accumulation was asynchronous with an order of .alpha.-gliadins, .beta.-, .gamma.- and some .omega.-gliadins and finally the remaining .omega.-gliadins. In S deficiency, all gliadins reached a const. proportion of the dry wt. of the endosperm earlier than in normal wheat, while a more marked increase in the proportion of HMW glutenin occurred late in grain development. The protein blot studies also identified a putative .omega.-gliadin polypeptide which was detectable late in seed development and only in S-deficient seeds.

L9 ANSWER 41 OF 51 CAPLUS COPYRIGHT 2003 ACS on STN

ACCESSION NUMBER: 1987:194871 CAPLUS

DOCUMENT NUMBER: 106:194871

TITLE: Monoclonal **antibodies** in agricultural testing: quantitation of specific wheat gliadins affected by sulfur deficiency

AUTHOR(S): Skerriitt, John H.; Martinuzzi, Ornella; Wrigley, Colin W.

CORPORATE SOURCE: Wheat Res. Unit, CSIRO, North Ryde, 2113, Australia
SOURCE: Canadian Journal of Plant Science (1987), 67(1), 121-9
CODEN: CPLSAY; ISSN: 0008-4220

DOCUMENT TYPE: Journal

LANGUAGE: English

AB Proteins correlation with end-use quality in wheat (*Triticum aestivum* L.) flour samples have been quantitated using a panel of monoclonal **antibodies** (MCA) with specificities for different gliadins (grain endosperm storage proteins which are sol. in aq. alc.). A beta-gliadin specific **antibody** was found suitable for measuring sulfur-related quality loss in sets of flours from three wheat cultivars grown under varying conditions of sulfur fertilization. Binding of this monoclonal **antibody**, measured in a competitive enzyme-immunoassay, was highly correlated with flour sulfur and with the extensibility of, and resistance to stretching of doughs prepd. from these flour samples. These results demonstrate that monoclonal **antibodies** may be used to measure levels of specific components which vary as the technol. quality of the food varies. Rapid spot-tests based on the reaction of seed proteins with specific monoclonal **antibodies** may aid progeny selection in plant breeding program.

L9 ANSWER 42 OF 51 CAPLUS COPYRIGHT 2003 ACS on STN

ACCESSION NUMBER: 1987:135178 CAPLUS

DOCUMENT NUMBER: 106:135178

TITLE: Distinction between barley varieties by grain characteristics, electrophoresis, chromatography and **antibody** reaction

AUTHOR(S): Burbidge, M. J.; Batey, I. L.; Campbell, W. P.; Skerriitt, J. H.; Wrigley, C. W.

CORPORATE SOURCE: Rohstoffabt., VLB, Berlin, D-1000/65, Fed. Rep. Ger.
SOURCE: Seed Science and Technology (1986), 14(3), 619-29
CODEN: SSTCBK; ISSN: 0251-0952

DOCUMENT TYPE: Journal; General Review

LANGUAGE: English

AB A review and discussion with 10 refs. of methods of identification of barley varieties, e.g., visual examn., gel electrophoresis, HPLC, and immunol.

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L9 ANSWER 43 OF 51 CAPLUS COPYRIGHT 2003 ACS on STN

ACCESSION NUMBER: 1987:115996 CAPLUS

DOCUMENT NUMBER: 106:115996

TITLE: Improved staining and characterization of proteins

following gel electrophoresis and electroblotting

Wrigley, Colin W.; Skerritt, John H.

CORPORATE SOURCE: Wheat Res. Unit, CSIRO, North Ryde, 2113, Australia

SOURCE: Electrophor. '86 [Eighty-Six], Proc. Meet. Int.

Electrophor. Soc., 5th (1986), 291-303. Editor(s):

Dunn, Michael J. VCH: Weinheim, Fed. Rep. Ger.

CODEN: 55IZAB

DOCUMENT TYPE: Conference

LANGUAGE: English

AB Improvements in immunol. techniques for characterizing protein zones after gel electrophoresis and electrophoretic transfer to nitrocellulose are illustrated, using wheat grain proteins as antigens and monoclonal or serum antibodies. Techniques included alkali enhancement of protein staining and immunol. reactivity of electroblotted proteins, avoidance of nonspecific antibody binding, and preparative use of electroblotting for protein purifn.

L9 ANSWER 44 OF 51 CAPLUS COPYRIGHT 2003 ACS on STN

ACCESSION NUMBER: 1987:48365 CAPLUS

DOCUMENT NUMBER: 106:48365

TITLE: Specificity characteristics of monoclonal

antibodies to wheat grain storage

proteins

AUTHOR(S): Skerritt, John H.; Underwood, P. Anne

CORPORATE SOURCE: Div. Mol. Biol., CSIRO, North Ryde, 2113, Australia

SOURCE: Biochimica et Biophysica Acta (1986), 874(3), 245-54

CODEN: BBACAQ; ISSN: 0006-3002

DOCUMENT TYPE: Journal

LANGUAGE: English

AB A variety of monoclonal antibodies was prepd. to wheat (Triticum aestivum) gluten proteins, and their antigenic specificities were assessed using non-denaturing polyacrylamide gradient and SDS-PAGE and immunoblotting techniques. While most anti-gliadin monoclonal antibodies bound to all gliadin protein bands sepd. by 1-dimensional electrophoresis, several antibodies binding to small groups of gliadin proteins were identified. At high concns., these specific antibodies bound to an increasing no. of gliadins; this is likely due to the very high sequence homologies between groups of gliadin proteins. Several monoclonal antibodies with specificities for glutenin proteins were produced. These antibodies bound to all major glutenin subunits, although at low antibody concns. some bound selectively to a single subunit. Other anti-glutenin antibodies bound to minor glutenin subunits and a variety of gliadin proteins. Several bound to .gamma.-gliadins and high-mol.-wt. glutenins, suggesting that these groups of proteins bear considerable homol. The results are reviewed in relation to known information on gluten protein structure, derived from DNA-sequencing studies.

L9 ANSWER 45 OF 51 CAPLUS COPYRIGHT 2003 ACS on STN

ACCESSION NUMBER: 1986:624490 CAPLUS

DOCUMENT NUMBER: 105:224490

TITLE: New approaches to barley variety identification and quality studies

AUTHOR(S): Skerritt, J. H.; Batey, I. L.; Wrigley, C.

W.

CORPORATE SOURCE: Wheat Res. Unit, CSIRO, North Ryde, Australia

SOURCE: Proceedings of the Convention - Institute of Brewing

(Asia Pacific Section) (1986), 19th, 55-62

CODEN: IBAZA2; ISSN: 0367-6897

DOCUMENT TYPE: Journal

LANGUAGE: English

AB Three new approaches, which rely on differences in hordein compn. or

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properties, were investigated for their suitability as barley variety identification methods, to supplement visual and electrophoretic methods. High-performance liq. chromatog. on either ion-exchange or reversed-phase columns can differentiate barley varieties that cannot be distinguished by electrophoresis. Differences in the interaction of hordeins from various varieties with a set of monoclonal antibodies may form the basis for rapid spot-test for confirmation of variety or quality type. In addn., a very simple test based upon differences in the turbidity of grain exts. will be of use in preliminary screening of barley samples. There is potential for these new methods to be applied to malt anal.: both varietal identification of malts and detn. of the extent of (protein) modification. Components yielding processing problems can be identified and quantitated in malt samples.

L9 ANSWER 46 OF 51 CAPLUS COPYRIGHT 2003 ACS on STN

ACCESSION NUMBER: 1986:570903 CAPLUS

DOCUMENT NUMBER: 105:170903

TITLE: Molecular comparison of alcohol-soluble wheat and buckwheat proteins

AUTHOR(S): Skerritt, J. H.

CORPORATE SOURCE: Wheat Res. Unit, CSIRO, North Ryde, 2113, Australia

SOURCE: Cereal Chemistry (1986), 63(4), 365-9

CODEN: CECHAF; ISSN: 0009-0352

DOCUMENT TYPE: Journal

LANGUAGE: English

AB Comparisons of buckwheat and wheat proteins according to amino acid compn., electrophoresis, and immunol. reaction revealed little or no similarities. Whereas most of the material extd. from wheat flour by 70% EtOH (following salt extn.) was protein in nature, similar exts. from buckwheat contained only 2.4% N. Unlike wheat gliadin, the corresponding buckwheat fraction was rich in lysine, arginine, and glycine; it was not electrophoretically resolvable into gliadinlike bands on lactate-buffered polyacrylamide gels, and on SDS polyacrylamide gels; it had only minor components in the gliadin mol. size range. Immunol. studies with rabbit polyclonal and mouse monoclonal antibodies showed little cross-reactivity between cereal prolamins and buckwheat proteins. Celiac sera with high IgG anti-gliadin titers also reacted very weakly with buckwheat proteins. These results suggest that alc.-sol. buckwheat proteins (which are only minor components of the endosperm) bear little mol. similarity to wheat prolamins; descriptions of the former as glutenlike are misleading.

L9 ANSWER 47 OF 51 CAPLUS COPYRIGHT 2003 ACS on STN

ACCESSION NUMBER: 1986:49930 CAPLUS

DOCUMENT NUMBER: 104:49930

TITLE: A sensitive monoclonal-antibody-based test for gluten detection: choice of primary and secondary antibodies

AUTHOR(S): Skerritt, John H.; Diment, John A.; Wrigley, Colin W.

CORPORATE SOURCE: Wheat Res. Unit, CSIRO, North Ryde, NSW 2113, Australia

SOURCE: Journal of the Science of Food and Agriculture (1985), 36(10), 995-1003

CODEN: JSFAAE; ISSN: 0022-5142

DOCUMENT TYPE: Journal

LANGUAGE: English

AB Of a series of monoclonal antibodies prepd. to cereal proteins, 2 antibodies with specificity for low-mobility, heat-stable prolamins in wheat and related cereals were investigated as possible probes for a test for gluten in cooked or processed foods. Urea-based solvents were superior to iso-PrOH or SDS extractants in allowing sensitive detection of trace amts. of prolamins. The antibodies detected bread and durum wheat and rye prolamins most strongly, followed by barley then oats; detection of corn and rice was quite weak. This selectivity is suitable for a test for prolamins toxic to coeliac-disease patients. Several enzyme-labeled 2nd

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antibodies, for detection of monoclonal antibody bound to cereal protein, were unsuitable reagents since an appreciable fraction of the 2nd antibodies bound directly to the cereal proteins. Sensitive, artifact-free detection of antibody binding could be performed using the peroxidase-antiperoxidase technique or by direct conjugation of horseradish peroxidase to the monoclonal antibodies.

L9 ANSWER 48 OF 51 CAPLUS COPYRIGHT 2003 ACS on STN

ACCESSION NUMBER: 1986:49929 CAPLUS

DOCUMENT NUMBER: 104:49929

TITLE: A sensitive monoclonal-antibody-based test for gluten detection: quantitative immunoassay

AUTHOR(S): Skerritt, John H.

CORPORATE SOURCE: Wheat Res. Unit, CSIRO, North Ryde, NSW 2113, Australia

SOURCE: Journal of the Science of Food and Agriculture (1985), 36(10), 987-94

CODEN: JSFAAE; ISSN: 0022-5142

DOCUMENT TYPE: Journal

LANGUAGE: English

AB An enzyme-coupled monoclonal antibody has been used to quantify gliadin-like immunoreactivity in a variety of foods. Small discs of nitrocellulose are soaked in food ext. or a series of std. gliadin solns., and incubated with antibody and an enzyme substrate yielding a sol. product. By use of a photometer, std. curves for gliadin may be constructed and the apparent gliadin content of samples calcd. The reproducibility of the procedure was examd. using a variety of common foods and food proteins. The limit of detection for wheat gliadin was .apprx.20 .mu.g/mL ext.; gliadin levels in excess of this value were found in some gluten-free bread mixes and starch [9005-25-8] sources. The overall time for anal. is 5-6 h, although for large nos. of samples, overnight blocking of non-specific antibody binding may be used. It is possible that a library of enzyme-linked monoclonal antibodies could be developed as useful tools for specific food anal.

L9 ANSWER 49 OF 51 CAPLUS COPYRIGHT 2003 ACS on STN

ACCESSION NUMBER: 1986:49928 CAPLUS

DOCUMENT NUMBER: 104:49928

TITLE: A sensitive monoclonal-antibody-based test for gluten detection: studies with cooked or processed foods

AUTHOR(S): Skerritt, John H.; Smith, Robyn A.

CORPORATE SOURCE: Wheat Res. Unit, CSIRO, North Ryde, NSW 2113, Australia

SOURCE: Journal of the Science of Food and Agriculture (1985), 36(10), 980-6

CODEN: JSFAAE; ISSN: 0022-5142

DOCUMENT TYPE: Journal

LANGUAGE: English

AB A method for detection of wheat, rye, barley and oat proteins in a wide range of foods, including baked goods and processed meats has been developed. The procedure requires immobilization of food exts. on nitrocellulose paper followed by treatment with an enzyme-conjugated monoclonal antibody. Upon addn. of the appropriate enzyme substrate, gluten-contg. foods yield purple spots; a wide range of non-gluten common food proteins did not react. The method has several advantages over other means of detecting cereal protein, such as electrophoresis. It is rapid, requiring little sample prepn., and does not require sophisticated equipment or prior knowledge of electrophoretic patterns of common non-cereal food proteins. Since the method may be used with cooked or baked foods, it should be suitable for food-monitoring applications.

L9 ANSWER 50 OF 51 CAPLUS COPYRIGHT 2003 ACS on STN

ACCESSION NUMBER: 1986:33153 CAPLUS

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DOCUMENT NUMBER: 104:33153
 TITLE: Detection and quantitation of **cereal** protein in foods using specific enzyme-linked monoclonal **antibodies**
 AUTHOR(S): Skerriitt, John H.
 CORPORATE SOURCE: Wheat Res. Unit, CSIRO, North Ryde, 2113, Australia
 SOURCE: Food Technology in Australia (1985), 37(12), 570-2
 CODEN: FTAUAC; ISSN: 0015-6647
 DOCUMENT TYPE: Journal
 LANGUAGE: English
 AB A simple test for the presence and level of **cereal** gluten proteins in foods has been developed using monoclonal **antibodies** with specificity for heat-stable proteins from wheat, rye, barley, and oat **grain**. The test is faster, more sensitive and more reliable than other methods, such as electrophoresis, and may be applied to both cooked or processed as well as raw foods. The ability of monoclonal **antibodies** to act as sensitive reagents having reproducible specificities should allow their use in a wide range of immunochem. methods in food anal.

L9 ANSWER 51 OF 51 CAPLUS COPYRIGHT 2003 ACS on STN
 ACCESSION NUMBER: 1985:59452 CAPLUS
 DOCUMENT NUMBER: 102:59452
 TITLE: Monoclonal **antibodies** to gliadin proteins used to examine **cereal** **grain** protein homologies
 AUTHOR(S): Skerriitt, John H.; Smith, Robyn A.; Wrigley, Colin W.; Underwood, P. Anne
 CORPORATE SOURCE: Wheat Res. Unit, CSIRO, North Ryde, 2113, Australia
 SOURCE: Journal of Cereal Science (1984), 2(4), 215-24
 CODEN: JCSCDA; ISSN: 0733-5210
 DOCUMENT TYPE: Journal
 LANGUAGE: English
 AB Monoclonal **antibodies** were prepd. to a gliadin protein ext. of bread wheat (*Triticum aestivum* cv Timgalen) and specific **antibody**-**cereal** protein interactions were detected using horseradish peroxidase-coupled second **antibodies** after transfer of proteins to nitrocellulose following electrophoresis. Whereas some **antibodies** had broad specificity for gliadin protein, other **antibodies** of narrower specificity were investigated further. The latter **antibodies** were selective for .omega.-gliadins and bound neither high-mol.-wt. glutenin subunits albumin and globulin wheat proteins, nor a wide variety of other proteins. However, certain related **cereal** species such as durum wheat, barley, and rye contained endosperm proteins recognized by these monoclonal **antibodies**. This observation confirms that sequence homologies exist between prolamins from wheat and related **cereal** species as well as between certain gliadins from hexaploid wheat.

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L16 ANSWER 1 OF 1 CAPLUS COPYRIGHT 2003 ACS on STN
 ACCESSION NUMBER: 2000:335649 CAPLUS
 DOCUMENT NUMBER: 132:333681
 TITLE: Detection of preharvest sprouting in cereal grains by immunoassay of .alpha.-amylase
 INVENTOR(S): Skerritt, John Howard
 PATENT ASSIGNEE(S): Quality Wheat CRC Limited, Australia
 SOURCE: PCT Int. Appl., 51 pp.
 CODEN: PIXXD2
 DOCUMENT TYPE: Patent
 LANGUAGE: English
 FAMILY ACC. NUM. COUNT: 1
 PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2000028319	A1	20000518	WO 1999-AU995	19991111
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RW: AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE				
CA 2345403	AA	20000518	CA 1999-2345403	19991111
EP 1137935	A1	20011004	EP 1999-957719	19991111
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, FI				
JP 2002529735	T2	20020910	JP 2000-581446	19991111
AU 757926	B2	20030313	AU 2000-15341	19991111
PRIORITY APPLN. INFO.: AU 1998-7058 A 19981111				
WO 1999-AU995 W 19991111				

AB A two-site immunoassay for the qual. or quant. detection of .alpha.-amylase in a test sample comprises: (i) exposing the test sample to a first ("capture") antibody or antibody fragment which specifically or preferentially binds to a first epitope on the .alpha.-amylase under conditions permitting binding; (ii) subsequently exposing bound .alpha.-amylase to a second ("detection") antibody or antibody fragment which specifically or preferentially binds to a second epitope on the .alpha.-amylase that is distinct from the first epitope, under conditions permitting binding of the second antibody or its fragment to the bound .alpha.-amylase; and (iii) detecting any binding of the second antibody or its fragment to the bound .alpha.-amylase, wherein either of the first or second epitopes is an epitope comprising one or more of the amino acid sequences: IDRLVSIRTRGQIHS, CRDDRPYADG, or VNWVNKVGGS and variants thereof showing .gtoreq.80% (preferably .gtoreq.90%) sequence identity. The immunoassay is useful for detecting weather damage (i.e., preharvest sprouting) in cereal grain. Thus, a rapid tube sandwich ELISA detected .alpha.-amylase in preharvest-sprouted wheat exts. at .apprx.4 ng/mL.

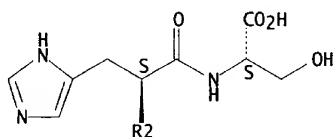
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 RL: ANT (Analyte); ANST (Analytical study)
 (detection of preharvest sprouting in cereal grains by immunoassay of .alpha.-amylase)

RN 268202-94-4 CAPLUS

CN L-Serine, L-isoleucyl-L-.alpha.-aspartyl-L-alanyl-L-leucyl-L-valyl-L-seryl-L-isoleucyl-L-arginyl-L-threonyl-L-arginylglycyl-L-glutamyl-L-isoleucyl-L-histidyl- (9CI) (CA INDEX NAME)

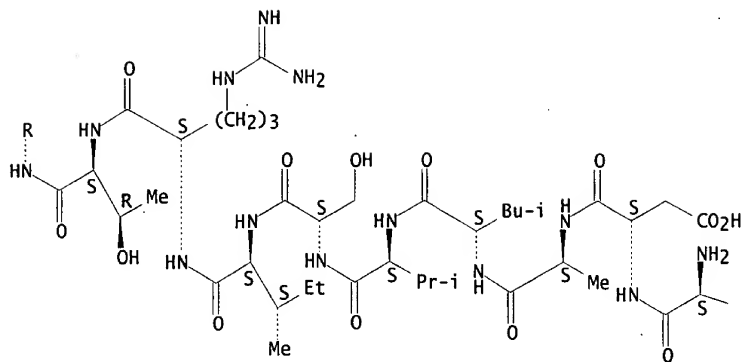
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PAGE 1-A



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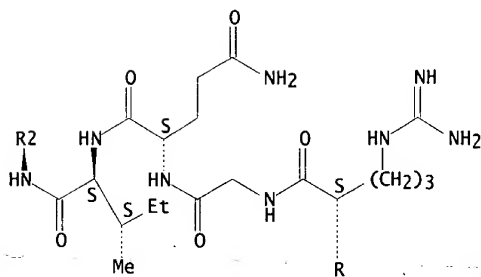
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PAGE 2-B



PAGE 3-A



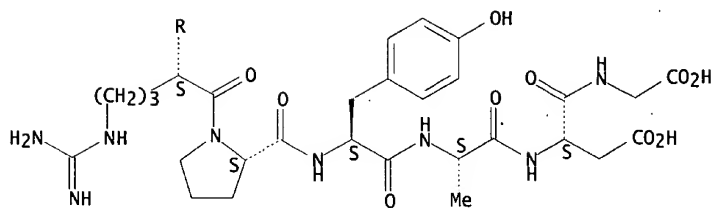
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CN Glycine, L-cysteinyl-L-arginyl-L-.alpha.-aspartyl-L-.alpha.-aspartyl-L-arginyl-L-prolyl-L-tyrosyl-L-alanyl-L-.alpha.-aspartyl- (9CI) (CA INDEX NAME)

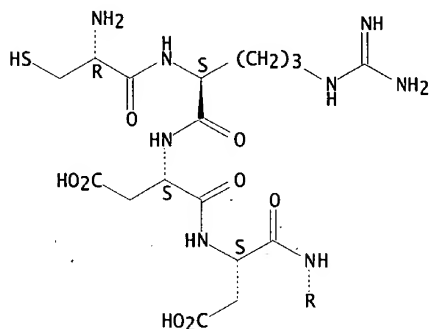
Absolute stereochemistry.

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PAGE 1-A



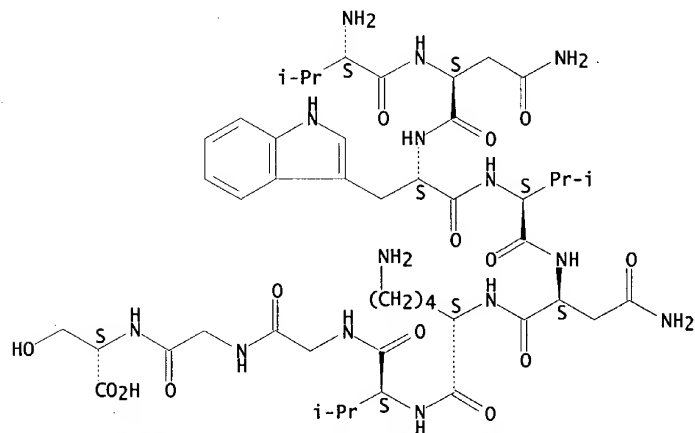
PAGE 2-A



RN 268202-96-6 CAPLUS

CN L-Serine, L-valyl-L-asparaginy1-L-tryptophyl-L-valyl-L-asparaginy1-L-lysy1-L-valylglycylglycyl- (9CI) (CA INDEX NAME)

Absolute stereochemistry.



REFERENCE COUNT:

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THERE ARE 3 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

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GenCore version 5.1.6
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OK protein - protein search, using sw model

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(Without alignments)
51.920 Million cell updates/sec

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Total number of hits satisfying chosen parameters: 1107863

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Post-processing: Minimum Match 0%
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Listing first 100 summaries

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PD 13-JUN-2000.
XX
PE 04-NOV-1993; 99JP-0356560.
XX
PR 05-NOV-1992; 92JP-0321274.
XX 04-NOV-1993; 93JP-0297607.
XX
PA (NASC-) NAT SCI COUNCIL.
XX
DR WPI: 2000-468171/41.
XX N-PSDB; AAA72947.
XX
PT A gene expression system containing the promoter region of
PT alpha-amylase gene, useful for mass production of a desired gene
PT product in a plant host cell
XX
PS Example 1; Page 27-30; 39pp; Japanese.
XX
XX The present invention describes a gene expression system containing the
CC promoter region of an alpha-amylase gene. Also described is a method for
CC preparing a transgenic rice plant comprising: (1) infecting Agrobacterium
CC into an untransformed embryo of a rice plant; (2) simultaneously culturing
CC the embryo with a suspended culture of a dicotyledon during the
CC transforming step; (3) growing the transformed embryo to a callus in a
CC selective medium containing a plant growth hormone; and (4) regenerating
CC the callus to roots and sprouts in a regeneration medium. The method can
CC be used for mass production of a desired gene product in a plant host
CC cell. The present sequence represents the rice alpha-Amy7-C protein,
CC which is used in an example from the present invention.
XX
SO Sequence 428 AA;

Query Match
Best Local Similarity 71.4%; Score 45; DB 21; Length 428;
Matches 10; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 TDRVSTRTGQIH 14
DB 359 IERLVSTIRNGQIH 372

RESULT 4
AAB50251
ID AAB50251 standard; Protein; 428 AA.
XX
AC AAB50251;
XX
DT 21-JAN-2002 (first entry)
XX
DE Rice alpha-amylase (alpha-Amy7-C gene product).
XX
KM Alpha-amylase; promoter; rice; transgenic plant; angiosperm;
XX monocot; cereal; brewing.
XX
OS Oryza sativa.
XX
FH Key Location/Qualifiers

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FT Peptide 1-25
FT /label= Signal_peptide
FM Protein 26-428
FM /label= Mature_protein
XX
XX US6288302-B1.
XX
PD 11-SEP-2001.
XX
PE 04-MAY-1998; 98US-0072917.
XX
XX 04-NOV-1992; 92US-0973324.
XX 01-AUG-1995; 95US-0509962.
XX 08-OCT-1997; 97US-0947201.
XX 22-NOV-1994; 94US-0343380.
XX
XX (NASC-) NAT SCI COUNCIL ROC.
XX
XX Yu S, Liu L, Chan M;
XX
XX WPI: 2001-647191/74.
XX N-PSDB; AA170537.
XX
XX Producing a transgenic monocot plant comprising a transgene under
PT control of an alpha amylase promoter and signal peptide sequences,
PT provides transgenic plants particularly cereals for the brewing
PT industry
XX
XX Example 1; Column 61-64; 44pp; English.
XX
XX The present sequence is that of rice (Oryza sativa) cv. M202
CC alpha-amylase, encoded by isolated genomic DNA clone alpha-Amy7-C
CC (see AA170537). Expression of alpha-Amy7-C in cultured suspension
CC cells of rice was induced 6-fold at day 12 after sugar depletion,
CC and continued to increase up to day 14. The invention relates to
CC the use of an alpha-amylase gene promoter and signal sequence in
CC the production of recombinant proteins in transgenic plants and
CC transgenic plant seeds. In a claimed method, a transgenic monocot
CC is obtained by: transforming an immature embryo of the plant via
CC Agrobacterium-mediated transformation with DNA comprising a plant
CC alpha-amylase promoter (e.g. the rice alpha-Amy7-C promoter) that
CC is induced under sugar-depleted or sugar-free conditions, a signal
CC peptide sequence, and an exogenous sequence encoding a gene product;
CC regenerating the transformed plant; and growing the transgenic
CC plant, which expresses the gene product under sugar-depleted or
CC sugar-free conditions. The gene product may also be obtained by
CC cultivating an angiosperm host cell. The transgenic monocot plants
CC are especially useful in brewing and to produce glucose from starch.
XX
SO Sequence 428 AA;

Query Match
Best Local Similarity 71.4%; Score 45; DB 22; Length 428;
Matches 10; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 TDRVSTRTGQIH 14
DB 359 IERLVSTIRNGQIH 372

RESULT 5
AAB97245
ID AAB97245 standard; Protein; 428 AA.
XX
AC AAB97245;
XX
DT 31-JUL-2001 (first entry)
XX
DE Alpha-amylase related protein #1.
XX
KM Alpha-amylase; promoter; expression vector; rice.
XX
XX Unidentified.
XX
OS

```

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XX XX TW402638-A.
PN XX
XX XX 21-AUG-2000.
PD XX
XX XX 13-FEB-1992; 97TW-0101436.
PE XX
XX XX 13-FEB-1992; 97TW-0101436.
PR XX
XX XX (NASC-) NAT SCI COUNCIL.
PA XX
XX XX Yu S, Liou L;
PI XX
XX XX WPI; 2001-167365/17.
DR XX
XX N-PSDB; AAH20283.
PT Gene expression system comprising the promoter region of alpha-amylase
PT gene, produces large quantities of alpha-amylase in culture medium of
PT sugar starved rice -
XX
XX PS Disclosure; Fig 8; 104pp; Chinese.
XX
XX CC This invention relates to a gene expression system comprising the
XX alpha-amylase gene promoter. DNA encoding the signal peptide of
XX alpha-amylase and the promoter along with the glucuronidase reporter gene
XX and hygromycin resistance gene are used in the construction of a GUS gene
XX expression vector, which when transformed into rice suspension-cultured
XX cells, can be used to investigate the expression of the vector under the
XX control of the promoter. The gene expression system can be used to
XX conduct gene regulation and protein expression and secretion using the
XX characteristics of the alpha-amylase gene promoter and the DNA sequence
XX encoding the signal peptide. The present sequence represents an
XX alpha-amylase related protein used in the course of the present
XX invention.
XX
XX SO Sequence 428 AA;

Query Match 61.6%; Score 45; DB 22; Length 428;
Best Local Similarity 71.4%; Pred. NO. 5;
Matches 10; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 1 IDRLVSTRRGQIH 14
   |:||||| | | |
Db 359 IERLVSTRRGQIH 372

RESULT 6
AAR76520
ID AAR76520 standard; Protein: 429 AA.
XX
XX AC AAR76520;
XX
XX DT 14-FEB-1996 (first entry) -
XX
XX DE Alpha-amylase-7-C.
XX
XX KW Alpha-Amy-6-C; amylase; promoter; vector; heterologous;
KW gene expression system.
XX
XX OS Oryza sativa.
XX
XX PH Key Location/Qualifiers
FT Misc-difference 35
FT /note= "corresp. to GAC codon"
FT Misc-difference 83
FT /note= "corresp. to CAG codon"
FT Misc-difference 158
FT /note= "corresp. to GAC codon"
FT Misc-difference 218
FT /note= "corresp. to TAC codon"
FT Misc-difference 224
FT /note= "corresp. to CGG codon"
FT Misc-difference 233

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FT FT /note= "corresp. to CGT codon"
FT FT Misc-difference 294 /note= "corresp. to CAG codon"
XX XX
XX XX JP07143895-A.
XX XX
XX XX 06-JUN-1995.
PD XX
XX XX 04-NOV-1993; 93JP-0297607.
PE XX
XX XX 05-NOV-1992; 92JP-0321274.
PR XX
XX XX (NASC-) NAT SCI COUNCIL.
PA XX
XX XX WPI; 1995-236472/31.
DR XX
XX N-PSDB; AAQ92806.
XX
XX PT Gene expression system config. alpha-amylase gene promoter - for use
XX in plants for expression of heterologous genes
XX
XX PS Claim 3; Page 27-30; 42pp; Japanese.
XX
XX CC AAR76519-R76521 represent the amylase gene products alpha-amylase-6-C,
XX alpha-amylase-7-C and alpha-amylase-8-C respectively. The promoter
XX regions of these amylase genes are used in a new gene expression system.
XX The system may be used for the expression of heterologous genes in plant
XX cells and for the large scale production of the encoded products of such
XX genes.
XX CC NI. some amino acids in this sequence appear to have been wrongly
XX entered, see feature table and the corresp. DNA file AAQ92806.
XX
XX SO Sequence 429 AA;

Query Match 61.6%; Score 45; DB 16; Length 429;
Best Local Similarity 71.4%; Pred. NO. 5.1;
Matches 10; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 1 IDRLVSTRRGQIH 14
   |:||||| | | |
Db 360 IERLVSTRRGQIH 373

RESULT 7
AAR55130
ID AAR55130 standard; Protein: 433 AA.
XX
XX AC AAR55130;
XX
XX DT 25-MAR-2003 (updated)
XX DT 12-JAN-1995 (first entry)
XX
XX DE Rice alpha-amylase coding.
XX
XX KW Virus; recombination; plant virus; alpha trichosanthin; phenotype;
KW alpha amylase; alpha haemoglobin; bromo mosaic virus; gemini virus;
KW rice necrosis virus tobamovirus; gene expression; chinese cucumber.
XX
XX OS Oryza sativa.
XX
XX PN US5316931-A.
XX
XX PD 31-MAY-1994.
XX
XX PF 31-JUL-1992; 92US-0923692.
XX
XX PR 26-FEB-1988; 88US-0160766.
XX PR 26-FEB-1988; 88US-0160771.
XX PR 15-JUL-1988; 88US-0219279.
XX PR 17-FEB-1989; 89US-0310861.
XX PR 05-MAY-1989; 89US-0347637.
XX PR 08-JUN-1989; 89US-0363138.
XX PR 22-OCT-1990; 90US-0600244.
XX PR 16-JAN-1991; 91US-0641617.

```

PR 26-JUL-1991; 91US-0737899.
 XX 01-AUG-1991; 91US-0739143.
 PA (BIOS-) BIOSOURCE GENETICS CORP.
 XX
 PI Dawson MO, Donson J, Garger SJ, Grantham GL, Grill LK;
 PI Turpen AM, Turpen TH;
 XX
 DR WPI: 1994-176269/21.
 DR N-PSDB; AAQ65574.
 XX
 PT New recombinant plant viral nucleic acid - capable of systemic
 PT infection and stable expression of non-native nucleic acid in
 PT plant host
 XX
 PS Example 4; Columns 53-56; 44pp; English.
 CC The rice alpha-amylase gene may be inserted into a recombinant plant
 CC virus which can then be used to infect plants for the production of
 CC non-native products (i.e. this case alpha amylase). Other genes which
 CC may be inserted into the virus are those which control a phenotypic
 CC trait, such as male sterility, or sequences encoding anti-sense RNA
 CC which can be useful to prevent the expression of undesired phenotypic
 CC traits. The recombinant virus is derived from a plus sense, single
 CC stranded virus selected from tobamovirus, Drome mosaic virus, rice
 CC necrosis virus or a gemini virus.
 CC (updated on 25-MAR-2003 to correct PF field.)
 CC
 SO Sequence 433 AA:
 Query Match 61.6%; Score 45; DB 15; Length 433;
 Best Local Similarity 71.4%; Pred. No. 5.1;
 Matches 10; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 OY 1 IDRLVSTRRCQIH 14
 1:||||| 1 1
 Db 364 IERLVSTRRCQIH 377
 RESULT 8
 AAR32987
 ID AAR32987 standard; Protein: 434 AA.
 XX
 AC AAR32987;
 XX
 DT 25-MAR-2003 (updated)
 DT 17-JUN-1993 (first entry)
 XX
 DE Rice alpha-amylase.
 XX
 KM Recombinant products; commercial production; fermentation;
 KM biosynthesis; natural products; recombinant proteins;
 KM Product expression; protein expression; expressed proteins.
 XX
 OS Oryza sativa.
 XX
 PM WO9303161-A1.
 PD 18-FEB-1993.
 XX
 PP 31-JUL-1992; 92MO-US06359.
 PR 01-AUG-1991; 91US-0739143.
 XX
 PA (DAMS/) DAMSON W O.
 PA (DONS/) DONSON J.
 PA (GARG/) GARGER S J.
 PA (GRAN/) GRANTHAM G L.
 PA (GRIL/) GRILLE L K.
 PA (TURP/) TURPEN A M.
 PA (TURP/) TURPEN T H.
 PI Donson J, Dawson MO, Grantham GL, Turpen TH, Turpen AM, Garger SJ;

PI Grille LK;
 XX
 DR WPI: 1993-076518/09.
 DR N-PSDB; AAQ37680.
 XX
 PT Recombinant plant viral nucleic acids - used to express a prod.,
 PT e.g. antibody or IL-1 in a plant
 XX
 PS Example 4; Page 96; 30pp; English.
 CC This sequence is rice alpha amylase. The coding sequence was inserted
 CC into a recombinant plant viral nucleic acid which was then used to
 CC express a recombinant product (i.e. this case rice alpha-amylase) in a
 CC plant. The plant viral sequence may be from tobacco mosaic, cucumber
 CC green mottle, plant virus, Drome mosaic, broad bean mottle, rice
 CC necrosis, geminiviruses, tomato golden mosaic, Cassava latent and
 CC rice streak viruses.
 CC (updated on 25-MAR-2003 to correct PF field.)
 CC (updated on 25-MAR-2003 to correct PI field.)
 CC
 SO Sequence 434 AA:
 Query Match 61.6%; Score 45; DB 14; Length 434;
 Best Local Similarity 71.4%; Pred. No. 5.1;
 Matches 10; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 OY 1 IDRLVSTRRCQIH 14
 1:||||| 1 1
 Db 365 IERLVSTRRCQIH 378
 RESULT 9
 AAM10469
 ID AAM10469 standard; Protein: 434 AA.
 XX
 AC AAM10469;
 XX
 DT 26-APR-1997 (first entry)
 XX
 DE Rice alpha-amylase.
 XX
 KM Recombinant viral nucleic acid; RNA virus; vector;
 KM tobacco mosaic virus; TMV; rice; alpha-amylase; transgenic plant.
 XX
 OS Oryza sativa.
 XX
 PM WO9640867-A1.
 PD 19-DEC-1996.
 XX
 PP 06-JUN-1996; 96WO-US09299.
 PR 07-JUN-1995; 95US-0483502.
 XX
 PA (BIOS-) BIOSOURCE TECHNOLOGIES INC.
 XX
 PI Dawson MO, Donson J, Garger SJ, Grantham GL, Grill LK;
 PI Turpen AM, Turpen TH;
 XX
 DR WPI: 1997-065181/06.
 DR N-PSDB; AAT47095.
 XX
 PT Recombinant viral nucleic acid producing, e.g. male sterility in
 PT plants - comprises nucleic acid whose transcription is controlled by
 PT another sequence
 XX
 PS Example 4; Page 127-129; 149pp; English.
 CC A DNA sequence (AAT47095) codes for rice alpha-amylase (AAM10469).
 CC Novel viral nucleic acids can be constructed in which the alpha-
 CC amylase coding sequence is placed under control of the promoter
 CC of the tobacco mosaic virus coat protein gene, which has been
 CC deleted. The recombinant viral nucleic acid is capable of self-

CC replication, encapsidation and systemic spread in infected tobacco
CC plants, and directs expression of the alpha-amylase in plant
CC tissue.

XX Sequence 434 AA;

Query Match 61.6%; Score 45; DB 18; Length 434;
Best Local Similarity 71.4%; Pred. No. 5.1;
Matches 10; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 1 IDRLVSIRRGQIH 14
|:||||| |
Db 365 IERLVSIRNRQGIH 378

RESULT 10
AAW1871
ID AAW1871 standard; Protein: 434 AA.

XX AAW1871;

XX 25-MAR-2003 (updated)
DT 21-APR-1997 (first entry)

XX Rice alpha-amylase.

XX Recombinant virus; alpha-haemoglobin; human; chinese cucumber;
KW alpha-trichosanthin; rice; alpha amylase; beta-haemoglobin;
XX subgenomic promoter; coat protein.

OS Oryza sativa.

XX US5589367-A.

XX 31-DEC-1996.

XX 19-JAN-1994; 94US-0184237.

XX 17-FEB-1989; 89US-0310881.

XX 05-MAY-1989; 89US-0347637.

XX 08-JUN-1989; 89US-0363138.

XX 31-JUL-1992; 92US-0923692.

XX 26-FEB-1988; 88US-0160766.

XX 26-FEB-1988; 88US-0160771.

XX 15-JUL-1988; 88US-0219279.

XX 22-OCT-1990; 90US-0600244.

XX 16-JAN-1991; 91US-0641617.

XX 26-JUL-1991; 91US-0737899.

XX 01-AUG-1991; 91US-0739143.

XX (BIOS-) BIOSOURCE TECHNOLOGIES INC.

XX Dawson WO, Donson J, Garger SJ, Grantham GL, Grill LK;

XX Turpen AM, Turpen TH;

XX WPI: 1997-076845/07.

XX N-PSDB: AAT61377.

XX Recombinant viral DNA for altering plant phenotype or protein prodn

CC - contains non-native sub-genomic promoter for expression of

CC heterologous protein and native promoter for expression of coat

CC protein

CC Example 4; Column 49-52; 42pp; English.

CC involving germ cell. The recombinant viruses are stable and can
CC cause systemic infection, with stable expression/transcription in
CC plants that are hosts for the non-native part of the vector. The
CC nucleotide sequences encoding these protein preferably integrated
CC in plant viruses having either the O-coat protein or the U1-coat
CC protein gene.

CC (Updated on 25-MAR-2003 to correct PF field.)
CC (Updated on 25-MAR-2003 to correct PR field.)

XX Sequence 434 AA;

Query Match 61.6%; Score 45; DB 18; Length 434;
Best Local Similarity 71.4%; Pred. No. 5.1;
Matches 10; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 1 IDRLVSIRRGQIH 14
|:||||| |
Db 365 IERLVSIRNRQGIH 378

RESULT 11
AAV01375
ID AAV01375 standard; Protein: 434 AA.

XX AAV01375;

XX 20-MAR-2003 (updated)
DT 04-JUN-1999 (first entry)

XX O. sativa alpha-amylase.

XX Recombinant; plant virus; coat protein; systemic infection;

XX transcription; therapeutic; rice; alpha-amylase.

XX Oryza sativa.

XX US5889190-A.

XX 30-MAR-1999.

XX 07-JUN-1995; 95US-0480432.

XX 17-FEB-1989; 89US-0310881.

XX 05-MAY-1989; 89US-0347637.

XX 08-JUN-1989; 89US-0363138.

XX 31-JUL-1992; 92US-0923692.

XX 19-JAN-1994; 94US-0184237.

XX 26-FEB-1988; 88US-0160766.

XX 26-FEB-1988; 88US-0160771.

XX 15-JUL-1988; 88US-0219279.

XX 22-OCT-1990; 90US-0600244.

XX 16-JAN-1991; 91US-0641617.

XX 26-JUL-1991; 91US-0737899.

XX 01-AUG-1991; 91US-0739143.

XX (BIOS-) BIOSOURCE TECHNOLOGIES INC.

XX Dawson WO, Donson J, Garger SJ, Grantham GL, Grill LK;

XX Turpen AM, Turpen TH;

XX WPI: 1999-243290/20.

XX N-PSDB: AAX29144.

XX Recombinant plant viral nucleic acid derived from a plus sense,

CC single stranded RNA plant virus - useful for the transcription of

CC products in a host

CC Example 4; Columns 47-51; 46pp; English.

CC The invention relates to a recombinant plant viral nucleic acid derived

CC from a plus sense, single stranded RNA plant virus. The recombinant plant

CC viral nucleic acid comprises: (a) a first plant viral subgenomic promoter

CC that is native to the plus sense, single stranded RNA plant virus and

CC operably joined to a first nucleic acid expression sequence; and (b) a
 CC second plant viral subgenomic promoter that is non-native and is operably
 CC joined to a second nucleic acid expression sequence; where, (i) (a) and
 CC (b) are incapable of recombination with one another, (ii) either the
 CC first or the second nucleic acid expression sequence is a plant viral
 CC coat protein coding sequence. The recombinant plant viral nucleic acid
 CC allows the transcription of products in a host, such as therapeutic acid
 CC and ribozymes. It also gives the option of applying the coding sequence
 CC to the desired organism, tissue, organ or cell, is stable for the foreign
 CC coding sequences and is capable of systemic infection in the plant host.
 CC The transformation and regeneration of target organisms become
 CC unnecessary.
 CC (Updated on 20-MAR-2003 to correct PR field.)

SQ Sequence 434 AA;
 Query Match 61.6%; Score 45; DB 20; Length 434;
 Best Local Similarity 71.4%; Pred. No. 5.1;
 Matches 10; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 QY 1 IDRLVSIPTRGQIH 14
 DB 365 IERLVSIRNRQGIH 378

RESULT 12

AAW84383
 ID AAW84383 standard; Protein: 434 AA.

AC AAW84383;

DT 01-APR-1999 (first entry)

DE Rice alpha-amylase sequence.

KV Rice: alpha-amylase; plant virus: RNA plant virus promoter;

KW Systemic infection; foreign gene expression; AIDS therapeutic drug.

OS Oryza sativa.

PM US866785-A.

PD 02-FEB-1999.

PF 07-JUN-1995; 9505-0482920.

PR 31-JUL-1992; 9205-0923692.

PR 26-FEB-1988; 8805-0160766.

PR 26-FEB-1988; 8805-0160771.

PR 15-JUL-1988; 8805-0219279.

PR 17-FEB-1989; 8905-0310881.

PR 05-MAY-1989; 8905-0347637.

PR 08-JUN-1989; 8905-0363138.

PR 22-OCT-1990; 9005-0600244.

PR 16-JAN-1991; 9105-0641617.

PR 26-JUL-1991; 9105-0737899.

PR 01-AUG-1991; 9105-0739143.

PR 19-JAN-1994; 9405-0184237.

PR 07-JUN-1995; 9505-0482920.

(BIOS-) BIOSOURCE TECHNOLOGIES INC.

PA Dawson WO, Donson J, Garger SJ, Grantham GL, Grill LK;

PI Turpen AM, Turpen TH;

DR WPI: 1999-142035/12.

DR N-PSDB: AAW03386.

PT Recombinant plant viral vector - that is capable of systemic

PT infection in host plant and stable production of heterologous DNA

PT useful for producing therapeutic proteins for treating e.g. AIDS

PS Example 4; Columns 51-54; 45pp; English.

XX The present sequence represents rice alpha-amylase. The nucleic
 CC acid sequence can be expressed in the plant viral constructs of the
 CC invention. The specification describes a recombinant plant viral
 CC nucleic acid derived from a positive (+)-sense RNA plant virus comprising
 CC a native (+)-sense RNA plant virus promoter that is linked to an
 CC expression sequence and a heterologous (+)-sense RNA plant virus
 CC promoter that is linked to an expression sequence. The promoters are
 CC incapable of recombination with each other, and one of the expression
 CC sequences encodes a plant viral coat protein while the other is
 CC optionally a heterologous coding sequence. The plant viral nucleic acid
 CC is capable of systemic infection in a host plant. The viral construct is
 CC useful for the introduction and expression of non-viral foreign genes
 CC in plants and the production of e.g. potential AIDS therapeutic drugs.

SQ Sequence 434 AA;
 Query Match 61.6%; Score 45; DB 20; Length 434;
 Best Local Similarity 71.4%; Pred. No. 5.1;
 Matches 10; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 QY 1 IDRLVSIPTRGQIH 14
 DB 365 IERLVSIRNRQGIH 378

RESULT 13

AAV87792
 ID AAV87792 standard; Protein: 434 AA.

AC AAV87792;

DT 24-AUG-2000 (first entry)

DE Rice alpha-amylase protein.

KV Animal RNA virus: viral coat protein; plant: male sterility;

KW Interleukin; EPO; erythropoietin; CSF; colony stimulating factor;

KW Factor VIII; hGH; human growth hormone; melanin; insulin; vaccine;

KW stereo specific catalysts; alpha-amylase; rice.

OS Oryza sativa.

PM US6054566-A.

PD 25-APR-2000.

PF 07-JUN-1995; 9505-0484341.

PR 17-FEB-1989; 8905-0310881.

PR 08-JUN-1989; 8905-0363138.

PR 26-FEB-1988; 8805-0160766.

PR 15-JUL-1988; 8805-0219279.

PR 05-MAY-1989; 8905-0347637.

PR 22-OCT-1990; 9005-0600244.

PR 16-JAN-1991; 9105-0641617.

PR 26-JUL-1991; 9105-0737899.

PR 01-AUG-1991; 9105-0739143.

PR 31-JUL-1992; 9205-0923692.

(BIOS-) BIOSOURCE TECHNOLOGIES INC.

PA Garger SJ, Grill LK, Turpen TH, Grantham GL, Dawson WO, Turpen AM;

PI Donson J;

DR WPI: 2000-338510/29.

DR N-PSDB: AAV12394.

PT Recombinant non-retroviral nucleic acid for producing proteins such as

PT interleukin, melanin and vaccines, comprises subgenomic promoters

PT linked to sequences coding for viral coat protein and heterologous

PT proteins -
 PS Example 4; Column 65-68; 51pp; English.
 XX
 CC This invention describes a novel recombinant viral nucleic acid (1)
 CC from a non-retroviral (+) sense, single stranded animal RNA virus
 CC comprising a nucleic acid sequence coding for a viral coat protein
 CC regulated by a native subgenomic promoter and other two heterologous
 CC nucleic acid sequences regulated by two other subgenomic promoters.
 CC (1) is useful for expressing foreign genes e.g. genes inducing male
 CC sterility in plants. (1) is also useful for producing proteins such as
 CC interleukin, EPO (erythropoietin), CSF (colony stimulating factor),
 CC Factor VIII, hGH (human growth hormone), melanin, insulin, vaccines
 CC etc., and compounds that are useful for stereo specific catalysis of,
 CC organic compounds. (1) is stable and transcribed systemically. The dual
 CC subgenomic promoter system reduces the frequency of recombination thus
 CC reducing regeneration of the wild type virus. This sequence represents
 CC a rice alpha-amylase protein which is described in the method of the
 CC invention.
 XX
 SQ Sequence 434 AA;
 Query Match 61.6%; Score 45; DB 21; Length 434;
 Best Local Similarity 71.4%; Pred. No. 5.1;
 Matches 10; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 QY 1 IDRLVSIRTRQGIH 14
 ||:||||| | ||
 Db 365 IERLVSIRNRGCIH 378
 RESULT 14
 AAY35541
 ID AAY35541 standard; Protein; 460 AA.
 XX
 AC AAY35541;
 XX
 DT 13-SEP-1999 (first entry)
 XX
 DE C. pneumoniae protein involved in intermediate metabolism.
 XX
 KW Respiratory disease; pneumonia; bronchitis; heart disease; sarcoidosis;
 KW sinusitis; purulent otitis media; erythema nodosum; pharyngitis;
 KW vaccine; neutralising epitope.
 XX
 OS Chlamydia pneumoniae.
 XX
 PN WO9927105-A2.
 XX
 PD 03-JUN-1999.
 XX
 PF 20-NOV-1998; 98WO-IB01890.
 XX
 PR 04-NOV-1998; 98US-0107078.
 PR 21-NOV-1997; 97FR-0014673.
 XX
 PA (GEST) GENSET.
 XX
 PI Griffiths R;
 XX
 DR WPI: 1999-357842/30.
 XX
 PT Genome sequence of Chlamydia pneumoniae
 PS Page 1288-1289; Disclosure; 1912pp; English.
 XX
 CC AA34584-Y35879 represent the proteins encoded by all the open reading
 CC frames in the complete genome (see AA34584-Y35879) of Chlamydia pneumoniae.
 CC C. pneumoniae causes respiratory disease such as pneumonia and
 CC bronchitis and is thought to be a contributing factor in heart
 CC disease, sarcoidosis, sinusitis, purulent otitis media, erythema
 CC nodosum or pharyngitis. The polypeptides encoded by the open reading
 CC frames of the C. pneumoniae genome (see AA34584-Y35879) can be used in

CC immunogenic compositions as vaccines. Vectors containing C. pneumoniae
 CC nucleotide sequences can also be used as immunogenic compositions,
 CC especially where the vector directs the expression of a neutralising
 CC epitope of C. pneumoniae.
 XX
 SQ Sequence 460 AA;
 Query Match 60.3%; Score 44; DB 20; Length 460;
 Best Local Similarity 57.1%; Pred. No. 8.5;
 Matches 8; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
 QY 2 DRLVSIRTRQGIHS 15
 |||:|:| | |||:
 Db 407 DRLSMETGELIHN 420
 RESULT 15
 AAU31870
 ID AAU31870 standard; Protein; 386 AA.
 XX
 AC AAU31870;
 XX
 DT 18-DEC-2001 (first entry)
 XX
 DE Novel human secreted protein #2361.
 XX
 KW Human; vaccination; gene therapy; nutritional supplement;
 KW stem cell proliferation; haematopoiesis; nerve tissue regeneration;
 KW immune suppression; immune stimulation; anti-inflammatory; leukaemia.
 XX
 OS Homo sapiens.
 XX
 PN WO200179449-A2.
 XX
 PD 25-OCT-2001.
 XX
 PF 16-APR-2001; 2001WO-US08656.
 XX
 PR 18-APR-2000; 2000US-0552929.
 PR 26-JAN-2001; 2001US-0770160.
 XX
 PA (HYSE-) HYSEQ INC.
 XX
 PI Tang YT, Liu C, Dymnac RT;
 XX
 DR WPI: 2001-611725/70.
 XX
 PT Nucleic acids encoding a range of human polypeptides, useful in genetic
 PT vaccination, testing and therapy -
 XX
 PS Claim 20; Page 521; 765pp; English.
 XX
 CC The invention relates to novel human secreted polypeptides. The
 CC polypeptides and antibodies to the polypeptides are useful for
 CC determining the presence of or predisposition to a disease associated
 CC with altered levels of polypeptide. The polypeptides are also useful for
 CC identifying agents (agonists and antagonists) that bind to them. Cells
 CC expressing the proteins are useful for identifying a therapeutic agent
 CC for use in treatment of a pathology related to aberrant expression or
 CC physiological interactions of the polypeptide. Vectors comprising
 CC the nucleic acids encoding the polypeptides and cells genetically
 CC engineered to express them are also useful for producing the proteins.
 CC The proteins are useful in genetic vaccination, testing and
 CC therapy, and can be used as nutritional supplements. They may be used to
 CC increase stem cell proliferation; to regulate haematopoiesis; and in
 CC bone, cartilage, tendon and/or nerve tissue growth or regeneration;
 CC immune suppression and/or stimulation; as anti-inflammatory agents; and
 CC in treatment of leukaemia. AAU29510-AAU33304 represent the amino acid
 CC sequences of novel human secreted proteins of the invention.
 XX
 SQ Sequence 386 AA;
 Query Match 58.9%; Score 43; DB 22; Length 386;

Best Local Similarity 46.7%; Pred. No. 11;
Matches 7; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

OY 1 DRLVSIRTRGQIHS 15
:111:111:11
DB 163 MDRLQLRSRNETHS 177

RESULT 16

AAAB10652
ID AAB10652 standard; Protein: 167 AA.

AAAB10652;
AC

DT 19-JAN-2001 (first entry)

DE Human VEGF-X protein derived from clone 41.

XX VEGF-X; vascular endothelial growth factor; human; vulnary; cytostatic;
KW antihemetic; antiarthritic; antipsoriatic; antidiabetic; treatment;
KW angiogenesis regulator; vascularization regulator; cancer; psoriasis;
KW rheumatoid arthritis; diabetic retinopathy; blood vessel; organ repair;
KW tissue regeneration; tissue repair; wound; dermal ulcer; pressure sore;
KW venous sore; diabetic ulcer; burns; skin graft growth.

OS Homo sapiens.

PN W0200037641-A2.

PD 29-JUN-2000.

PF 21-DEC-1999; 99MO-US30503.

PR 22-DEC-1998; 98GB-0028377.

PR 18-MAR-1999; 990S-0124967.

PR 08-NOV-1999; 990S-0164131.

PA (JANSEN PHARM NV.

PI Gordon RD, Sprengel JJ, Yon JR, Dijkmans JH, Gosiowska A;

PI Dhanaraj SN, Xu J;

DR WPI: 2000-442669/38.

XX New vascular endothelial growth factor protein, useful for treating or

XX preventing diseases associated with inappropriate angiogenesis activity

XX such as cancer, rheumatoid arthritis, psoriasis and wounds -

XX Disclosure: Fig 12; 127pp; English.

XX This invention describes a novel vascular endothelial growth factor-X
CC (VEGF-X) protein (Ia) and its encoding polynucleotide (IIa) which has
CC vulnary, cytostatic, antihemetic, antiarthritic, antipsoriatic and
CC antidiabetic activity and acts as an angiogenesis and vascularization
CC regulator. An antisense molecule of the invention is useful for treating
CC or preventing cancer, rheumatoid arthritis, psoriasis and diabetic
CC retinopathy by inhibiting angiogenic activity or inappropriate
CC vascularization including formation and proliferation of new blood
CC vessels, growth and development of tissues, tissue regeneration and organ
CC for preparing medicaments for treating wounds such as dermal ulcers,
CC skin graft growth, venous sores, diabetic ulcers and burns and to promote
CC tissue regeneration and organ repair by promoting angiogenic activity or
CC vascularization. This sequence represents the human VEGF-X protein
CC derived from clone 41 which is described in the method of the invention.

XX Sequence 167 AA;

Query Match 57.5%; Score 42; DB 21; Length 167;

Best Local Similarity 42.9%; Pred. No. 6.4; Mismatches 3; Indels 0; Gaps 0;

Matches 6; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

OY 2 DRLVSIRTRGQIHS 15
:111:111:111
DB 47 ERITVSTNGSIHS 60

RESULT 17

AAAB10643
ID AAB10643 standard; Protein: 168 AA.

AAAB10643;
AC

DT 19-JAN-2001 (first entry)

DE Human VEGF-X CUB-like domain protein.

XX VEGF-X; vascular endothelial growth factor; human; vulnary; cytostatic;
KW antihemetic; antiarthritic; antipsoriatic; antidiabetic; treatment;
KW angiogenesis regulator; vascularization regulator; cancer; psoriasis;
KW rheumatoid arthritis; diabetic retinopathy; blood vessel; organ repair;
KW tissue regeneration; tissue repair; wound; dermal ulcer; pressure sore;
KW venous sore; diabetic ulcer; burns; skin graft growth.

OS Homo sapiens.

PN W0200037641-A2.

PD 29-JUN-2000.

PF 21-DEC-1999; 99MO-US30503.

PR 22-DEC-1998; 98GB-0028377.

PR 18-MAR-1999; 990S-0124967.

PR 08-NOV-1999; 990S-0164131.

PA (JANSEN PHARM NV.

PI Gordon RD, Sprengel JJ, Yon JR, Dijkmans JH, Gosiowska A;

PI Dhanaraj SN, Xu J;

DR N-PSDB: AAA71987.

XX New vascular endothelial growth factor protein, useful for treating or

XX preventing diseases associated with inappropriate angiogenesis activity

XX such as cancer, rheumatoid arthritis, psoriasis and wounds -

XX Disclosure: Fig 26; 127pp; English.

XX This invention describes a novel vascular endothelial growth factor-X
CC (VEGF-X) protein (Ia) and its encoding polynucleotide (IIa) which has
CC vulnary, cytostatic, antihemetic, antiarthritic, antipsoriatic and
CC antidiabetic activity and acts as an angiogenesis and vascularization
CC regulator. An antisense molecule of the invention is useful for treating
CC or preventing cancer, rheumatoid arthritis, psoriasis and diabetic
CC retinopathy by inhibiting angiogenic activity or inappropriate
CC vascularization including formation and proliferation of new blood
CC vessels, growth and development of tissues, tissue regeneration and organ
CC for preparing medicaments for treating wounds such as dermal ulcers,
CC skin graft growth, venous sores, diabetic ulcers and burns and to promote
CC tissue regeneration and organ repair by promoting angiogenic activity or
CC vascularization. This sequence represents a human VEGF-X protein
CC described in the method of the invention.

XX Sequence 168 AA;

Query Match 57.5%; Score 42; DB 21; Length 168;

Best Local Similarity 42.9%; Pred. No. 6.4; Mismatches 3; Indels 0; Gaps 0;

Matches 6; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

OY 2 DRLVSIRTRGQIHS 15

Db :|:|:| | | | |
44 ERITVSTNGSIHS 57

RESULT 18

AA10653
ID AAB10653 standard; Protein; 282 AA.

AC AAB10653;

DT 19-JAN-2001 (first entry)

DE Human VEGF-X protein derived from clone 20.

XX VEGF-X; vascular endothelial growth factor; human; vulnerrary; cytosatic;
XX antirhematic; antiarthritic; antipsoriatic; antidiabetic; treatment;
XX angiogenesis regulator; vascularization regulator; cancer; psoriasis;
XX rheumatoid arthritis; diabetic retinopathy; blood vessel; organ repair;
XX tissue regeneration; tissue repair; wound; dermal ulcer; pressure sore;
XX venous sore; diabetic ulcer; burns; skin graft growth.

XX Homo sapiens.

OS WO200037641-A2.

PN 29-JUN-2000.

PD 21-DEC-1999; 99WO-US30503.

PF 22-DEC-1998; 98GB-0028377.

PR 18-MAR-1999; 99US-0124967.

PR 08-NOV-1999; 99US-0164131.

XX (JANC) JANSSEN PHARM NV.

XX Gordon RD, Sprengel JU, Yon JR, Dijkmans JTH, Gosiewska A;

PI Dhanaraj SN, Xu J;

DR WPI; 2000-442669/38.

XX New vascular endothelial growth factor protein, useful for treating or

PT preventing diseases associated with inappropriate angiogenesis actively

PT such as cancer, rheumatoid arthritis, psoriasis and wounds -

XX Disclosure; Fig 12; 127pp; English.

XX This invention describes a novel vascular endothelial growth factor-X

CC (VEGF-X) protein (Ia) and its encoding polynucleotide (IIa) which has

CC vulnerary, cytosatic, antirhematic, antiarthritic, antipsoriatic and

CC antidiabetic activity and acts as an angiogenesis and vascularization

CC regulator. An antisense molecule of the invention is useful for treating

CC or preventing cancer, rheumatoid arthritis, psoriasis and diabetic

CC retinopathy by inhibiting angiogenic activity or inappropriate

CC vascularization including formation and proliferation of new blood

CC vessels, growth and development of tissues, tissue regeneration and organ

CC and tissue repair in a subject. The products of the invention are useful

CC for preparing medicaments for treating wounds such as dermal ulcers,

CC pressure sores, venous sores, diabetic ulcers and burns and to promote

CC skin graft growth, tissue repair, proliferation of new blood vessels,

CC tissue regeneration and organ repair by promoting angiogenic activity or

CC vascularization. This sequence represents the human VEGF-X protein

CC derived from clone 20 which is described in the method of the invention.

XX Sequence 282 AA;

XX Query Match 57.5%; Score 42; DB 21; Length 282;

XX Best Local Similarity 42.9%; Pred. No. 12;

XX Matches 6; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

XX 2 DRVLSIRTRGOIHS 15

XX :|:|:| | | | |

XX 47 ERITVSTNGSIHS 60

RESULT 19

AA59286
ID AAY59286 standard; Protein; 297 AA.

AC AAY59286;

DT 25-APR-2000 (first entry)

DE Bone morphogenic protein (BMP) (clone HSYAE36).

XX Bone morphogenic protein; BMP; cytosatic; osteopathic; angiogenic;

XX vulnerary; bone disorder; osteoarthritis; cartilage defect; human;

XX tissue repair; gene therapy.

XX Homo sapiens.

OS Key Location/Qualifiers

FT Peptide 1..22 "signal peptide"

FT Peptide 15..23 "immunogenic epitope"

FT Protein 23..297 "mature protein"

FT Peptide 34..39 "immunogenic epitope"

FT Peptide 51..57 "immunogenic epitope"

FT Peptide 60..66 "immunogenic epitope"

FT Peptide 153..158 "immunogenic epitope"

FT Peptide 234..240 "immunogenic epitope"

FT Peptide 269..274 "immunogenic epitope"

FT Peptide 281..290 "immunogenic epitope"

FT Peptide "immunogenic epitope"

PN WO200004183-A1.

XX 27-JAN-2000.

PD 14-JUL-1999; 99WO-US15783.

PF 15-JUL-1998; 98US-0092922.

PR (HUMA-) HUMAN GENOME SCI INC.

XX Ruben SM, Young PE;

XX WPI; 2000-182442/16.

DR N-PSDB; AA248600.

XX Novel cDNA encoding human bone morphogenic proteins, vectors, host

PT cells and methods of recombinant production, useful for diagnosis and

PT treatment of, e.g. bone disorders -

XX Claim 11; Page 184-185; 187pp; English.

XX The invention provides novel human bone morphogenic proteins (BMP) and

CC nucleic acids encoding the BMPs. The BMP polypeptides can be expressed

CC by standard recombinant methodology. Determining the presence or absence

CC of a mutation in the polynucleotides or determining the presence or

CC amount of expression of the polypeptides is useful for diagnosing a

CC pathological condition or a susceptibility to a pathological condition

CC in a subject. The polynucleotides can also be used to prevent, treat or

CC ameliorate a medical condition. The proteins are useful for diagnosis

CC and/or treatment of diseases associated with BMPs, in particular bone

CC disorders (e.g. osteoarthritis, cartilage defects and tissue repair),

CC and in particular for stimulation of angiogenesis. The polynucleotides

CC are useful as reagents for differential identification of tissues or cell

CC types present in biological samples. The polynucleotides can be used in

CC gene therapy to promote the growth of endothelial cells. The present
 CC sequence represents a BMP of the invention (clone H51A36).
 XX
 SQ Sequence 297 AA: 57.5%; Score 42; DB 21; Length 297;
 Query Match Best Local Similarity 42.9%; Pred. No. 12;
 Matches 6; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

OY 2 DRVLSIRTRQGIHS 15
 :|:::| | | | |
 Db 67 ERITVSTNGSIHS 80

RESULT 20
 AAU02751
 ID AAU02751 standard; Protein: 305 AA.
 XX
 AC AAU02751;
 XX
 DT 29-AUG-2001 (first entry)
 XX
 DE Novel Human Protein, NHP #3.
 XX
 KW Human: Novel Human Protein; NHP; diagnostic; drug screening; cancer;
 KW clinical trial monitoring; physiological disorder; behavioural disorder;
 KW infectious disease; gene therapy.
 XX
 OS Homo sapiens.
 XX
 PN MO200129084-A2.
 XX
 PD 26-APR-2001.
 XX
 PE 18-OCT-2000; 2000MO-US28803.
 XX
 PR 18-OCT-1999; 99US-0160106.
 BR 29-OCT-1999; 99US-0162547.
 XX
 PA (LEXI-) LEXICON GENETICS INC.
 XX
 PI Turner CA, Donoho G, Nehls M, Hilbun E, Zambrowicz B, Sands AT;
 DR N-PSDB: AAS03539.
 XX
 DR N-PSDB: AAS03539.
 XX
 PT Nucleic acids encoding novel human proteins (NHP), useful for treating
 PT physiological or behavioural disorders, cancers and infectious diseases
 PT
 PS
 PS Claim 6; Page 62; 63pp; English.

CC The sequence represents the amino acid sequence of novel human protein,
 CC NHP #3, isolated from a human adrenal gland cDNA library. NHP nucleotides
 CC are useful for drug screening and clinical trial monitoring, and for the
 CC diagnosis and treatment of physiological or behavioural disorders, cancer
 CC and infectious disease. Nucleotide constructs encoding functional NHPs,
 CC mutant NHPs, as well as antisense and ribozyme molecules can also be used
 CC in gene therapy for the modulation of NHP expression. NHP polypeptides
 CC may be used to produce agonists, antagonists and antibodies for the
 CC regulation of NHP expression in the treatment and/or diagnosis of
 CC disease.
 CC
 XX
 XX Sequence 305 AA:
 Query Match 57.5%; Score 42; DB 22; Length 305;
 Best Local Similarity 42.9%; Pred. No. 13;
 Matches 6; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

OY 2 DRVLSIRTRQGIHS 15
 :|:::| | | | |
 Db 47 ERITVSTNGSIHS 60

RESULT 21
 AAY84558
 ID AAY84558 standard; Protein: 318 AA.
 XX
 AC AAY84558;
 XX
 DT 25-JUL-2000 (first entry)
 XX
 DE A fragment of platelet-derived growth factor C (PDGF-C).
 XX
 DE Platelet-derived growth factor C; PDGF-C; cell proliferation;
 KW growth factor; heparin; connective tissue; wound healing; VEGF-F;
 KW fibroblast mitogenesis; PDGF alpha receptor activation; tumour growth;
 KW choriocarcinoma; Wilms tumour; megakaryoblastic leukaemia;
 KW lung carcinoma; erythroleukemia; tissue remodelling.
 XX
 OS Homo sapiens.
 XX
 XX Key Location/Qualifiers
 FT Misc-difference 287 /note="encoded by AAS"
 FT
 XX
 PN MO20018212-A2.
 XX
 PD 06-APR-2000.
 XX
 PE 30-SEP-1999; 99MO-US22668.
 XX
 PR 30-SEP-1998; 98US-0102461.
 PR 12-NOV-1998; 98US-0108109.
 PR 03-DEC-1998; 98US-0110749.
 PR 18-DEC-1998; 98US-0113002.
 PR 21-MAY-1999; 98US-0135436.
 PR 15-JUL-1999; 99US-0144022.
 XX
 PA (LUDM-) LUDMIG INST CANCER RES.
 PA (UTHE-) UNIV HELSINKI LICENSING LTD.
 XX
 PI Eriksson A, Aase K, Lee X, Ponten A, Uuteala M, Alltalo K;
 PI Oestman U, Heidn C, Betsholz G;
 DR WPI: 2000-292954/25.
 DR N-PSDB: AAA12524.
 XX
 PT Novel DNA encoding PDGF-C useful to stimulate or enhance proliferation,
 PT differentiation, growth and motility of cells expressing the PDGF-C
 PT receptor -
 XX
 PS Disclosure; Fig 4; 135pp; English.

CC The present sequence represents a human platelet-derived growth factor C
 CC (PDGF-C) (formally designated VEGF-F) fragment. PDGF-C polypeptides have
 CC the ability to stimulate and enhance proliferation or differentiation,
 CC and/or growth or motility of cells expressing a PDGF-C receptor.
 CC PDGF-C polypeptides can be used in pharmaceuticals for promoting cell
 CC proliferation, preferably in combination with one other growth factor
 CC and heparin. Pharmaceuticals comprising PDGF-C polypeptides can also
 CC be used for stimulating connective tissue or wound healing. The
 CC PDGF-C polypeptide can be enzymatically processed to generate the active
 CC truncated form of PDGF-C. PDGF-C can also be used to regulate the receptor-binding
 CC specificity of PDGF-C. PDGF-C can also be used to promote fibroblast
 CC mitogenesis in a mammal and to induce PDGF alpha receptor activation.
 CC PDGF-C antagonists can be used to inhibit tumour growth of a tumour
 CC expressing PDGF-C in a mammal. Specific types of human tumours, e.g.
 CC choriocarcinoma, Wilms tumour, megakaryoblastic leukaemia, lung carcinoma
 CC and erythroleukemia, can be identified by testing for expression of
 CC PDGF-C. PDGF-C antagonists can also be used to inhibit tissue
 CC remodelling during invasion of tumour cells into a normal population of
 CC cells. Antagonists can also be used to treat fibrotic conditions,
 CC especially found in the lung, kidney or liver.
 CC
 XX
 XX Sequence 318 AA:

Query Match 57.5%; Score 42; DB 21; Length 318;
 Best Local Similarity 42.9%; Pred. No. 13;
 Matches 6; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 2 DRVLSIRTRGOIHS 15
 :|:::| | | | |
 Db 20 ERITVSTNGSIHS 33

RESULT 22

AAB58438
 ID AAB58438 standard; Protein; 339 AA.

AC AAB58438;

DT 14-MAR-2001 (first entry)

DE Lung cancer associated polypeptide sequence SEQ ID 776.

XX Human; lung cancer associated protein; neuroprotective; cytosstatic;

KW cardiactive; immunomodulatory; muscular active; vulnery;

KM gastrointestinal; nephrotropic; antiinfective; gynecological;

KM antibacterial; diagnosis; neural disorder; immune disorder; reproductive;

KM proliferative disorder; wound healing; infectious disease.

OS Homo sapiens.

PN WO20005180-A2.

PD 21-SEP-2000.

PF 08-MAR-2000; 2000WO-US05918.

PR 12-MAR-1999; 99US-0124270.

PI (HUMA-) HUMAN GENOME SCI INC.

PA (ROSE/) ROSEN C A.

PI Ruben SM;

DR WPI: 2000-587514/55.

DR N-PSDB: AAF18314.

PS Claim 11; Page 1305-1306; 1425pp; English.

XX Polynucleotide sequences AAF17982 - AAF18424 encode human lung cancer
 CC associated proteins represented in AAB58106 - AAB58548. Lung cancer
 CC associated proteins and polynucleotide sequences, their agonists, and
 CC antagonists may have neuroprotective; cytosstatic; cardiactive;
 CC immunomodulatory; muscular active general; vulnery; gastrointestinal
 CC general; nephrotropic; antiinfective; gynecological; or antibacterial
 CC activity. The invention also includes antibodies specific for the
 CC protein or polynucleotide sequences. The lung cancer associated
 CC polynucleotide sequences may be used for detection of lung cancer,
 CC chromosome identification, as chromosome markers, and for numerous other
 CC diagnostic or research purposes. The proteins may be used to treat
 CC disorders such as neural, immune, muscular, reproductive,
 CC gastrointestinal, pulmonary, cardiovascular, renal, and proliferative
 CC disorders. The proteins may also be used in the treatment of wounds and
 CC infectious diseases. Polynucleotide sequences AAF18425 - AAF18433 and
 CC peptide AAB5549 are used in the course of the invention for the
 CC identification and characterisation of the polynucleotide and protein
 CC sequences.

XX Sequence 339 AA;

Query Match 57.5%; Score 42; DB 21; Length 339;
 Best Local Similarity 42.9%; Pred. No. 14;

Matches 6; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 2 DRVLSIRTRGOIHS 15
 :|:::| | | | |
 Db 41 ERITVSTNGSIHS 54

RESULT 23

AAV33679

ID AAV33679 standard; Protein; 345 AA.

AC AAV33679;

DT 11-JAN-2000 (first entry)

DE Human VEGF-E protein.

XX VEGF-E; human; vascular endothelial cell growth factor; wound repair;

KW treatment; cardiovascular disorder; endothelial disorder; therapy;

KW tissue generation; regeneration; cardiac hypertrophy; cancer; detection;

KM angiogenic disorder; age-related macular degeneration; vascular disease;

XX neovascularization; tumor; gene mapping.

OS Homo sapiens.

PN WO947677-A2.

PD 23-SEP-1999.

PF 10-MAR-1999; 99WO-US05190.

PR 17-MAR-1998; 98US-0040220.

PR 02-NOV-1998; 98US-0184216.

PA (GETH) GENENTECH INC.

PI Ferrara N, Kuo SS;

DR WPI: 1999-560306/49.

DR N-PSDB: AA223691.

PS Claim 1; Fig 2; 122pp; English.

XX This invention describes the isolation of a novel human vascular
 CC endothelial cell growth factor-E (VEGF-E) polypeptide which has
 CC tranquilizer, vulnery and cardiant activity. VEGF-E can be administered
 CC therapeutically, especially by expressing encoding polynucleotides, to
 CC treat cardiovascular or endothelial disorders in mammals, especially
 CC humans. It is useful in wound repair and tissue generation and
 CC regeneration, and may especially be used to treat cardiac hypertrophy
 CC It can be combined with a carrier in pharmaceutical compositions, which
 CC can be administered to treat disorders as above. VEGF-E can be used to
 CC screen for antagonists and agonists, and the antagonists administered to
 CC treat angiogenic disorders in mammals (especially humans) e.g. cancer or
 CC age-related macular degeneration. It can be used to generate antibodies,
 CC useful therapeutically as antagonists, as above. The antibodies are also
 CC useful to detect VEGF-E polypeptide, especially to diagnose
 CC cardiovascular, endothelial or angiogenic disorders in mammals (e.g.
 CC vascular disease, or neovascularization associated with tumor formation),
 CC by contacting the antibody with a tissue sample and detecting formation
 CC of an antibody-VEGF-E polypeptide complex. Polynucleotides encoding
 CC VEGF-E can be used to diagnose cardiovascular and endothelial disorders
 CC in mammals, by detecting abnormally high or low VEGF-E gene expression in
 CC tissue samples. They can also be used to diagnose a disease or
 CC susceptibility to a disease related to a mutated form of VEGF-E (e.g. a
 CC cardiovascular, endothelial or angiogenic disorder such as a tumor), by
 CC detecting a mutation in the VEGF-E-encoding sequence isolated from a
 CC sample. They may also be used to produce probes useful to detect related
 CC sequences or for gene mapping. This sequence represents the human VEGF-E
 CC protein described in the method of the invention.


```

CC invention.
XX
SQ Sequence 345 AA;
Query Match 57.5%; Score 42; DB 20; Length 345;
Best Local Similarity 42.9%; Pred. No. 15;
Matches 6; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

OY 2 DRLVSIRTRQIHS 15
   :|:::| | | | |
Db 47 ERITVSTNGSIHS 60

RESULT 25
AAY30023
ID AAY30023 standard; Protein: 345 AA.
XX
AC AAY30023;
XX
DT 11-OCT-1999 (first entry)
XX
DE Human vascular endothelial growth factor related protein.
XX
KW Vascular endothelial growth factor related protein; VEGF-R protein;
KW tissue growth inhibition; tumour growth; cancer; tissue growth;
KW angiogenesis; coronary artery blockage.
XX
OS Homo sapiens.
XX
PN MO9937671-A1.
XX
PD 29-JUL-1999.
XX
PE 26-JAN-1999; 99WO-US01574.
XX
PR 31-AUG-1998; 98US-0098548.
PR 27-JAN-1998; 98US-0072635.
PR 05-JUN-1998; 98US-0088089.
PR 24-JUN-1998; 98US-0090544.
XX
PA (ELIL ) LILLY & CO ELI.
XX
PT Dou S, Na S, Song HY;
XX
DR WPI; 1999-458680/38.
DR N-PSDB; AAX86352.
XX
PT A vascular endothelial growth factor related protein and related
PT polynucleotide, useful for identifying antagonists and binding
PT compounds
XX
PS Claim 1; Page 56-58; 62pp; English.
XX
CC The present sequence represents a vascular endothelial growth factor
CC related (VEGF-R) protein. VEGF-R can be used in assays to identify
CC compounds that bind to it or that antagonize its activity. VEGF-R
CC antagonists (e.g. anti-VEGF-R antibodies) are useful for inhibiting
CC tissue growth. This is useful for inhibiting tumour growth and for
CC treating cancer. VEGF-R itself can be used to stimulate tissue
CC growth, angiogenesis and to treat coronary artery blockage. The
CC VEGF-R coding sequence can be used for the recombinant production of
CC the VEGF-R protein.
XX
SQ Sequence 345 AA;
Query Match 57.5%; Score 42; DB 20; Length 345;
Best Local Similarity 42.9%; Pred. No. 15;
Matches 6; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

OY 2 DRLVSIRTRQIHS 15
   :|:::| | | | |
Db 47 ERITVSTNGSIHS 60

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RESULT 26
AAB48657
ID AAB48657 standard; Protein: 345 AA.
XX
AC AAB48657;
XX
DT 09-MAR-2001 (first entry)
XX
DE Human zvegf3, SEQ ID NO:33.
XX
KW Human: zvegf3; zvegf4 fusion; growth factor homologue; VEGF/PDGF family;
KW CUB domain; PDGF-like activity; mitogenic; osteogenic;
KW neovascularisation; tissue repair; proliferation; differentiation;
KW liver damage; neurodegenerative; Alzheimer's disease; multiple sclerosis;
KW periodontal disease; bone fracture; wound healing; vulnerability; ischaemia;
KW immunomodulation; hepatic.
XX
OS Homo sapiens.
XX
PN WO200066736-A1.
XX
PD 09-NOV-2000.
XX
PE 03-MAY-2000; 2000WO-US40047.
XX
PR 03-MAY-1999; 99US-0304216.
PR 10-NOV-1999; 99US-0164463.
PR 04-FEB-2000; 2000US-0180169.
XX
PA (ZYMO ) ZYMOGENETICS INC.
XX
PT Gilbert T, Hart CE, Sheppard PO, Gilbertson DG;
XX
DR WPI; 2000-687541/67.
DR N-PSDB; AAC81582.
XX
PT Growth factor homologs and the nucleic acids that encode them, useful
PT e.g. for treating liver damage, ischaemia, multiple sclerosis and
PT Alzheimer's disease.
XX
PS Claim 48; Page 125-126; 143pp; English.
XX
CC The invention relates to the human growth factor homologue zvegf4
CC (AAB48653), and nucleic acids encoding it (AAC81555). Zvegf4 is a member
CC of the PDGF (platelet-derived growth factor)/VEGF (vascular endothelial
CC growth factor) family. Zvegf4 has a growth factor domain (AAB48654)
CC characterised by a PDGF cysteine knot structure, and a CUB domain
CC (AAB48655) which has a beta barrel structure. Zvegf4 has PDGF-like
CC activity, having mitogenic activity on fibroblasts, vascular smooth
CC muscle cells and pericytes, and has also been shown to stimulate bone
CC growth. The invention also relates to fusion proteins comprising human
CC zvegf4 or fragments thereof, particularly human zvegf4/human zvegf3
CC fusions; expression constructs and host cells comprising human zvegf4
CC nucleic acids; the recombinant expression of human zvegf4; an antibody
CC which binds to human zvegf4 or a fragment thereof; a method of activating
CC a cell-surface PDGF receptor using a zvegf4-derived polypeptide; a
CC method of modulating the proliferation, differentiation, migration or
CC metabolism of bone cells, comprising exposing bone cells to
CC zvegf4-derived polypeptides; and a method of detecting a genetic
CC abnormality in the zvegf4 gene of a patient. Zvegf4 proteins and derived
CC fragments may be used to stimulate tissue development or repair, or
CC cellular differentiation or proliferation. They are particularly used for
CC the treatment or repair of liver damage, and may also be used to
CC modulate neurite growth (e.g., in the treatment of Alzheimer's disease or
CC multiple sclerosis). Due to their osteogenic activity, they may also be
CC used in the treatment of periodontal disease and fractures. They may also be
CC used to enhance expansion and mobilisation of haematopoietic stem cells
CC and endothelial precursor stem cells, which may be useful in the
CC treatment of ischaemia, in wound healing, and in the modulation of the
CC immune system. The present sequence represents human zvegf3.
XX
SQ Sequence 345 AA;

```

Query Match 57.5%; Score 42; DB 21; Length 345;
 Best Local Similarity 42.9%; Pred. No. 15;
 Matches 6; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

OY 2 DRLVSTRTGQIHS 15
 :|:::| | | | |
 DB 47 ERITVSTNGSIHS 60

RESULT 27
 AAB24250
 ID AAB24250 standard; Protein; 345 AA.
 AC AAB24250;
 DT 08-FEB-2001 (first entry)
 DE Human platelet-derived growth factor related protein LP8.
 DE Human: platelet derived growth factor related protein; LP8; VEGF;
 KW vascular endothelial growth factor b; tissue regeneration; vulnery;
 KW atherosclerosis; PDGF-related protein; antiatherosclerotic.
 XX
 OS Homo sapiens.
 XX
 PM W0200059940-R2.
 XX
 PD 12-OCT-2000.
 XX
 PF 24-MAR-2000; 2000MO-US06427.
 XX
 PR 06-APR-1999; 9905-0127913.
 XX
 PA (ELIL) LILLY & CO ELI.
 XX
 PI Hammond LJ, Na S;
 DR WPI: 2000-664991/64.
 XX
 N-PSDB: AAC64426.
 XX
 PT Enhancing tissue growth and promoting wound healing by administering
 platelet-derived growth factor related protein, LP8 or its analog and
 treating atherosclerosis by administering LP8 antagonist -
 XX
 PS Claim 4; Page 63-64; 64pp; English.
 XX
 CC The present invention describes a method for enhancing tissue growth,
 CC promoting wound healing or stimulating smooth muscle growth by
 CC administering a platelet-derived growth factor (PDGF) related protein,
 CC designated LP8 or its analogue. Also described is a method of slowing
 CC the progress of atherosclerosis or treating atherosclerosis comprising
 CC the administration of an LP8 antagonist. The method is useful for
 CC enhancing tissue growth, promoting wound healing and stimulating smooth
 CC muscle growth. Antagonists of LP8 are useful for treating
 CC atherosclerosis. The present sequence represents human LP8, which is
 CC also called VEGFh.
 XX
 SO Sequence 345 AA;
 Query Match 57.5%; Score 42; DB 21; Length 345;
 Best Local Similarity 42.9%; Pred. No. 15;
 Matches 6; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

OY 2 DRLVSTRTGQIHS 15
 :|:::| | | | |
 DB 47 ERITVSTNGSIHS 60

RESULT 28
 AAB44322
 ID AAB44322 standard; Protein; 345 AA.

AC AAB44322;
 XX 08-FEB-2001 (first entry)
 DT
 DE Human PRO200 (UNQ174) protein sequence SEQ ID NO:488.
 XX
 XX Human PRO200 (UNQ174) protein sequence SEQ ID NO:488.
 DE
 KW Human; secreted protein; transmembrane protein; PRO; EST; cytosolic;
 KW expressed sequence tag; detection; cancer.
 XX
 OS Homo sapiens.
 XX
 PN W0200053756-R2.
 XX
 PD 14-SEP-2000.
 XX
 PF 18-FEB-2000; 2000MO-US04341.
 XX
 PR 08-MAR-1999; 99MO-US05028.
 PR 12-MAR-1999; 99US-0123957.
 PR 26-MAR-1999; 99US-0126773.
 PR 21-APR-1999; 99US-0130232.
 PR 26-APR-1999; 99US-0131445.
 PR 14-MAY-1999; 99US-0134287.
 PR 23-JUN-1999; 99US-0141037.
 PR 26-JUL-1999; 99US-0145898.
 PR 28-OCT-1999; 99US-0162506.
 PR 30-NOV-1999; 99MO-US28313.
 PR 02-DEC-1999; 99MO-US28351.
 PR 16-DEC-1999; 99MO-US28365.
 PR 30-DEC-1999; 99MO-US30095.
 PR 30-DEC-1999; 99MO-US31243.
 PR 05-JAN-2000; 2000MO-US00219.
 PR 06-JAN-2000; 2000MO-US00277.
 PR 06-JAN-2000; 2000MO-US00376.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Ashkenazi AJ, Baker KP, Bolstein D, Desnoyers LJ, Eaton DL;
 PI Ferrara N, Filvaroff E, Fong S, Gao W, Gerber H, Gertlsen ME;
 PI Goddard A, Godowski PJ, Grimaldi CJ, Gurney AL, Hillan KJ;
 PI Kijavlin IY, Kuo SS, Napier MA, Pan J, Paoni NF, Roy MA;
 PI Shelton DL, Stewart TA, Tumas D, Williams PM, Wood WT;
 DR WPI: 2000-611443/58.
 DR N-PSDB: AAC78582.
 XX
 PT Novel PRO polypeptides and polynucleotides used in detection methods,
 PT to target bioactive molecules to specific cells, and to modulate
 PT cellular activities -
 XX
 PS Claim 12; Fig 207; 636pp; English.
 XX
 CC AAC78458 to AAC78599 represent polynucleotide and EST (expressed
 CC sequence tag) sequences which encode secreted or transmembrane PRO
 CC polypeptides. The PRO polynucleotides and polypeptides have cytostatic
 CC activity. The polynucleotides and polypeptides can be used for detecting
 CC the presence of PRO polypeptides in samples, for linking bioactive
 CC molecules to cells and for modulating biological activities of cells,
 CC using the polypeptides for specific targeting. The polypeptide targeting
 CC can be used to kill the target cells, e.g. for the treatment of cancers.
 CC The polypeptide pairs provide specific targeting of bioactive molecules
 CC to cells. AAC78600 to AAC78987 represent PCR primers and probes used in
 CC the isolation of the PRO polynucleotide sequences.
 XX
 SO Sequence 345 AA;
 Query Match 57.5%; Score 42; DB 21; Length 345;
 Best Local Similarity 42.9%; Pred. No. 15;
 Matches 6; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

OY 2 DRLVSTRTGQIHS 15
 :|:::| | | | |

Db 47 ERITVSTNGSIHS 60

RESULT 29
AAB10633
ID AAB10633 standard; Protein; 345 AA.
XX
AC AAB10633;
XX
DT 19-JAN-2001 (first entry)
XX
DE Human VEGF-X protein.
XX
KW VEGF-X; vascular endothelial growth factor; human; vulnary; cytostatic;
KW antirheumatic; antiarthritic; antipsoriatic; antidiabetic; treatment;
KW angiogenesis regulator; vascularization regulator; cancer; psoriasis;
KW rheumatoid arthritis; diabetic retinopathy; blood vessel; organ repair;
KW tissue regeneration; tissue repair; wound; dermal ulcer; pressure sore;
KW venous sore; diabetic ulcer; burns; skin graft growth.
XX
OS Homo sapiens.
XX
PN WO200037641-A2.
XX
PD 29-JUN-2000.
XX
PF 21-DEC-1999; 99WO-US30503.
XX
PR 22-DEC-1998; 98GB-0028377.
PR 18-MAR-1999; 99US-0124967.
PR 08-NOV-1999; 99US-0164131.
XX
PA (JANC) JANSSEN PHARM NV.
PI Gordon RD, Sprengel JJ, Yon JR, Dijkmans JH, Gosiowska A;
PI Dhanaraj SN, Xu J;
XX
DR WPI: 2000-442669/38.
DR N-PSDB; AAA71951.
XX
PT New vascular endothelial growth factor protein, useful for treating or
PT preventing diseases associated with inappropriate angiogenesis activity
PT such as cancer, rheumatoid arthritis, psoriasis and wounds -
XX
PS Disclosure; Fig 6; 127pp; English.
XX
CC This invention describes a novel vascular endothelial growth factor-X
CC (VEGF-X) protein (Ia) and its encoding polynucleotide (IIa) which has
CC vulnary, cytostatic, antirheumatic, antiarthritic, antipsoriatic and
CC antidiabetic activity and acts as an angiogenesis and vascularization
CC regulator. An antisense molecule of the invention is useful for treating
CC or preventing cancer, rheumatoid arthritis, psoriasis and diabetic
CC retinopathy by inhibiting angiogenic activity or inappropriate
CC vascularization including formation and proliferation of new blood
CC vessels, growth and development of tissues, tissue regeneration and organ
CC and tissue repair in a subject. The products of the invention are useful
CC for preparing medicaments for treating wounds such as dermal ulcers,
CC pressure sores, venous sores, diabetic ulcers and burns and to promote
CC skin graft growth, tissue repair, proliferation of new blood vessels,
CC tissue regeneration and organ repair by promoting angiogenic activity or
CC vascularization. This sequence represents the RACE generated human VEGF-X
CC protein described in the method of the invention.
XX
SQ Sequence 345 AA;

Query Match 57.5%; Score 42; DB 21; Length 345;
Best Local Similarity 42.9%; Pred. No. 15;
Matches 6; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 2 DRVSVIRTRQIHS 15
:|:::| | | | |
Db 47 ERITVSTNGSIHS 60

RESULT 30
AAB10634
ID AAB10634 standard; Protein; 345 AA.
XX
AC AAB10634;
XX
DT 19-JAN-2001 (first entry)
XX
DE Human VEGF-X homologue protein.
XX
KW VEGF-X; vascular endothelial growth factor; human; vulnary; cytostatic;
KW antirheumatic; antiarthritic; antipsoriatic; antidiabetic; treatment;
KW angiogenesis regulator; vascularization regulator; cancer; psoriasis;
KW rheumatoid arthritis; diabetic retinopathy; blood vessel; organ repair;
KW tissue regeneration; tissue repair; wound; dermal ulcer; pressure sore;
KW venous sore; diabetic ulcer; burns; skin graft growth.
XX
OS Homo sapiens.
XX
PN WO200037641-A2.
XX
PD 29-JUN-2000.
XX
PF 21-DEC-1999; 99WO-US30503.
XX
PR 22-DEC-1998; 98GB-0028377.
PR 18-MAR-1999; 99US-0124967.
PR 08-NOV-1999; 99US-0164131.
XX
PA (JANC) JANSSEN PHARM NV.
PI Gordon RD, Sprengel JJ, Yon JR, Dijkmans JH, Gosiowska A;
PI Dhanaraj SN, Xu J;
XX
DR WPI: 2000-442669/38.
DR N-PSDB; AAA71952.
XX
PT New vascular endothelial growth factor protein, useful for treating or
PT preventing diseases associated with inappropriate angiogenesis activity
PT such as cancer, rheumatoid arthritis, psoriasis and wounds -
XX
PS Disclosure; Fig 7; 127pp; English.
XX
CC This invention describes a novel vascular endothelial growth factor-X
CC (VEGF-X) protein (Ia) and its encoding polynucleotide (IIa) which has
CC vulnary, cytostatic, antirheumatic, antiarthritic, antipsoriatic and
CC antidiabetic activity and acts as an angiogenesis and vascularization
CC regulator. An antisense molecule of the invention is useful for treating
CC or preventing cancer, rheumatoid arthritis, psoriasis and diabetic
CC retinopathy by inhibiting angiogenic activity or inappropriate
CC vascularization including formation and proliferation of new blood
CC vessels, growth and development of tissues, tissue regeneration and organ
CC and tissue repair in a subject. The products of the invention are useful
CC for preparing medicaments for treating wounds such as dermal ulcers,
CC pressure sores, venous sores, diabetic ulcers and burns and to promote
CC skin graft growth, tissue repair, proliferation of new blood vessels,
CC tissue regeneration and organ repair by promoting angiogenic activity or
CC vascularization. This sequence represents the human VEGF-X protein
CC homologue described in the method of the invention.
XX
SQ Sequence 345 AA;

Query Match 57.5%; Score 42; DB 21; Length 345;
Best Local Similarity 42.9%; Pred. No. 15;
Matches 6; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 2 DRVSVIRTRQIHS 15
:|:::| | | | |
Db 47 ERITVSTNGSIHS 60

Search completed: August 29, 2003, 18:43:56

Wed Sep 3 13:06:20 2003

Job time : 48.8571 secs

us-09-830-876-1_1.rag

Page 17

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 29, 2003, 18:38:06 ; Search time 15.8571 Seconds
(without alignments)
40.024 Million cell updates/sec

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Sequence: 1 IDRLVSRTRQIHS 15

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Searched: 328717 seqs, 4231058 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 08
Maximum Match 1008

Listing first 100 summaries

Database :

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Query Length	DB ID	Description
1	45	61.6	428	1	US-07-973-324A-4
2	45	61.6	428	1	US-08-343-380-4
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4	45	61.6	428	3	US-09-072-917A-4
5	45	61.6	434	1	US-07-923-692C-6
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9	45	61.6	434	3	US-08-483-502-6
10	45	61.6	434	3	US-09-726-651A-6
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18	45	57.5	345	4	US-09-564-595D-33
19	45	57.5	345	4	US-09-706-968-2
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77	34	46.6	529	1	US-08-484-105-8
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95	33	45.2	98	4	US-09-252-991A-25260
96	33	45.2	122	4	US-09-732-210-241
97	33	45.2	122	4	US-09-732-210-585
98	33	45.2	154	4	US-09-134-001C-3873
99	33	45.2	168	4	US-09-198-452A-1079
100	33	45.2	239	4	US-09-252-991A-21942

ALIGNMENTS

```
RESULT 1
US-07-973-324A-4
; Sequence 4, Application US/07973324A
; Patent No. 5460952
; GENERAL INFORMATION:
; APPLICANT: Yu, Su-May
; APPLICANT: Liu, Li-Fei
; TITLE OF INVENTION: Gene Expression System Comprising the
; TITLE OF INVENTION: Promoter Region of the Alpha-Amylase Genes
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/973,324A
; FILING DATE: 04-NOV-1992
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Borun, Michael F.
; REGISTRATION NUMBER: 25447
; REFERENCE/DOCKET NUMBER: 31149
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 428 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-07-973-324A-4
Query Match 61.6%; Score 45; DB 1; Length 428;
Best local Similarity 71.4%; Pred. No. 0.78;
Matches 10; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 IDRLVSIRTRGQIH 14
|:||||| |
Db 359 IERLVSIRNRGQIH 372

RESULT 2
US-08-343-380-4
; Sequence 4, Application US/08343380
; Patent No. 5712112
; GENERAL INFORMATION:
; APPLICANT: Yu, Su-May
; APPLICANT: Liu, Li-Fei
; TITLE OF INVENTION: Gene Expression System Comprising the
; TITLE OF INVENTION: Promoter Region of the Alpha-Amylase Genes
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
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; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/343,380
; FILING DATE: 22-NOV-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/973,324
; FILING DATE: 04-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Borun, Michael F.
; REGISTRATION NUMBER: 25447
; REFERENCE/DOCKET NUMBER: 31149
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 428 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-343-380-4
Query Match 61.6%; Score 45; DB 1; Length 428;
Best local Similarity 71.4%; Pred. No. 0.78;
Matches 10; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 IDRLVSIRTRGQIH 14
|:||||| |
Db 359 IERLVSIRNRGQIH 372

RESULT 3
US-09-072-435-4
; Sequence 4, Application US/09072435
; Patent No. 6215051
; GENERAL INFORMATION:
; APPLICANT: Yu, Su-May
; APPLICANT: Liu, Li-Fei
; TITLE OF INVENTION: GENE EXPRESSION SYSTEM COMPRISING THE
; TITLE OF INVENTION: PROMOTER REGION OF THE ALPHA-AMYLASE GENES
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 233 South Wacker Drive/6300 Sears tower
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/072,435
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/639,792
; FILING DATE: 29-APR-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/973,324
; FILING DATE: 04-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Gass, David A.
; REGISTRATION NUMBER: 38,153
```

REFERENCE/DOCKET NUMBER: 28123/34274
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 428 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-072-435-4

Query Match 61.6%; Score 45; DB 3; Length 428;
Best Local Similarity 71.4%; Pred. No. 0.78;
Matches 10; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 IDRLVSTRGQIH 14
DB 359 IERLVSTRNGQIH 372

RESULT 4

US-09-072-917A-4
Sequence 4, Application US/09072917A
Request No. 6288302
GENERAL INFORMATION:
APPLICANT: Iu, Su-May
APPLICANT: Iu, Su-May
APPLICANT: Chu, Ming-Tsair
TITLE OF INVENTION: Application of Alpha-Amylase Gene
TITLE OF INVENTION: Promoter and Signal Sequence in the Production of
Patent No. 6288302
TITLE OF INVENTION: Recombinant Proteins in Transgenic Plants and Transgenic
TITLE OF INVENTION: Plant Seeds
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Marshall, O'Toole, Gersteln, Murray & Borun
STREET: 233 South Wacker Drive/6300 Sears Tower
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/072.917A
FILING DATE:
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/509,962
FILING DATE: 01-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: Gass, David A.
REGISTRATION NUMBER: 38,153
REFERENCE/DOCKET NUMBER: 28123/34257
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 428 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-072-917A-4

Query Match 61.6%; Score 45; DB 3; Length 428;
Best Local Similarity 71.4%; Pred. No. 0.78;
Matches 10; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 IDRLVSTRGQIH 14
DB 359 IERLVSTRNGQIH 372

RESULT 5

US-07-923-692C-6
Sequence 6, Application US/07923692C
Patent No. 5316931
GENERAL INFORMATION:
APPLICANT: Donson, Jon
APPLICANT: Dawson, William O.
APPLICANT: Grantham, George L.
APPLICANT: Tulpen, Thomas H.
APPLICANT: Tulpen, Ann Myers
APPLICANT: Gargner, Stephen R.
APPLICANT: Gail, Lawrence K.
TITLE OF INVENTION: RECOMBINANT PLANT VIRAL NUCLEIC ACIDS
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Limbach & Limbach
STREET: 2001 Ferry Building
CITY: San Francisco
STATE: CAL
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/923,692C
FILING DATE: 31-JUL-1992
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 600,244
FILING DATE: 22-OCT-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 641,617
FILING DATE: 16-JAN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 310,881
FILING DATE: 17-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 160,766
FILING DATE: 26-FEB-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 160,771
FILING DATE: 26-FEB-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 347,637
FILING DATE: 05-MAY-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 363,138
FILING DATE: 08-JUN-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 219,279
FILING DATE: 15-JUL-1988
ATTORNEY/AGENT INFORMATION:
NAME: Halluin, Albert P.
REGISTRATION NUMBER: 28,957
REFERENCE/DOCKET NUMBER: BIOG-20121
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-433-8716
TELEFAX: 415-433-8716
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 434 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-923-692C-6

Query Match 61.6%; Score 45; DB 1; Length 434;
Best Local Similarity 71.4%; Pred. No. 0.79;
Matches 10; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 IDRLVSIPTRGQIH 14
1:||||| 1 11
DB 365 IERLVSIRNRGQIH 378

RESULT 6

US-08-184-237-6
Sequence 6, Application US/08184237
Patent No. 5589367
GENERAL INFORMATION:
APPLICANT: Donson, Jon
APPLICANT: Dawson, William O.
APPLICANT: Grantham, George L.
APPLICANT: Turpen, Thomas H.
APPLICANT: Turpen, Ann Myers
APPLICANT: Garger, Stephen J.
APPLICANT: Grill, Laurence K.
TITLE OF INVENTION: RECOMBINANT PLANT VIRAL NUCLEIC ACIDS
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lambach & Lambach
STREET: 2001 Ferry Building
CITY: San Francisco
STATE: CAL
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/184,237
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 923,692
FILING DATE: 31-JUL-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 600,244
FILING DATE: 22-OCT-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 641,617
FILING DATE: 16-JAN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 310,881
FILING DATE: 17-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 160,766
FILING DATE: 26-FEB-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 160,771
FILING DATE: 26-FEB-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 347,637
FILING DATE: 05-MAY-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 363,138
FILING DATE: 08-JUN-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 219,279
FILING DATE: 15-JUL-1988
ATTORNEY/AGENT INFORMATION:
NAME: Halluin, Albert P.
REGISTRATION NUMBER: 28,957
REFERENCE/DOCKET NUMBER: BIOG-20121 USA
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-433-4150
TELEFAX: 415-433-8716

INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 434 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-184-237-6

Query Match 61.6%; Score 45; DB 1; Length 434;
Best Local Similarity 71.4%; Pred. No. 0.79;
Matches 10; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 IDRLVSIPTRGQIH 14
1:||||| 1 11
DB 365 IERLVSIRNRGQIH 378

RESULT 7

US-08-482-920-6
Sequence 6, Application US/08482920
Patent No. 5866785
GENERAL INFORMATION:
APPLICANT: Donson, Jon
APPLICANT: Dawson, William O.
APPLICANT: Grantham, George L.
APPLICANT: Turpen, Thomas H.
APPLICANT: Turpen, Ann Myers
APPLICANT: Garger, Stephen J.
APPLICANT: Grill, Laurence K.
TITLE OF INVENTION: RECOMBINANT PLANT VIRAL NUCLEIC ACIDS
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,920
FILING DATE: 07-JUNE-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 184,237
FILING DATE: 19-JAN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 600,244
FILING DATE: 22-OCT-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 641,617
FILING DATE: 16-JAN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 310,881
FILING DATE: 17-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 160,766
FILING DATE: 26-FEB-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 160,771
FILING DATE: 26-FEB-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 347,637
FILING DATE: 05-MAY-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 363,138
FILING DATE: 08-JUN-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 219,279
FILING DATE: 15-JUL-1988
ATTORNEY/AGENT INFORMATION:

NAME: Halluin, Albert P.
REGISTRATION NUMBER: 28,957
REFERENCE/DOCKET NUMBER: 8129-112
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-854-3660
TELEFAX: 415-854-3694
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 434 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-482-920-6

Query Match 61.6%; Score 45; DB 2; Length 434;
Best Local Similarity 71.4%; Pred. No. 0.79;
Matches 10; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 IDRLVSIIRNGQIH 14
|:||||| |
Db 365 IERLVSIIRNGQIH 378

RESULT 8
US-08-484-341-6
Sequence 6, Application US/08484341
GENERAL INFORMATION:
APPLICANT: Dawson, Jon
Grantham, William O.
Turpen, Thomas H.
Turpen, Ann Myers
Garger, Stephen J.
Grill, Laurence K.
TITLE OF INVENTION: RECOMBINANT PLANT VIRAL NUCLEIC ACIDS
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lambach & Lambach
STREET: 2001 Ferry Building
CITY: San Francisco
STATE: CAL
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,341
FILING DATE: 07-Jun-1995
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/184,237
FILING DATE: <Unknown>
APPLICATION NUMBER: US 600,244
FILING DATE: 22-OCT-1990
APPLICATION NUMBER: US 641,617
FILING DATE: 16-JAN-1991
APPLICATION NUMBER: US 310,881
FILING DATE: 17-FEB-1989
APPLICATION NUMBER: US 160,766
FILING DATE: 26-FEB-1988
APPLICATION NUMBER: US 160,771
FILING DATE: 26-FEB-1988
APPLICATION NUMBER: US 347,637
FILING DATE: 05-MAY-1989
APPLICATION NUMBER: US 363,138
FILING DATE: 08-JUN-1989
APPLICATION NUMBER: US 219,279
FILING DATE: 15-JUL-1988
ATTORNEY/AGENT INFORMATION:
NAME: Halluin, Albert P.
REGISTRATION NUMBER: 28,957

REFERENCE/DOCKET NUMBER: BIOG-20121 USA
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-433-4150
TELEFAX: 415-433-8716
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 434 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-08-484-341-6

Query Match 61.6%; Score 45; DB 3; Length 434;
Best Local Similarity 71.4%; Pred. No. 0.79;
Matches 10; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 IDRLVSIIRNGQIH 14
|:||||| |
Db 365 IERLVSIIRNGQIH 378

RESULT 9
US-08-483-502-6
Sequence 6, Application US/08483502
Patent No. 6284492
GENERAL INFORMATION:
APPLICANT: Dawson, Jon
Grantham, William O.
Turpen, Thomas H.
Turpen, Ann Myers
Garger, Stephen J.
Grill, Laurence K.
TITLE OF INVENTION: RECOMBINANT PLANT VIRAL NUCLEIC ACIDS
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Venable, Baetjer, Howard & Civiletti
STREET: 1201 New York Avenue N.W., Suite 1000
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/483,502
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/739,143
FILING DATE:
APPLICATION NUMBER: US 600,244
FILING DATE: 22-OCT-1990
APPLICATION NUMBER: US 641,617
FILING DATE: 16-JAN-1991
APPLICATION NUMBER: US 310,881
FILING DATE: 17-FEB-1989
APPLICATION NUMBER: US 160,766
FILING DATE: 26-FEB-1988
APPLICATION NUMBER: US 160,771
FILING DATE: 26-FEB-1988
APPLICATION NUMBER: US 347,637
FILING DATE: 05-MAY-1989
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 363,138
FILING DATE: 08-JUN-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 219,279
FILING DATE: 15-JUL-1988
ATTORNEY/AGENT INFORMATION:
NAME: Thnen, Jeffrey L.
REGISTRATION NUMBER: 28,957
REFERENCE/DOCKET NUMBER: 18604-090574
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-962-4810
TELEFAX: 202-962-8300
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 434 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-483-502-6

Query Match 61.6%; Score 45; DB 3; Length 434;
Best Local Similarity 71.4%; Pred. No. 0.79;
Matches 10; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 IDRLVSIRTRGOIH 14
:|||||:|
DB 365 IERLVSIRTRGOIH 378

RESULT 10
US-09-726-651A-6
Sequence 6, Application US/09726651A
Patent No. 6448046
GENERAL INFORMATION:
APPLICANT: Dawson, William O.
APPLICANT: GRANTHAM, GEORGE L.
APPLICANT: TURPEN, Thomas H.
APPLICANT: TURPEN, Ann M.
APPLICANT: GARGER, Stephen J.
APPLICANT: GRILL, Laurence K.
TITLE OF INVENTION: RECOMBINANT ANIMAL VIRUS NUCLEIC ACIDS
FILE REFERENCE: 008010023CNU01
CURRENT APPLICATION NUMBER: US/09/726,651A
CURRENT FILING DATE: 2002-05-02
PRIOR APPLICATION NUMBER: 08/483,502
PRIOR FILING DATE: 1995-06-07
PRIOR APPLICATION NUMBER: 08/184,237
PRIOR FILING DATE: 1994-01-19
PRIOR APPLICATION NUMBER: 07/923,692
PRIOR FILING DATE: 1992-07-31
PRIOR APPLICATION NUMBER: 07/600,244
PRIOR FILING DATE: 1990-10-22
PRIOR APPLICATION NUMBER: 07/641,617
PRIOR FILING DATE: 1991-01-16
PRIOR APPLICATION NUMBER: 07/737,899
PRIOR FILING DATE: 1991-07-26
NUMBER OF SEQ ID NOS: 19
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 6
LENGTH: 434
TYPE: PRT
ORGANISM: Oryza sativa
FEATURE:
OTHER INFORMATION: CLONE: alpha-amylase
OTHER INFORMATION: protein
US-09-726-651A-6

Query Match 61.6%; Score 45; DB 4; Length 434;
Best Local Similarity 71.4%; Pred. No. 0.79;
Matches 10; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 IDRLVSIRTRGOIH 14

DB 365 IERLVSIRTRGOIH 378

RESULT 11
US-09-198-452A-959
Sequence 959, Application US/09198452A
Patent No. 6559294
GENERAL INFORMATION:
APPLICANT: Griffiths, R.
TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragment of invention: thereof and uses thereof, in particular for the diagnosis, prevention and treatment of infection
FILE REFERENCE: 9710-003-999
CURRENT APPLICATION NUMBER: US/09/198,452A
CURRENT FILING DATE: 1998-11-24
NUMBER OF SEQ ID NOS: 6849
SEQ ID NO 959
LENGTH: 460
TYPE: PRT
ORGANISM: Chlamydia pneumoniae
FEATURE:
NAME/KEY: SITE
LOCATION: 1...460
OTHER INFORMATION: Xaa-unknown or other
US-09-198-452A-959

Query Match 60.3%; Score 44; DB 4; Length 460;
Best Local Similarity 57.1%; Pred. No. 1.3;
Matches 8; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 2 DRLVSIRTRGOIHS 15
:|||||:|
DB 407 DRLVSIRTRGOIHS 420

RESULT 12
US-09-564-595D-54
Sequence 54, Application US/09564595D
Patent No. 6495668
GENERAL INFORMATION:
APPLICANT: Gilbert, Teresa
APPLICANT: Hart, Charles E.
APPLICANT: Sheppard, Paul O.
TITLE OF INVENTION: GROWTH FACTOR HOMOLOGY ZVEGF4
FILE REFERENCE: 99-19
CURRENT APPLICATION NUMBER: US/09/564,595D
CURRENT FILING DATE: 2000-05-03
PRIOR APPLICATION NUMBER: US 09/304,216
PRIOR FILING DATE: 1999-05-03
PRIOR APPLICATION NUMBER: US 60/164,463
PRIOR FILING DATE: 1999-11-10
PRIOR APPLICATION NUMBER: US 60/180,169
PRIOR FILING DATE: 2000-02-04
NUMBER OF SEQ ID NOS: 57
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 54
LENGTH: 302
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: fusion polypeptide
US-09-564-595D-54

Query Match 57.5%; Score 42; DB 4; Length 302;
Best Local Similarity 42.9%; Pred. No. 2.1;
Matches 6; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 2 DRLVSIRTRGOIHS 15
:|||||:|
DB 2 ERLVSTNGSIHS 15


```
RESULT 13
US-09-564-595D-55
; Sequence 55, Application US/09564595D
; Patent No. 6495668
; GENERAL INFORMATION:
; APPLICANT: Gilbert, Teresa
; APPLICANT: Hart, Charles E.
; APPLICANT: Sheppard, Paul O.
; TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF4
; FILE REFERENCE: 99-19
; CURRENT APPLICATION NUMBER: US/09/564,595D
; PRIOR FILING DATE: 2000-05-03
; PRIOR FILING DATE: 1999-05-03
; PRIOR FILING DATE: 1999-11-10
; PRIOR FILING DATE: 1999-11-10
; PRIOR FILING DATE: 2000-02-04
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 55
; LENGTH: 316
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion polypeptide
US-09-564-595D-55

Query Match
Best Local Similarity 57.5%; Score 42; DB 4; Length 316;
Matches 6; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

OY 2 DRLVSIRTRQIHS 15
DB 2 ERITVSTNGSIHS 15

RESULT 14
US-09-040-220D-2
; Sequence 2, Application US/09040220D
; Patent No. 6391311
; GENERAL INFORMATION:
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Kuo, Sophia S.
; TITLE OF INVENTION: NOVEL POLYPEPTIDES HAVING HOMOLOGY TO VASCULAR
; TITLE OF INVENTION: ENDOTHELIAL CELL GROWTH FACTOR AND BONE MORPHOGENETIC
; TITLE OF INVENTION: PROTEIN 1 AND NUCLEIC ACIDS ENCODING SAME, THEIR USES,
; FILE REFERENCE: P1122
; CURRENT APPLICATION NUMBER: US/09/040,220D
; PRIOR FILING DATE: 1998-03-17
; NUMBER OF SEQ ID NOS: 8
; SEQ ID NO 2
; LENGTH: 345
; TYPE: PRT
; ORGANISM: Human
US-09-040-220D-2

Query Match
Best Local Similarity 57.5%; Score 42; DB 4; Length 345;
Matches 6; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

OY 2 DRLVSIRTRQIHS 15
DB 47 ERITVSTNGSIHS 60

RESULT 15
US-09-457-066-2
; Sequence 2, Application US/09457066
; Patent No. 6432673
; GENERAL INFORMATION:
; APPLICANT: Gao, Zeren
US-09-457-066-2

APPLICANT: Hart, Charles E.
APPLICANT: Piddington, Christopher S.
APPLICANT: Sheppard, Paul O.
APPLICANT: Shoemaker, Kimberly E.
APPLICANT: Gilbertson, Debra G.
APPLICANT: West, James W.
; TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF3
; FILE REFERENCE: 98-60
; CURRENT APPLICATION NUMBER: US/09/457,066
; PRIOR FILING DATE: 1999-12-07
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 345
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-457-066-2

Query Match
Best Local Similarity 57.5%; Score 42; DB 4; Length 345;
Matches 6; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

OY 2 DRLVSIRTRQIHS 15
DB 47 ERITVSTNGSIHS 60

RESULT 16
US-09-265-686-2
; Sequence 2, Application US/09265686
; Patent No. 6455283
; GENERAL INFORMATION:
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Kuo, Sophia S.
; TITLE OF INVENTION: POLYPEPTIDES HOMOLOGOUS TO VEGF AND BMP1
; FILE REFERENCE: P1122P2
; CURRENT APPLICATION NUMBER: US/09/265,686
; PRIOR FILING DATE: 1999-03-10
; PRIOR FILING DATE: 1998-03-17
; PRIOR FILING DATE: 1998-03-17
; PRIOR FILING DATE: US 09/184,216
; NUMBER OF SEQ ID NOS: 8
; SEQ ID NO 2
; LENGTH: 345
; TYPE: PRT
; ORGANISM: Human
US-09-265-686-2

Query Match
Best Local Similarity 57.5%; Score 42; DB 4; Length 345;
Matches 6; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

OY 2 DRLVSIRTRQIHS 15
DB 47 ERITVSTNGSIHS 60

RESULT 17
US-09-540-224-5
; Sequence 5, Application US/09540224
; Patent No. 6468543
; GENERAL INFORMATION:
; APPLICANT: Gilbertson, Debra G.
; APPLICANT: Hart, Charles E.
; TITLE OF INVENTION: METHODS FOR PROMOTING GROWTH OF BONE,
; TITLE OF INVENTION: LIGAMENT AND CARTILAGE USING ZVEGF4
; FILE REFERENCE: 00-28
; CURRENT APPLICATION NUMBER: US/09/540,224
; PRIOR FILING DATE: 2000-03-31
; EARLIER APPLICATION NUMBER: US 60/180,169
; PRIOR FILING DATE: 2000-02-04
; NUMBER OF SEQ ID NOS: 9
US-09-540-224-5
```

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; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 345
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-540-224-5

```

```

Query Match          57.5%; Score 42; DB 4; Length 345;
Best Local Similarity 42.9%; Pred. No. 2.4;
Matches 6; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

```

```

OY      2 DLVSIRTRQIHS 15
        :|:::| | | |
Db      47 ERITVSTNGSIHS 60

```

```

RESULT 18
US-09-564-595D-33
; Sequence 33, Application US/09564595D
; Patent No. 6495668
; GENERAL INFORMATION:
; APPLICANT: Gilbert, Teresa
; APPLICANT: Hart, Charles E.
; APPLICANT: Sheppard, Paul O.
; TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGFA
; FILE REFERENCE: 99-19
; CURRENT APPLICATION NUMBER: US/09/564,595D
; CURRENT FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: US 09/304,216
; PRIOR FILING DATE: 1999-05-03
; PRIOR APPLICATION NUMBER: US 60/164,463
; PRIOR FILING DATE: 1999-11-10
; PRIOR APPLICATION NUMBER: US 60/180,169
; PRIOR FILING DATE: 2000-02-04
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 33
; LENGTH: 345
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-564-595D-33

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Query Match          57.5%; Score 42; DB 4; Length 345;
Best Local Similarity 42.9%; Pred. No. 2.4;
Matches 6; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

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```

OY      2 DLVSIRTRQIHS 15
        :|:::| | | |
Db      47 ERITVSTNGSIHS 60

```

```

RESULT 19
US-09-706-968-2
; Sequence 2, Application US/09706968
; Patent No. 6528050
; GENERAL INFORMATION:
; APPLICANT: Gao, Zeren
; APPLICANT: Hart, Charles E.
; APPLICANT: Piddington, Christopher S.
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Shoemaker, Kimberly E.
; APPLICANT: Gilbertson, Debra G.
; APPLICANT: West, James W.
; TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGFS
; FILE REFERENCE: 98-60C1
; CURRENT APPLICATION NUMBER: US/09/706,968
; CURRENT FILING DATE: 2000-11-06
; PRIOR APPLICATION NUMBER: US/09/541,752
; PRIOR FILING DATE: 2000-03-31
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 345

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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-706-968-2

```

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Query Match          57.5%; Score 42; DB 4; Length 345;
Best Local Similarity 42.9%; Pred. No. 2.4;
Matches 6; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

```

```

OY      2 DLVSIRTRQIHS 15
        :|:::| | | |
Db      47 ERITVSTNGSIHS 60

```

```

RESULT 20
US-08-466-120-2
; Sequence 2, Application US/08466120
; Patent No. 5869284
; GENERAL INFORMATION:
; APPLICANT: CAO, ET AL.
; TITLE OF INVENTION: Retinoid Acid Receptor Epsilon
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
; ADDRESSEE: CECCHI, STEWART & OLSTEIN
; STREET: 6 BECKER FARM ROAD
; CITY: ROSELAND
; STATE: NEW JERSEY
; COUNTRY: USA
; ZIP: 07068

```

```

; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 INCH DISKETTE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WORD PERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/466,120
; FILING DATE: June 6, 1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/07266
; FILING DATE: 24 JUN 94
; ATTORNEY/AGENT INFORMATION:
; NAME: FERRARO, GREGORY D.
; REGISTRATION NUMBER: 36,134
; REFERENCE/DOCKET INFORMATION:
; TELEPHONE: 201-994-1744
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 433 AMINO ACIDS
; TYPE: AMINO ACID
; STRANDEDNESS:
; TOPOLOGY: LINEAR
; MOLECULE TYPE: PROTEIN
US-08-466-120-2

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```

Query Match          53.4%; Score 39; DB 2; Length 433;
Best Local Similarity 53.8%; Pred. No. 12;
Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

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```

OY      3 RLVSIRTRQIHS 15
        :|:::| | | |
Db      396 KLVSLRTSSVHS 408

```

```

RESULT 21
PCT-US94-07266-2
; Sequence 2, Application PC/TUS9407266
; GENERAL INFORMATION:
; APPLICANT: CAO, ET AL.
; TITLE OF INVENTION: Retinoid Acid Receptor Epsilon
; NUMBER OF SEQUENCES: 2

```

CORRESPONDENCE ADDRESS:
ADDRESSER: CARELLA, BYRNE, BAIN, GILFILLAN,
ADDRESSEE: CECCHI, STEWART & OLSTEIN
STREET: 6 BECKER FARM ROAD
CITY: ROSELAND
STATE: NEW JERSEY
COUNTRY: USA
ZIP: 07068
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/07266
FILING DATE: Concurrently
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: FERRARO, GREGORY D.
REGISTRATION NUMBER: 36,134
REFERENCE/DOCKET NUMBER: 325800-125
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1744
TELEFAX: 201-994-1700
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 433 AMINO ACIDS
TYPE: AMINO ACID
STRANDEDNESS:
TOPOLOGY: LINEAR
MOLECULE TYPE: PROTEIN
PCT-US94-07266-2

Query Match 53.4%; Score 39; DB 5; Length 433;
Best local similarity 53.8%; Pred. No. 12;
Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 3 RLVSIRTRQIHS 15
Db 396 KLVSLRTLSVHS 408

RESULT 22
US-08-333-358-8
Sequence 8, Application US/08333358
Patent No. 5571696
GENERAL INFORMATION:
APPLICANT: EVANS Ph.D., RONALD M.
APPLICANT: MANGELSDORF Ph.D., DAVID J.
APPLICANT: ONG MS., ESTELITA S.
APPLICANT: ORO Ph.D., ANTHONY E.
APPLICANT: BORGMEYER Ph.D., UWE K.
APPLICANT: GIGUERE Ph.D., VINCENT NMN
APPLICANT: YAO Mr., TSO-PANG NMN
TITLE OF INVENTION: NOVEL RECEPTORS
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pretly, Schroeder, Brueggemann & Clark
STREET: 444 So. Flower St., Suite 2000
CITY: Los Angeles
STATE: CA
COUNTRY: US
ZIP: 90071-2921
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/333,358

FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/761,068
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Reiter Ph.D., Stephen E.
REGISTRATION NUMBER: 31192
REFERENCE/DOCKET NUMBER: P31 8936
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 440 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-333-358-8

Query Match 53.4%; Score 39; DB 1; Length 440;
Best local similarity 53.8%; Pred. No. 12;
Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 3 RLVSIRTRQIHS 15
Db 403 KLVSLRTLSVHS 415

RESULT 23
US-08-463-694-8
Sequence 8, Application US/08463694
Patent No. 566233
GENERAL INFORMATION:
APPLICANT: EVANS Ph.D., RONALD M.
APPLICANT: MANGELSDORF Ph.D., DAVID J.
APPLICANT: ONG MS., ESTELITA S.
APPLICANT: ORO Ph.D., ANTHONY E.
APPLICANT: BORGMEYER Ph.D., UWE K.
APPLICANT: GIGUERE Ph.D., VINCENT NMN
APPLICANT: YAO Mr., TSO-PANG NMN
TITLE OF INVENTION: NOVEL RECEPTORS
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pretly, Schroeder, Brueggemann & Clark
STREET: 444 So. Flower St., Suite 2000
CITY: Los Angeles
STATE: CA
COUNTRY: US
ZIP: 90071-2921
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/463,694
FILING DATE: 05-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/761,068
FILING DATE: 17-SEP-1991
ATTORNEY/AGENT INFORMATION:
NAME: Reiter Ph.D., Stephen E.
REGISTRATION NUMBER: 31192
REFERENCE/DOCKET NUMBER: P31 8936
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 440 amino acids
TYPE: amino acid

TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-463-694-8

Query Match
Best Local Similarity 53.4%; Score 39; DB 1; Length 440;
Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

OY 3 RLVSIRTRQIHS 15
:||||:||||
Db 403 KLVSLRTRSSVHS 415

RESULT 24
US-08-694-501-8
Sequence 8, Application US/08694501
Patent No. 5710004
GENERAL INFORMATION:
APPLICANT: EVANS, Ph.D., RONALD M.
APPLICANT: MANGELSDORF, Ph.D., DAVID J.
APPLICANT: ONG, Ms., ESTELITA S.
APPLICANT: ORO, Ph.D., ANTHONY E.
APPLICANT: BORGMAYER, Ph.D., UWE K.
APPLICANT: GIGUERE, Ph.D., VINCENT NMN
APPLICANT: YAO, Mr., TSO-PANG NMN
TITLE OF INVENTION: NOVEL RECEPTORS
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Pretly, Schroeder, Brueggemann & Clark
STREET: 444 So. Flower St., Suite 2000
CITY: Los Angeles
STATE: CA
COUNTRY: US
ZIP: 90071-2921
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/694,501
FILING DATE: 07-AUG-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/333,358
FILING DATE:
APPLICATION NUMBER: US/07/761,068
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Reiter Ph.D., Stephen E.
REGISTRATION NUMBER: 31192
REFERENCE/DOCKET NUMBER: P31 8936
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ. ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 440 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-694-501-8

Query Match
Best Local Similarity 53.4%; Score 39; DB 1; Length 440;
Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

OY 3 RLVSIRTRQIHS 15
:||||:||||
Db 403 KLVSLRTRSSVHS 415

RESULT 25

US-08-342-411A-4
Sequence 4, Application US/08342411A
Patent No. 5639616
GENERAL INFORMATION:
APPLICANT: LIAO, Shutsung
APPLICANT: SONG, Ching
TITLE OF INVENTION: UBQUITOUS NUCLEAR RECEPTOR:
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/342,411A
FILING DATE: 18-NOV-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: KITCHELL, BARBARA S.
REGISTRATION NUMBER: 33,928
REFERENCE/DOCKET NUMBER: ARCD154
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (713) 789-2679
TELEX: 79-0924
INFORMATION FOR SEQ. ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 443 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-342-411A-4

Query Match
Best Local Similarity 53.4%; Score 39; DB 1; Length 443;
Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

OY 3 RLVSIRTRQIHS 15
:||||:||||
Db 406 KLVSLRTRSSVHS 418

RESULT 26
US-08-372-652-3
Sequence 3, Application US/08372652
Patent No. 5932699
GENERAL INFORMATION:
APPLICANT: Moore, David
APPLICANT: Seol, Wongi
APPLICANT: Choi, Hwang-sik
TITLE OF INVENTION: RETINOID X RECEPTOR-INTERACTING
TITLE OF INVENTION: POLYPEPTIDES AND RELATED MOLECULES AND METHODS
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street, Suite 3100
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/372,652
FILING DATE: 13-JAN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 00786/246001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 446 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-372-652-3

Query Match 53.4%; Score 39; DB 2; Length 446;
Best Local Similarity 53.8%; Pred. No. 13;
Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

OY 3 RLVSIPTRQIHS 15
:|||||:|
DB 409 KLVSLRTLSVHS 421

RESULT 27
US-08-776-844-2
Sequence 2, Application US/08776844
Patent No. 6277926
GENERAL INFORMATION:
APPLICANT: ENMARK, EVA
TITLE OF INVENTION: OR-1 ON ORPHAN RECEPTOR BELONGING
TO THE NUCLEAR RECEPTOR FAMILY
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Banner & Witcoff
STREET: 1001 G Street, NW
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20001
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/776,844
FILING DATE: 24-JUN-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP95/03247
FILING DATE: 16-AUG-1995
APPLICATION NUMBER: UK 9413536.2
FILING DATE: 16-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Kagan, Sarah A
REGISTRATION NUMBER: 32141
REFERENCE/DOCKET NUMBER: 00487.04029
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-508-9100
TELEFAX: 202-508-9299
TELEX:
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 446 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein

MOLECULE TYPE: protein
US-08-776-844-2

Query Match 53.4%; Score 39; DB 3; Length 446;
Best Local Similarity 53.8%; Pred. No. 13;
Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

OY 3 RLVSIPTRQIHS 15
:|||||:|
DB 409 KLVSLRTLSVHS 421

RESULT 28
US-09-909-325-2
Sequence 2, Application US/09909325
Patent No. 6525188
GENERAL INFORMATION:
APPLICANT: ENMARK, EVA
GUSTAFSSON, JAN
TITLE OF INVENTION: OR-1 ON ORPHAN RECEPTOR BELONGING
TO THE NUCLEAR RECEPTOR FAMILY
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Banner & Witcoff
STREET: 1001 G Street, NW
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20001
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/909,325
FILING DATE: 19-JUL-2001
CLASSIFICATION: <unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/776,844
FILING DATE: <unknown>
APPLICATION NUMBER: UK 9413536.2
FILING DATE: 16-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Kagan, Sarah A
REGISTRATION NUMBER: 32141
REFERENCE/DOCKET NUMBER: 00487.04029
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-508-9100
TELEFAX: 202-508-9299
TELEX: <unknown>
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 446 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-909-325-2

Query Match 53.4%; Score 39; DB 4; Length 446;
Best Local Similarity 53.8%; Pred. No. 13;
Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

OY 3 RLVSIPTRQIHS 15
:|||||:|
DB 409 KLVSLRTLSVHS 421

RESULT 29
PCT-US95-16311-3
Sequence 3, Application PC/TUS9516311

GENERAL INFORMATION:
APPLICANT: Moore, David
APPLICANT: Seol, Wongi
APPLICANT: Choi, Hwang-Sik
TITLE OF INVENTION: RETINOID X RECEPTOR-INTERACTING
TITLE OF INVENTION: POLYPEPTIDES AND RELATED MOLECULES AND METHODS
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street, Suite 3100
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/16311
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/372,652
FILING DATE: 13-JAN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 00786/246001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 446 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US95-16311-3

Query Match 53.4%; Score 39; DB 5; Length 446;
Best Local Similarity 53.8%; Pred. No. 13;
Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 3 RLVSIIRTRGQIHS 15
DB 409 KLVSLRTLSVHS 421

RESULT 30
US-08-373-935-1
Sequence 1, Application US/08373935
Patent No. 5747661
GENERAL INFORMATION:
APPLICANT: Evans, Ronald M.
APPLICANT: Mangelsdorf, David J.
APPLICANT: Willy, Patricia J.
TITLE OF INVENTION: IDENTIFICATION OF A DISTINCT
TITLE OF INVENTION: RETINOID-RESPONSIVE PATHWAY AND USES THEREFOR
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Priety, Schroeder, Brueggemann & Clark
STREET: 444 South Flower Street, Suite 2000
CITY: Los Angeles
STATE: CA
COUNTRY: USA
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/373,935
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Reiter, Stephen E.
REGISTRATION NUMBER: 31,192
REFERENCE/DOCKET NUMBER: P41 9894
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-546-4737
TELEFAX: 619-546-4737
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 447 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-373-935-1

Query Match 53.4%; Score 39; DB 1; Length 447;
Best Local Similarity 53.8%; Pred. No. 13;
Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 3 RLVSIIRTRGQIHS 15
DB 410 KLVSLRTLSVHS 422

Search completed: August 29, 2003, 18:44:39
Job time : 17.8571 secs

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OM protein - protein search, using sw model

Run on: August 29, 2003, 18:42:11 ; Search time 23.5714 Seconds

(without alignments)
87.043 Million cell updates/sec

Title: US-09-830-876-1

Perfect score: 73

Sequence: 1 IDRLVSIKRGQIHS 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 510680 seqs, 136781880 residues

Total number of hits satisfying chosen parameters: 510680

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

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3: /cgn2_6/ptodata/2/pubpaa/US06_NEM_PUB.pep:*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
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11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*
12: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
13: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
14: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
16: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
17: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
18: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	45	61.6	434	12	US-10-280-679B-6
2	42	57.5	117	10	US-09-852-209A-19
3	42	57.5	117	15	US-10-131-600-19
4	42	57.5	297	15	US-10-103-197-5
5	42	57.5	318	10	US-09-852-209A-5
6	42	57.5	318	15	US-10-131-600-5
7	42	57.5	339	9	US-09-925-302-776
8	42	57.5	345	9	US-09-823-033-2
9	42	57.5	345	9	US-09-818-943-1
10	42	57.5	345	9	US-09-923-995-4
11	42	57.5	345	10	US-09-795-006A-149
12	42	57.5	345	10	US-09-978-295A-488
13	42	57.5	345	10	US-09-852-209A-3
14	42	57.5	345	10	US-09-978-697-488
15	42	57.5	345	10	US-09-978-192A-488

16	42	57.5	345	10	US-09-999-832A-488	Sequence 488, App
17	42	57.5	345	11	US-09-978-189-488	Sequence 488, App
18	42	57.5	345	11	US-09-796-753-6	Sequence 6, App11
19	42	57.5	345	11	US-09-978-608A-488	Sequence 488, App
20	42	57.5	345	11	US-09-978-585A-488	Sequence 488, App
21	42	57.5	345	11	US-09-978-191A-488	Sequence 488, App
22	42	57.5	345	11	US-09-978-403A-488	Sequence 488, App
23	42	57.5	345	11	US-09-999-832A-488	Sequence 488, App
24	42	57.5	345	11	US-09-981-912A-488	Sequence 488, App
25	42	57.5	345	11	US-09-978-824-488	Sequence 488, App
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28	42	57.5	345	11	US-09-978-824-488	Sequence 488, App
29	42	57.5	345	11	US-09-978-824-488	Sequence 488, App
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31	42	57.5	345	11	US-09-978-824-488	Sequence 488, App
32	42	57.5	345	11	US-09-978-824-488	Sequence 488, App
33	42	57.5	345	11	US-09-978-824-488	Sequence 488, App
34	42	57.5	345	11	US-09-978-824-488	Sequence 488, App
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36	42	57.5	345	11	US-09-978-824-488	Sequence 488, App
37	42	57.5	345	11	US-09-978-824-488	Sequence 488, App
38	42	57.5	345	11	US-09-978-824-488	Sequence 488, App
39	42	57.5	345	11	US-09-978-824-488	Sequence 488, App
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47	42	57.5	345	11	US-09-978-824-488	Sequence 488, App
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49	42	57.5	345	11	US-09-978-824-488	Sequence 488, App
50	42	57.5	345	11	US-09-978-824-488	Sequence 488, App
51	42	57.5	345	11	US-09-978-824-488	Sequence 488, App
52	42	57.5	345	11	US-09-978-824-488	Sequence 488, App
53	42	57.5	345	11	US-09-978-824-488	Sequence 488, App
54	42	57.5	345	11	US-09-978-824-488	Sequence 488, App
55	42	57.5	345	11	US-09-978-824-488	Sequence 488, App
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57	42	57.5	345	11	US-09-978-824-488	Sequence 488, App
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59	42	57.5	345	11	US-09-978-824-488	Sequence 488, App
60	42	57.5	345	11	US-09-978-824-488	Sequence 488, App
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63	42	57.5	345	11	US-09-978-824-488	Sequence 488, App
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66	42	57.5	345	11	US-09-978-824-488	Sequence 488, App
67	42	57.5	345	11	US-09-978-824-488	Sequence 488, App
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69	42	57.5	345	11	US-09-978-824-488	Sequence 488, App
70	42	57.5	345	11	US-09-978-824-488	Sequence 488, App
71	42	57.5	345	11	US-09-978-824-488	Sequence 488, App
72	42	57.5	345	11	US-09-978-824-488	Sequence 488, App
73	42	57.5	345	11	US-09-978-824-488	Sequence 488, App
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78	42	57.5	345	11	US-09-978-824-488	Sequence 488, App
79	42	57.5	345	11	US-09-978-824-488	Sequence 488, App
80	42	57.5	345	11	US-09-978-824-488	Sequence 488, App
81	42	57.5	345	11	US-09-978-824-488	Sequence 488, App
82	42	57.5	345	11	US-09-978-824-488	Sequence 488, App
83	42	57.5	345	11	US-09-978-824-488	Sequence 488, App
84	42	57.5	345	11	US-09-978-824-488	Sequence 488, App
85	42	57.5	345	11	US-09-978-824-488	Sequence 488, App
86	42	57.5	345	11	US-09-978-824-488	Sequence 488, App
87	42	57.5	345	11	US-09-978-824-488	Sequence 488, App
88	42	57.5	345	11	US-09-978-824-488	Sequence 488, App

89	42	57.5	345	12	US-10-141-753-286	Sequence 286, App
90	42	57.5	345	12	US-10-141-758-286	Sequence 286, App
91	42	57.5	345	12	US-10-142-418-286	Sequence 286, App
92	42	57.5	345	12	US-10-142-420-286	Sequence 286, App
93	42	57.5	345	12	US-10-142-422-286	Sequence 286, App
94	42	57.5	345	12	US-10-142-427-286	Sequence 286, App
95	42	57.5	345	12	US-10-142-760-286	Sequence 286, App
96	42	57.5	345	12	US-10-143-030A-488	Sequence 488, App
97	42	57.5	345	12	US-10-145-821-286	Sequence 286, App
98	42	57.5	345	12	US-10-152-531-286	Sequence 286, App
99	42	57.5	345	12	US-10-127-840A-286	Sequence 286, App
100	42	57.5	345	12	US-10-142-424-286	Sequence 286, App

ALIGNMENTS

RESULT 1

US-10-280-679B-6

Sequence 6, Application US/10280679B

Publication No. US20030150019A1

GENERAL INFORMATION:

APPLICANT: Large Scale Biology Corporation

TITLE OF INVENTION: Monopartite RNA Virus Transformation Vectors

FILE REFERENCE: LSBC-0109-US03

CURRENT APPLICATION NUMBER: US/10/280,679B

PRIOR FILING DATE: 2000-10-24

PRIOR APPLICATION NUMBER: 09/557,941

PRIOR FILING DATE: 2000-04-24

PRIOR APPLICATION NUMBER: 08/484,341

PRIOR FILING DATE: 1995-06-07

PRIOR APPLICATION NUMBER: 07/923,692

PRIOR FILING DATE: 1992-07-31

PRIOR APPLICATION NUMBER: 07/600,244

PRIOR FILING DATE: 1990-10-22

PRIOR APPLICATION NUMBER: 07/641,617

PRIOR FILING DATE: 1991-01-16

PRIOR APPLICATION NUMBER: 07/737,899

PRIOR FILING DATE: 1991-07-26

PRIOR APPLICATION NUMBER: 07/739,143

PRIOR FILING DATE: 1991-08-01

PRIOR APPLICATION NUMBER: 07/310,881

PRIOR FILING DATE: 1989-02-17

PRIOR APPLICATION NUMBER: 07/160,766

PRIOR FILING DATE: 1988-02-26

PRIOR APPLICATION NUMBER: 07/160,771

PRIOR FILING DATE: 1988-02-26

Remaining Prior Application data removed - See File Wrapper or PALM.

NUMBER OF SEQ ID NOS: 11

SOFTWARE: PatentIn version 3.1

SEQ ID NO 6

LENGTH: 434

TYPE: PRT

ORGANISM: Rice alpha-amylase

US-10-280-679B-6

Query Match 61.6%; Score 45; DB 12; Length 434;
 Best Local Similarity 71.4%; Pred. No. 4.1;
 Matches 10; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 IDRLVSIIRRGQIH 14
 DB 365 IERLVSIRRGQIH 378

RESULT 2

US-09-852-209A-19

Sequence 19, Application US/09852209A

Patent No. US20020164687A1

GENERAL INFORMATION:

APPLICANT: ERIKSSON, Ulf

APPLICANT: AASE, Karin

APPLICANT: LEE, Xuri

APPLICANT: PONTEN, Annica
 APPLICANT: UUTELA, Marko
 APPLICANT: ALITALO, Kari
 APPLICANT: OESTMAN, Arne
 APPLICANT: HELDIN, Carl-Henrik
 APPLICANT: BETHSHOLTZ, Christer
 TITLE OF INVENTION: PLATELET-DERIVED GROWTH FACTOR C, DNA CODING
 FILE REFERENCE: 09-410349-Eriksson et al-1064-44740
 CURRENT APPLICATION NUMBER: US/09/852,209A
 PRIOR FILING DATE: 2001-05-10
 PRIOR APPLICATION NUMBER: 09/410,349
 PRIOR FILING DATE: 1999-09-30
 PRIOR APPLICATION NUMBER: 60/110,749
 PRIOR FILING DATE: 1998-12-03
 PRIOR APPLICATION NUMBER: 60/113,002
 PRIOR FILING DATE: 1998-12-18
 PRIOR APPLICATION NUMBER: 60/135,426
 PRIOR FILING DATE: 1999-05-21
 PRIOR APPLICATION NUMBER: 60/144,022
 PRIOR FILING DATE: 1999-07-15
 NUMBER OF SEQ ID NOS: 39
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO 19
 LENGTH: 117
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-09-852-209A-19

Query Match 57.5%; Score 42; DB 10; Length 117;
 Best Local Similarity 42.9%; Pred. No. 3.4;
 Matches 6; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 2 DRVLSIRTRGQIHS 15
 DB 1 ERLLTVSTNGSIHS 14

RESULT 3

US-10-131-600-19

Sequence 19, Application US/10131600

Publication No. US20030082670A1

GENERAL INFORMATION:

APPLICANT: ERIKSSON, Ulf

APPLICANT: AASE, Karin

APPLICANT: LEE, Xuri

APPLICANT: PONTEN, Annica

APPLICANT: UUTELA, Marko

APPLICANT: ALITALO, Kari

APPLICANT: OESTMAN, Arne

APPLICANT: HELDIN, Carl-Henrik

APPLICANT: BETHSHOLTZ, Christer

TITLE OF INVENTION: PLATELET-DERIVED GROWTH FACTOR C, DNA CODING

FILE REFERENCE: 09-410349-Eriksson et al-1064-44740

CURRENT APPLICATION NUMBER: US/10/131,600

PRIOR FILING DATE: 2002-04-25

PRIOR APPLICATION NUMBER: 09/410,349

PRIOR FILING DATE: 1999-09-30

PRIOR APPLICATION NUMBER: 60/108,109

PRIOR FILING DATE: 1998-11-12

PRIOR APPLICATION NUMBER: 60/110,749

PRIOR FILING DATE: 1998-12-03

PRIOR APPLICATION NUMBER: 60/113,002

PRIOR FILING DATE: 1998-12-18

PRIOR APPLICATION NUMBER: 60/135,426

PRIOR FILING DATE: 1999-05-21

PRIOR APPLICATION NUMBER: 60/144,022

PRIOR FILING DATE: 1999-07-15

NUMBER OF SEQ ID NOS: 39

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 19

LENGTH: 117


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; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-131-600-19

Query Match
Best local similarity 57.5%; Score 42; DB 15; Length 117;
Pred. No. 3.4;
Matches 6; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

OY 2 DRIVSIRTRGOIHS 15
DB 1 ERITVSTNGSIHS 14

RESULT 4
US-10-103-197-5
; Sequence 5, Application US/10103197
; Publication No. US20030032098A1
; GENERAL INFORMATION:
; APPLICANT: Young et al.
; TITLE OF INVENTION: Bone Morphogenic Proteins (BMP family)
; FILE REFERENCE: PR012P1
; CURRENT APPLICATION NUMBER: US/10/103,197
; PRIOR FILING DATE: 2002-03-22
; PRIOR APPLICATION NUMBER: 09/458,690
; PRIOR FILING DATE: 1998-12-10
; PRIOR APPLICATION NUMBER: 60/092,922
; PRIOR FILING DATE: 1998-07-15
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 297
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-103-197-5

Query Match
Best local similarity 57.5%; Score 42; DB 15; Length 297;
Pred. No. 9.6;
Matches 6; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

OY 2 DRIVSIRTRGOIHS 15
DB 67 ERITVSTNGSIHS 80

RESULT 5
US-09-852-209A-5
; Sequence 5, Application US/09852209A
; Patent No. US20020164687A1
; GENERAL INFORMATION:
; APPLICANT: ERIKSSON, Ulf
; APPLICANT: AASE, Karin
; APPLICANT: LEE, Xuri
; APPLICANT: PONTEN, Annica
; APPLICANT: TUTTELA, Marko
; APPLICANT: ALLTALO, Kari
; APPLICANT: OESTMAN, Arne
; APPLICANT: HELDIN, Carl-Henrik
; APPLICANT: BERTSHOLTZ, Christer
; TITLE OF INVENTION: PLATELET-DERIVED GROWTH FACTOR C,
; FILE REFERENCE: 09-410349-ERIKSSON et al-1064-44740
; CURRENT APPLICATION NUMBER: US/09/852,209A
; PRIOR FILING DATE: 2001-05-10
; PRIOR APPLICATION NUMBER: 09/410,349
; PRIOR FILING DATE: 1999-09-30
; PRIOR APPLICATION NUMBER: 60/110,749
; PRIOR FILING DATE: 1998-12-03
; PRIOR APPLICATION NUMBER: 60/113,002
; PRIOR FILING DATE: 1998-12-18
; PRIOR APPLICATION NUMBER: 60/135,426
; PRIOR FILING DATE: 1999-05-21
; PRIOR APPLICATION NUMBER: 60/144,022
; PRIOR FILING DATE: 1999-07-15

; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 318
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-131-600-5

Query Match
Best local similarity 57.5%; Score 42; DB 15; Length 318;
Pred. No. 10;
Matches 6; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

OY 2 DRIVSIRTRGOIHS 15
DB 20 ERITVSTNGSIHS 33

RESULT 7
US-09-925-302-776
; Sequence 776, Application US/09925302
; Patent No. US20020044941A1
; GENERAL INFORMATION:
; APPLICANT: ROSEN et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA104
```

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; CURRENT APPLICATION NUMBER: US/09/925,302
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05918
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 896
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 776
; LENGTH: 339
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-925-302-776
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Query Match      57.5%; Score 42; DB 9; Length 339;
Best Local Similarity 42.9%; Pred. No. 11;
Matches 6; Conservative 5; Mismatches 3; Indels 0; Gaps 0;
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QY      2 DRLVSIRTRGQIHS 15
        :|:::| | | | |
Db      41 ERITVSTNGSIHS 54
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```
RESULT 8
US-09-823-033-2
; Sequence 2, Application US/09823033
; Patent No. US20020004225A1
; GENERAL INFORMATION:
; APPLICANT: Hart, Charles E.
; APPLICANT: Gilbertson, Debra G.
; TITLE OF INVENTION: METHODS FOR PROMOTING GROWTH OF BONE,
; FILE REFERENCE: 00-12
; CURRENT APPLICATION NUMBER: US/09/823,033
; CURRENT FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 345
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-823-033-2
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Query Match      57.5%; Score 42; DB 9; Length 345;
Best Local Similarity 42.9%; Pred. No. 11;
Matches 6; Conservative 5; Mismatches 3; Indels 0; Gaps 0;
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```
QY      2 DRLVSIRTRGQIHS 15
        :|:::| | | | |
Db      47 ERITVSTNGSIHS 60
```

```
RESULT 9
US-09-818-943-1
; Sequence 1, Application US/09818943
; Patent No. US20020049987A1
; GENERAL INFORMATION:
; APPLICANT: ERIKSSON, ULF
; APPLICANT: LI, Xuri
; APPLICANT: PONTEN, Annica
; APPLICANT: AASE, Karin
; APPLICANT: LI, Hong
; TITLE OF INVENTION: NON-HUMAN TRANSGENIC ANIMALS EXPRESSING PLATELET-DERIVED GROWTH F
; FILE REFERENCE: 1064/48487
; CURRENT APPLICATION NUMBER: US/09/818,943
; CURRENT FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: US 60/192,507
; PRIOR FILING DATE: 2000-03-28
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 1
; LENGTH: 345
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-818-943-1
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Query Match      57.5%; Score 42; DB 9; Length 345;
Best Local Similarity 42.9%; Pred. No. 11;
Matches 6; Conservative 5; Mismatches 3; Indels 0; Gaps 0;
```

```
QY      2 DRLVSIRTRGQIHS 15
        :|:::| | | | |
Db      47 ERITVSTNGSIHS 60
```

```
RESULT 10
US-09-923-995-4
; Sequence 4, Application US/09923995
; Patent No. US20020081700A1
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; TITLE OF INVENTION: SNAKE VENOM POLYPEPTIDE ZSNK1
; FILE REFERENCE: 00-47
; CURRENT APPLICATION NUMBER: US/09/923,995
; CURRENT FILING DATE: 2001-08-07
; PRIOR APPLICATION NUMBER: US 60/223,164
; PRIOR FILING DATE: 2000-08-07
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 345
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-923-995-4
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```
Query Match      57.5%; Score 42; DB 9; Length 345;
Best Local Similarity 42.9%; Pred. No. 11;
Matches 6; Conservative 5; Mismatches 3; Indels 0; Gaps 0;
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```
QY      2 DRLVSIRTRGQIHS 15
        :|:::| | | | |
Db      47 ERITVSTNGSIHS 60
```

```
RESULT 11
US-09-795-006A-149
; Sequence 149, Application US/09795006A
; Patent No. US20020151680A1
; GENERAL INFORMATION:
; APPLICANT: Alltalo et al
; TITLE OF INVENTION: MATERIALS AND METHODS INVOLVING HYBRID VASCULAR
; FILE REFERENCE: 28967/35977B
; CURRENT APPLICATION NUMBER: US/09/795,006A
; CURRENT FILING DATE: 2001-02-26
; PRIOR APPLICATION NUMBER: US 60/205,331
; PRIOR FILING DATE: 2000-05-18
; PRIOR APPLICATION NUMBER: US 60/185,205
; PRIOR FILING DATE: 2000-02-25
; NUMBER OF SEQ ID NOS: 175
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 149
; LENGTH: 345
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-795-006A-149
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Query Match      57.5%; Score 42; DB 10; Length 345;
Best Local Similarity 42.9%; Pred. No. 11;
Matches 6; Conservative 5; Mismatches 3; Indels 0; Gaps 0;
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QY      2 DRLVSIRTRGQIHS 15
        :|:::| | | | |
Db      47 ERITVSTNGSIHS 60
```

RESULT 12
US-09-978-295A-488
Sequence 488, Application US/09978295A
Patent No. US2002015606A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnovers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gertlisen, Macy E.
APPLICANT: Goddard, Audrey
APPLICANT: Gonsky, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gutney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2630PIC11
CURRENT APPLICATION NUMBER: US/09/978,295A
CURRENT FILING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/064249
PRIOR FILING DATE: 1997-11-03
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066364
PRIOR FILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: 60/077450
PRIOR FILING DATE: 1998-03-10
PRIOR APPLICATION NUMBER: 60/077632
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077641
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077649
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077791
PRIOR FILING DATE: 1998-03-12
PRIOR APPLICATION NUMBER: 60/078004
PRIOR FILING DATE: 1998-03-13
PRIOR APPLICATION NUMBER: 60/078886
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/078936
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/078939
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/079294
PRIOR FILING DATE: 1998-03-25
PRIOR APPLICATION NUMBER: 60/079656
PRIOR FILING DATE: 1998-03-26
PRIOR APPLICATION NUMBER: 60/079664
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/079689
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/079663
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/079728
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/079786
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/079920
PRIOR FILING DATE: 1998-03-30
PRIOR APPLICATION NUMBER: 60/079923
PRIOR FILING DATE: 1998-03-30
PRIOR APPLICATION NUMBER: 60/080105
PRIOR FILING DATE: 1998-03-31
PRIOR APPLICATION NUMBER: 60/080107
PRIOR FILING DATE: 1998-03-31
PRIOR APPLICATION NUMBER: 60/080165
PRIOR FILING DATE: 1998-03-31
PRIOR APPLICATION NUMBER: 60/080194
PRIOR FILING DATE: 1998-03-31
PRIOR APPLICATION NUMBER: 60/080327
PRIOR FILING DATE: 1998-04-01
PRIOR APPLICATION NUMBER: 60/080328
PRIOR FILING DATE: 1998-04-01
PRIOR APPLICATION NUMBER: 60/080333
PRIOR FILING DATE: 1998-04-01
PRIOR APPLICATION NUMBER: 60/080334
PRIOR FILING DATE: 1998-04-01
PRIOR APPLICATION NUMBER: 60/081070
PRIOR FILING DATE: 1998-04-08
PRIOR APPLICATION NUMBER: 60/081049
PRIOR FILING DATE: 1998-04-08
PRIOR APPLICATION NUMBER: 60/081071
PRIOR FILING DATE: 1998-04-08
PRIOR APPLICATION NUMBER: 60/081195
PRIOR FILING DATE: 1998-04-08
PRIOR APPLICATION NUMBER: 60/081203
PRIOR FILING DATE: 1998-04-09
PRIOR APPLICATION NUMBER: 60/081229
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PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085704
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085697

Query Match 57.5%; Score 42; DB 10; Length 345;
Best Local Similarity 42.9%; Pred. No. 11;
Matches 6; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 2 DRVSIRTRGQIHS 15
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Db 47 ERITVSTNGSIHS 60

RESULT 13
US-09-852-209A-3
; Sequence 3, Application US/09852209A
; Patent No. US20020164687A1
; GENERAL INFORMATION:
; APPLICANT: ERIKSSON, ULF

APPLICANT: AASE, Karin
APPLICANT: LEE, Xuri
APPLICANT: PONTEN, Annica
APPLICANT: TUTELA, Marko
APPLICANT: ALITALO, Kari
APPLICANT: OESTMAN, Arne
APPLICANT: HELDIN, Carl-Henrik
APPLICANT: BETHSHOLTZ, Christer
TITLE OF INVENTION: PLATELET-DERIVED GROWTH FACTOR C, DNA CODING
FILE REFERENCE: 09-410349-ERIKSSON et al-1064-44740
CURRENT APPLICATION NUMBER: 05/09/852, 209A
PRIOR FILING DATE: 2001-05-10
PRIOR APPLICATION NUMBER: 09/410,349
PRIOR FILING DATE: 1999-09-30
PRIOR APPLICATION NUMBER: 60/110,749
PRIOR FILING DATE: 1998-12-03
PRIOR APPLICATION NUMBER: 60/113,002
PRIOR FILING DATE: 1998-12-18
PRIOR APPLICATION NUMBER: 60/135,426
PRIOR FILING DATE: 1999-05-21
PRIOR APPLICATION NUMBER: 60/144,022
PRIOR FILING DATE: 1999-07-15
NUMBER OF SEQ ID NOS: 39
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 3
LENGTH: 345
TYPE: PRT
ORGANISM: Homo sapiens
US-09-852-209A-3

Query Match 57.5%; Score 42; DB 10; Length 345;
Best Local Similarity 42.9%; Pred. No. 11;
Matches 6; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 2 DRVSIRTRGQIHS 15
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Db 47 ERITVSTNGSIHS 60

RESULT 14
US-09-978-697-488
; Sequence 488, Application US/09978697
; Patent No. US20020169284A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerlitsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kijavlin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James.
; APPLICANT: Paonl, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2630PIC27
CURRENT APPLICATION NUMBER: US/09/978,697
CURRENT FILING DATE: 2001-10-16
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
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Query Match 57.5%; Score 42; DB 10; Length 345;
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Matches 6; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

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RESULT 15
US-09-978-192A-488
; Sequence 488, Application US/09978192A
; Patent No. US20020177553A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferreira, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Garber, Hanspeter
; APPLICANT: Gerltsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kijavlin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630PIC9
; CURRENT APPLICATION NUMBER: US/09/978,192A
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
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PRIOR APPLICATION NUMBER: 60/085580
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Query Match 57.5%; Score 42; DB 10; Length 345;
Best Local Similarity 42.9%; Pred. No. 11;
Matches 6; Conservative 5; Mismatches 3; Indels 0; Gaps 0;
Oy 2 DRYVIRTRGOIHS 15
Db 47 ERITVSTNGSIHS 60
RESULT 16
US-09-832A-488
Sequence 488, Application US/09999832A
Publication No. US70020192706A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Bostein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eylon, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Grimsdahl, Paul J.
APPLICANT: Godowski, Audrey
APPLICANT: Grimsdahl, J. Christopher
APPLICANT: Gunney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kijavlin, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P4630PIC63
CURRENT APPLICATION NUMBER: US/09/999,832A
PRIOR FILING DATE: 2001-10-24
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PRIOR FILING DATE: 1997-10-17
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; PRIOR APPLICATION NUMBER: 60/085697

Query Match      57.5%: Score 42; DB 10; Length 345;
Best Local Similarity 42.9%; Pred. No. 11;
Matches 6; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

OY      2 DLVSTSTGSHS 15
DB      47 ERTTSTGSHS 60

RESULT 17
US-09-978-189-488
; Sequence 488, Application US/09978189
; Publication No. US2003004102A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Bolstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillman, Kenneth J.
; APPLICANT: Kijavlin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; TITLE OR INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P63091C7
; CURRENT APPLICATION NUMBER: US/09/978,189
; PRIOR FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/064249
; PRIOR FILING DATE: 1997-11-03
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
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; PRIOR APPLICATION NUMBER: 60/077450
; PRIOR FILING DATE: 1998-03-10
; PRIOR APPLICATION NUMBER: 60/077632
; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/077641
; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/077649

; PRIOR FILING DATE: 1998-03-11
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; PRIOR FILING DATE: 1998-04-21
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;; PRIOR APPLICATION NUMBER: 60/085580
;; PRIOR FILING DATE: 1998-05-15
;; PRIOR APPLICATION NUMBER: 60/085573
;; PRIOR FILING DATE: 1998-05-15
;; PRIOR APPLICATION NUMBER: 60/085704

;; PRIOR FILING DATE: 1998-05-15
;; PRIOR APPLICATION NUMBER: 60/085697
Query Match 57.5%; Score 42; DB 11; Length 345;
Best Local Similarity 42.9%; Pred. No. 11;
Matches 6; Conservative 5; Mismatches 3; Indels 0; Gaps 0;
Qy 2 DRVSIRTRGQIHS 15
Db 47 ERITVSTNGSIHS 60
RESULT 18
US-09-796-753-6
; Sequence 6, Application US/09796753
; Publication No. US20030027998A1
; GENERAL INFORMATION:
; APPLICANT: McCarthy, Sean A.
; TITLE OF INVENTION: SECRETED PROTEINS AND USES THEREOF
; FILE REFERENCE: 7853-227-999
; CURRENT APPLICATION NUMBER: US/09/796,753
; PRIOR FILING DATE: 2001-03-01
; PRIOR APPLICATION NUMBER: 09/183,175
; PRIOR FILING DATE: 1998-10-30
; PRIOR APPLICATION NUMBER: 09/223,094
; PRIOR FILING DATE: 1998-12-30
; PRIOR APPLICATION NUMBER: 09/223,546
; PRIOR FILING DATE: 1998-12-30
; PRIOR APPLICATION NUMBER: 09/224,246
; PRIOR FILING DATE: 1998-12-30
; PRIOR APPLICATION NUMBER: 09/259,388
; PRIOR FILING DATE: 1999-02-26
; PRIOR APPLICATION NUMBER: 60/122,458
; PRIOR FILING DATE: 1999-03-01
; PRIOR APPLICATION NUMBER: 09/312,359
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; PRIOR APPLICATION NUMBER: 09/336,536
; PRIOR FILING DATE: 1999-06-18
; PRIOR APPLICATION NUMBER: 09/342,687
; PRIOR FILING DATE: 1999-06-29
; PRIOR APPLICATION NUMBER: 09/345,464
; PRIOR FILING DATE: 1999-06-30
; PRIOR APPLICATION NUMBER: 09/365,164
; PRIOR FILING DATE: 1999-07-30
; PRIOR APPLICATION NUMBER: 09/399,723
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; PRIOR APPLICATION NUMBER: 09/409,634
; PRIOR FILING DATE: 1999-09-30
; PRIOR APPLICATION NUMBER: 09/471,179
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; PRIOR APPLICATION NUMBER: 09/572,002
; PRIOR FILING DATE: 2000-05-14
; PRIOR APPLICATION NUMBER: 09/597,993
; PRIOR FILING DATE: 2000-06-19
; PRIOR APPLICATION NUMBER: 09/599,596
; PRIOR FILING DATE: 2000-06-22
; PRIOR APPLICATION NUMBER: 09/630,334
; PRIOR FILING DATE: 2000-07-31
; PRIOR APPLICATION NUMBER: 09/606,565
; PRIOR FILING DATE: 2000-06-29
; PRIOR APPLICATION NUMBER: 09/606,317
; PRIOR FILING DATE: 2000-06-29
; PRIOR APPLICATION NUMBER: 09/665,666
; PRIOR FILING DATE: 2000-09-20
; PRIOR APPLICATION NUMBER: 09/677,751

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; PRIOR FILING DATE: 2000-09-30
; NUMBER OF SEQ ID NOS: 162
; SEQ ID NO 6
; LENGTH: 345
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-796-753-6
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Query Match          57.5%; Score 42; DB 11; Length 345;
Best Local Similarity 42.9%; Pred. No. 11;
Matches 6; Conservative 5; Mismatches 3; Indels 0; Gaps 0;
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OY      2 DRLVSIRTRGOIHS 15
        :|:::| | | | |
Db      47 ERITVSTNGSIHS 60
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RESULT 19

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US-09-978-608A-488
; Sequence 488, Application US/09978608A
; Publication No. US20030045462A1
; GENERAL INFORMATION:
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; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Bolstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kijavlin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630PIC22
; CURRENT APPLICATION NUMBER: US/09/978,608A
; CURRENT FILING DATE: 2001-10-16
; NUMBER OF SEQ ID NOS: 624
; Prior Application removed - See File Wrapper or Palm
; SEQ ID NO 488
; LENGTH: 345
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-978-608A-488
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Query Match          57.5%; Score 42; DB 11; Length 345;
Best Local Similarity 42.9%; Pred. No. 11;
Matches 6; Conservative 5; Mismatches 3; Indels 0; Gaps 0;
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OY      2 DRLVSIRTRGOIHS 15
        :|:::| | | | |
Db      47 ERITVSTNGSIHS 60
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RESULT 20
US-09-978-585A-488
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; Sequence 488, Application US/09978585A
; Publication No. US20030049633A1
; GENERAL INFORMATION:
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; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Bolstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kijavlin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630PIC15
; CURRENT APPLICATION NUMBER: US/09/978,585A
; CURRENT FILING DATE: 2001-10-16
; NUMBER OF SEQ ID NOS: 624
; Prior Application removed - See File Wrapper or Palm
; SEQ ID NO 488
; LENGTH: 345
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-978-585A-488
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Query Match          57.5%; Score 42; DB 11; Length 345;
Best Local Similarity 42.9%; Pred. No. 11;
Matches 6; Conservative 5; Mismatches 3; Indels 0; Gaps 0;
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OY      2 DRLVSIRTRGOIHS 15
        :|:::| | | | |
Db      47 ERITVSTNGSIHS 60
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RESULT 21

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US-09-978-191A-488
; Sequence 488, Application US/09978191A
; Publication No. US20030050239A1
; GENERAL INFORMATION:
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; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Bolstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
```

APPLICANT: Kljavin, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James;
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2630P1C4
CURRENT APPLICATION NUMBER: US/09/978,191A
CURRENT FILING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
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PRIOR APPLICATION NUMBER: 60/064249
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PRIOR FILING DATE: 1998-05-06
PRIOR APPLICATION NUMBER: 60/084441
PRIOR FILING DATE: 1998-05-06

Wed Sep 3 13:06:21 2003

us-09-830-876-1_1.rapb

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PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085573
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085704
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085697

Query Match      57.5%  Score 42;  DB 11;  Length 345;
Best Local Similarly 42.9%  Pred. No. 11;
Matches 6;  Conservative 5;  Mismatches 3;  Indels 0;  Gaps 0;

QY      2 DRLVSIRTRQOIH 15
:|:::|111
Db      47 ERIIVTNGSIHS 60

RESULT 22
US-09-978-403A-488
: Sequence 488, Application US/09978403A
: Publication No. US20030050240A1
: GENERAL INFORMATION:
: APPLICANT: Ashkenazi, Avi
: APPLICANT: Baker Kevin P.
: APPLICANT: Botstein, David
: APPLICANT: Desnovers, Luc
: APPLICANT: Eaton, Dan
: APPLICANT: Ferrara, Napoleon
: APPLICANT: Filvaroff, Ellen
: APPLICANT: Fong, Sherman
: APPLICANT: Gao, Wei-Qiang
: APPLICANT: Gerber, Hanspeter
: APPLICANT: Gertsen, Mary E.
: APPLICANT: Goddard, Audrey J.
: APPLICANT: Godowski, Paul Christopher
: APPLICANT: Gurley, Austin L.
: APPLICANT: Hillan, Kenneth J.
: APPLICANT: Kijavich, Iva J.
: APPLICANT: Kuo, Sophia S.
: APPLICANT: Napier, Mary A.
: APPLICANT: Pan, James Nicholas F.
: APPLICANT: Paoni, Nicholas Ann
: APPLICANT: Roy, Margaret Ann
: APPLICANT: Shelton, David L.
```

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APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William T.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2630P1C17 US/09/978,403A
CURRENT FILING DATE: 2002-03-19
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
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PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085573
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085704
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085697

Query Match 57.5%; Score 42; DB 11; Length 345;
Best Local Similarity 42.9%; Pred. No. 11;
Matches 6; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 2 DRLVSIRTRQIHS 15
Db 47 ERITVSTNGSIHS 60

RESULT 23
US-09-978-564A-488
Sequence 488, Application US/09978564A
Publication No. US2003050241A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
APPLICANT: Baker, Kevin P.
APPLICANT: Bolstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gunney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kijavlin, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paonli, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2630P1C25

1	CURRENT APPLICATION NUMBER: US/09/9718.5644	1	PRIOR FILING DATE: 1998-04-08
2	PRIOR FILING DATE: 2001-10-16	2	PRIOR APPLICATION NUMBER: 60/081203
3	PRIOR APPLICATION NUMBER: 09/918585	3	PRIOR FILING DATE: 1998-04-09
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5	PRIOR APPLICATION NUMBER: 60/062250	5	PRIOR FILING DATE: 1998-04-09
6	PRIOR FILING DATE: 1997-10-17	6	PRIOR APPLICATION NUMBER: 60/081955
7	PRIOR APPLICATION NUMBER: 60/064249	7	PRIOR FILING DATE: 1998-04-15
8	PRIOR FILING DATE: 1997-11-03	8	PRIOR APPLICATION NUMBER: 60/081817
9	PRIOR APPLICATION NUMBER: 60/065311	9	PRIOR FILING DATE: 1998-04-15
10	PRIOR FILING DATE: 1997-11-13	10	PRIOR APPLICATION NUMBER: 60/081819
11	PRIOR APPLICATION NUMBER: 60/066364	11	PRIOR FILING DATE: 1998-04-15
12	PRIOR FILING DATE: 1997-11-21	12	PRIOR APPLICATION NUMBER: 60/081952
13	PRIOR APPLICATION NUMBER: 60/077450	13	PRIOR FILING DATE: 1998-04-15
14	PRIOR FILING DATE: 1998-03-10	14	PRIOR APPLICATION NUMBER: 60/081838
15	PRIOR APPLICATION NUMBER: 60/077632	15	PRIOR FILING DATE: 1998-04-15
16	PRIOR FILING DATE: 1998-03-11	16	PRIOR APPLICATION NUMBER: 60/082568
17	PRIOR APPLICATION NUMBER: 60/077641	17	PRIOR FILING DATE: 1998-04-21
18	PRIOR FILING DATE: 1998-03-11	18	PRIOR APPLICATION NUMBER: 60/082569
19	PRIOR APPLICATION NUMBER: 60/077649	19	PRIOR FILING DATE: 1998-04-21
20	PRIOR FILING DATE: 1998-03-11	20	PRIOR APPLICATION NUMBER: 60/082704
21	PRIOR APPLICATION NUMBER: 60/077791	21	PRIOR FILING DATE: 1998-04-22
22	PRIOR FILING DATE: 1998-03-12	22	PRIOR APPLICATION NUMBER: 60/082804
23	PRIOR APPLICATION NUMBER: 60/078004	23	PRIOR FILING DATE: 1998-04-22
24	PRIOR FILING DATE: 1998-03-13	24	PRIOR APPLICATION NUMBER: 60/082700
25	PRIOR APPLICATION NUMBER: 60/078886	25	PRIOR FILING DATE: 1998-04-22
26	PRIOR FILING DATE: 1998-03-20	26	PRIOR APPLICATION NUMBER: 60/082797
27	PRIOR APPLICATION NUMBER: 60/078936	27	PRIOR FILING DATE: 1998-04-22
28	PRIOR FILING DATE: 1998-03-20	28	PRIOR APPLICATION NUMBER: 60/082796
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31	PRIOR APPLICATION NUMBER: 60/078939	31	PRIOR FILING DATE: 1998-04-27
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34	PRIOR FILING DATE: 1998-03-25	34	PRIOR APPLICATION NUMBER: 60/083392
35	PRIOR APPLICATION NUMBER: 60/079656	35	PRIOR FILING DATE: 1998-04-29
36	PRIOR FILING DATE: 1998-03-26	36	PRIOR APPLICATION NUMBER: 60/083435
37	PRIOR APPLICATION NUMBER: 60/079664	37	PRIOR FILING DATE: 1998-04-29
38	PRIOR FILING DATE: 1998-03-27	38	PRIOR APPLICATION NUMBER: 60/083499
39	PRIOR APPLICATION NUMBER: 60/079689	39	PRIOR FILING DATE: 1998-04-29
40	PRIOR FILING DATE: 1998-03-27	40	PRIOR APPLICATION NUMBER: 60/083545
41	PRIOR APPLICATION NUMBER: 60/079663	41	PRIOR FILING DATE: 1998-04-29
42	PRIOR FILING DATE: 1998-03-27	42	PRIOR APPLICATION NUMBER: 60/083554
43	PRIOR APPLICATION NUMBER: 60/079728	43	PRIOR FILING DATE: 1998-04-29
44	PRIOR FILING DATE: 1998-03-27	44	PRIOR APPLICATION NUMBER: 60/083558
45	PRIOR APPLICATION NUMBER: 60/079786	45	PRIOR FILING DATE: 1998-04-29
46	PRIOR FILING DATE: 1998-03-27	46	PRIOR APPLICATION NUMBER: 60/083559
47	PRIOR APPLICATION NUMBER: 60/079920	47	PRIOR FILING DATE: 1998-04-29
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49	PRIOR APPLICATION NUMBER: 60/079923	49	PRIOR FILING DATE: 1998-04-29
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51	PRIOR APPLICATION NUMBER: 60/080105	51	PRIOR FILING DATE: 1998-04-30
52	PRIOR FILING DATE: 1998-03-31	52	PRIOR APPLICATION NUMBER: 60/084366
53	PRIOR APPLICATION NUMBER: 60/080107	53	PRIOR FILING DATE: 1998-05-05
54	PRIOR FILING DATE: 1998-03-31	54	PRIOR APPLICATION NUMBER: 60/084414
55	PRIOR APPLICATION NUMBER: 60/080165	55	PRIOR FILING DATE: 1998-05-06
56	PRIOR FILING DATE: 1998-03-31	56	PRIOR APPLICATION NUMBER: 60/084639
57	PRIOR APPLICATION NUMBER: 60/080194	57	PRIOR FILING DATE: 1998-05-07
58	PRIOR FILING DATE: 1998-03-31	58	PRIOR APPLICATION NUMBER: 60/084639
59	PRIOR APPLICATION NUMBER: 60/080327	59	PRIOR FILING DATE: 1998-05-07
60	PRIOR FILING DATE: 1998-04-01	60	PRIOR APPLICATION NUMBER: 60/084660
61	PRIOR APPLICATION NUMBER: 60/080328	61	PRIOR FILING DATE: 1998-05-07
62	PRIOR FILING DATE: 1998-04-01	62	PRIOR APPLICATION NUMBER: 60/084660
63	PRIOR APPLICATION NUMBER: 60/080333	63	PRIOR FILING DATE: 1998-05-07
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PRIOR APPLICATION NUMBER: 60/085339
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PRIOR APPLICATION NUMBER: 60/085323
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PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085579
PRIOR FILING DATE: 1998-05-15
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Query Match 57.5%; Score 42; DB 11; Length 345;
Best Local Similarity 42.9%; Pred. No. 11;
Matches 6; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

Oy 2 DRVSIRTCQIHS 15
: : : : :
Db 47 ERITVSTNGSIHS 60

RESULT 24
US-09-999-833A-488

Sequence 488, Application US/09999833A
Publication No. US20030054405A1

GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Bolstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paonli, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2630PIC65
CURRENT FILING DATE: 2001-10-24
CURRENT APPLICATION NUMBER: US/09/999,833A
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/064249

PRIOR FILING DATE: 1997-11-03
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DB      47 ERLIVSTNGSIHS 60

RESULT 26
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; Publication No. US20030055216A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Bolstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gertsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kijaviv, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Raoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tamas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630PIC14
; CURRENT APPLICATION NUMBER: US/09/978, 824
; PRIOR FILING DATE: 2001-10-17
; PRIOR APPLICATION NUMBER: 09/918585
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Query Match 57.5%; Score 42; DB 11; Length 345;
Best Local Similarity 42.9%; Pred. No. 11;
Matches 6; Conservative 5; Mismatches 3; Indels 0; Gaps 0;
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Db 47 ERITVSTNGSIHS 60
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; Publication No. US20030060406A1
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; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Fillvaroff, Ellen
; APPLICANT: Fonzy, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerlitsen, Mary E.
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; APPLICANT: Gurney, Austin L.
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; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630P1C1
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PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/086023

Query Match 57.5%; Score 42; DB 11; Length 345;
Best Local Similarity 42.9%; Pred. No. 11;
Matches 6; Conservative 5; Mismatches 3; Indels 0; Caps 0;

0Y 2 DRVSIRRGQIHS 15
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Db 47 ERITVSTNGSIHS 60

RESULT 28
US-09-978-423A-488
Sequence 488, Application US/09978423A
Publication NO. US20030069178A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gottlieb, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Grimaldi, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kijavich, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James;
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OR INVENTION: Acids Encoding the Same
FILE REFERENCE: P2630PIC21
CURRENT APPLICATION NUMBER: US/09/978, 423A
CURRENT FILING DATE: 2002-05-16
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/064249
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Query Match      57.5%; Score 42; DB 11; Length 345;
Best Local Similarity 42.9%; Pred. NO. 11;
Matches      6; Conservative      5; Mismatches      3; Indels      0; Gaps      0;

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Db      47 ERLIVSTNGSIHS 60

RESULT 29
US-09-978-193A-488
; Sequence 488, Application US/09978193A
; Publication No. US20030073624A1

: GENERAL INFORMATION:
: APPLICANT: Ashkenazi, Avi
: APPLICANT: Baker Kevin P.
: APPLICANT: Botstein, David
: APPLICANT: Desnoyers, Luc
: APPLICANT: Eaton, Dan
: APPLICANT: Ferrara, Napoleon
: APPLICANT: Flivauff, Ellen
: APPLICANT: Fonq, Sherman
: APPLICANT: Geo, Wei-Qiang
: APPLICANT: Gerder, Hanspeter
: APPLICANT: Gertlisen, Mary E.
: APPLICANT: Goddard, Audrey
: APPLICANT: Godowski, Paul J.
: APPLICANT: Grimaldi, J. Christopher
: APPLICANT: Gurney, Austin L.
: APPLICANT: Hillan, Kenneth J.
: APPLICANT: Kijavlin, Ivar J.
: APPLICANT: Kuo, Sophia S.
: APPLICANT: Napier, Mary A.
: APPLICANT: Pan, James;
: APPLICANT: Paoul, Nicholas F.
: APPLICANT: Roy, Margaret Ann
: APPLICANT: Shelton, David L.
: APPLICANT: Stewart, Timothy A.
: APPLICANT: Tumas, Daniel
: APPLICANT: Williams, P. Mickey
: APPLICANT: Wood, William I.
: TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
: FILE REFERENCE: P2630P16
: CURRENT APPLICATION NUMBER: US/09/978,193A
: PRIOR FILING DATE: 2002-02-21
: PRIOR APPLICATION NUMBER: 09/918585
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Query Match 57.5%; Score 42; DB 11; Length 345;
 Best Local Similarity 42.9%; Pred. No. 11;
 Matches 6; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 2 DRLVSIRTRGQIHS 15
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RESULT 30
 US-09-999-830A-488
 ; Sequence 488, Application US/09999830A
 ; Publication No. US20030077700A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ashkenazi, Avi
 ; APPLICANT: Baker Kevin P.
 ; APPLICANT: Bolstein, David
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Eaton, Dan
 ; APPLICANT: Ferrara, Napoleon

APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gunney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kiljavin, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James;
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2630P1C70
CURRENT APPLICATION NUMBER: US/09/999,830A
PRIOR FILING DATE: 2001-08-31
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
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PRIOR APPLICATION NUMBER: 60/077641
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PRIOR APPLICATION NUMBER: 60/078004
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PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085697

Query Match

57.5%; Score 42; DB 11; Length 345;

Best Local Similarity 42.9%; Pred. No. 11;

Matches 6; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

Oy 2 DRLVSIPTRGQIHS 15
: : : : : | | | | |
DB 47 ERITVSTNGSIHS 60

Search completed: August 29, 2003, 18:47:45
Job time : 26.5714 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 29, 2003, 18:44:06 ; Search time 15.4286 Seconds
(without alignments)
93.497 Million cell updates/sec

Title: US-09-830-876-1

Perfect score: 73
Sequence: 1 IDRLVSIIRRGQIHS 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database :
1: pir1:**
2: pir2:**
3: pir3:**
4: pir4:**

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	58	79.5	429 1	JE0406
2	54	74.0	153 2	alpha-amylose (BC
3	54	74.0	427 1	ALBHB
4	51	69.9	135 2	alpha-amylose (BC
5	45	61.6	365 2	A69593
6	45	61.6	428 2	S10013
7	45	61.6	434 2	S12775
8	44	60.3	458 2	G86601
9	44	60.3	458 2	E72023
10	42	57.5	151 2	D87683
11	42	57.5	151 2	C90464
12	40	54.8	141 2	AR2812
13	40	54.8	141 2	B97591
14	40	54.8	246 2	E74581
15	39	53.4	443 2	SS9771
16	39	53.4	445 2	A56043
17	39	53.4	446 2	I49021
18	39	53.4	446 2	I59354
19	39	53.4	447 2	I38975
20	39	53.4	461 2	JC4014
21	39	53.4	585 2	S54506
22	39	53.4	1738 2	S54506
23	38	52.1	1373 2	B81407
24	38	52.1	223 2	S46537
25	38	52.1	319 2	H36792
26	38	52.1	368 2	JS0409
27	37	50.7	118 2	JE0398
28	37	50.7	119 2	S77863
29	37	50.7	142 2	AH3349

30	37	50.7	251 2	J01722
31	37	50.7	258 2	T36303
32	37	50.7	283 2	S41412
33	37	50.7	337 1	PAPGF
34	37	50.7	363 2	A31342
35	37	50.7	383 1	AIKROC
36	37	50.7	412 2	C96789
37	37	50.7	444 2	T50931
38	37	50.7	450 2	B70506
39	37	50.7	475 2	S34511
40	37	50.7	566 2	S64005
41	37	50.7	574 2	T16328
42	37	50.7	615 2	A83188
43	37	50.7	647 2	T49586
44	37	50.7	1804 2	S56247
45	37	50.7	2514 2	T37320
46	37	50.7	2619 2	T24588
47	36.5	50.0	250 2	G87404
48	36	49.3	83 2	G87393
49	36	49.3	232 2	T51408
50	36	49.3	253 2	J02255
51	36	49.3	257 2	G72648
52	36	49.3	267 2	F22794
53	36	49.3	283 2	T43146
54	36	49.3	292 2	D71364
55	36	49.3	319 2	C72406
56	36	49.3	319 2	AC1271
57	36	49.3	319 2	AE1633
58	36	49.3	331 2	C95998
59	36	49.3	353 2	D69001
60	36	49.3	438 2	S14957
61	36	49.3	511 1	S55198
62	36	49.3	546 1	C70393
63	36	49.3	572 2	T34658
64	36	49.3	591 2	T45713
65	36	49.3	600 2	F84129
66	36	49.3	639 2	S20867
67	36	49.3	639 2	AE1190
68	36	49.3	740 2	B30338
69	36	49.3	749 2	A82089
70	36	49.3	1195 2	E96615
71	36	49.3	2110 2	B44110
72	36	49.3	2111 2	A70668
73	35	47.9	119 1	R58517
74	35	47.9	193 2	D75331
75	35	47.9	207 2	H90339
76	35	47.9	229 2	T15359
77	35	47.9	272 2	T47354
78	35	47.9	298 2	A41381
79	35	47.9	315 2	A95412
80	35	47.9	337 2	S70469
81	35	47.9	338 2	A46666
82	35	47.9	379 2	AF0137
83	35	47.9	392 2	T45204
84	35	47.9	404 2	S57178
85	35	47.9	404 2	AB1832
86	35	47.9	532 2	JN0084
87	35	47.9	862 2	S30911
88	35	47.9	960 1	A39651
89	35	47.9	1259 2	JC5523
90	35	47.9	2311 2	T06161
91	35	47.9	2325 2	T02235
92	35	47.9	2831 2	T31419
93	35	47.9	2867 2	AC3481
94	34.5	47.3	814 2	T32223
95	34	46.6	120 1	F32207
96	34	46.6	120 1	T44411
97	34	46.6	128 2	H95027
98	34	46.6	128 2	H97898
99	34	46.6	153 2	S73561
100	34	46.6	159 2	E81726

3b protein - canin
probable indolegly
tetracycloroxymaph
fructose-bisphosph
fructose-bisphosph
alpha-amylose (BC
protein T23218.6
hypothetical prote
hypothetical prote
hypothetical prote
hypothetical prote
hypothetical prote
related to nif-spe
probable membrane
ataxia telangiecta
hypothetical prote
ribosomal protein
acyl carrier prote
hypothetical prote
triose-phosphate 1
hypothetical prote
tryptophan synthas
hypothetical prote
probable rRNA meth
6-phosphofructokin
hypothetical prote
probable sugar apt
conserved hypothet
alpha-amylose (BC
sulfate adenylyl-
probable adenylyl-
hypothetical prote
hypothetical prote
probable histidine
actin-assembly and
hypothetical prote
hypothetical prote
mycoerostate synth
mycoerostate synth
ribosomal protein
probable general s
drup-4-dehydroham
hypothetical prote
alcohol dehydrogen
beta-lactamase (BC
probable histidine
fructose-bisphosph
cytochrome D ubiq
probable sugar ABC
2-nitropropane dio
hypothetical prote
phytoene dehydroge
SMP2 protein - yea
disac-large tumor
transmembrane prot
acetyl-CoA carboxy
cyclic beta 1-2 gl
cellulobiose-phospho
hypothetical prote
ribosomal protein
ribosomal protein
50S ribosomal prot
hypothetical prote
conserved hypothet

ALIGNMENTS

```

RESULT 1
JE0406
alpha-amylase (EC 3.2.1.1) B precursor (gene Amy56 and others) - barley
N:Alternate names: 1,4-alpha-D-glucan glucanohydrolase
C:Species: Hordeum vulgare (barley)
C>Date: 17-Apr-1993 #sequence_revision 21-Jan-1997 #text_change 18-Jun-1999
C:Accession: JE0406; B30759; S06275; B31960; B21826
R:Rahmatullah, R.J.; Huang, J.K.; Clark, K.L.; Reeck, G.R.; Chandra, G.R.; Muthukrishnan
Plant Mol. Biol. 12, 119-121, 1989
A:Title: Nucleotide and predicted amino acid sequences of two different genes for high-E
A:Reference number: JE0405
A:Accession: JE0406
A:Molecule type: DNA
A:Residues: 1-429 <RAH>
A:Cross-references: EMBL:X15227; NID:g18899; PIDN:CAA33299.1; PID:g295805
A:Experimental source: gene Amy56 for alpha-amylase
A:Genetics: A36
R:Rogers, J.C.
submitted to GenBank, September 1988
A:Accession: B30759
A:Reference number: A94535
A:Status: not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-104,'G',106-154,'A',156-160,'PD',163,'G',167-196,'V',198-342,'T',344-392,'
A:Cross-references: GB:J04202; NID:g166984; PIDN:AAA98615.1; PID:g166985
A:Experimental source: cv. Himalaya gene Amy46 for alpha-amylase B
A:Genetics: A46
R:Knox, C.A.P.; Sonthayanon, B.; Chandra, G.R.; Muthukrishnan, S.
Plant Mol. Biol. 9, 3-17, 1987
A:Title: Structure and organization of two divergent alpha-amylase genes from barley.
A:Reference number: S06275
A:Accession: S06275
A:Molecule type: DNA
A:Residues: 1-11,'LI',14-32,'S',34-57,'I',59-79,'Y',81-139,'R',141-160,'PA',163-164,'R',
A:Cross-references: EMBL:M7125; NID:g166978; PIDN:AAA32926.1; PID:g166979
A:Experimental source: cv. Sundance gene for alpha-amylase 1 precursor (clone p141.117)
A:Genetics: A41
A:Note: the authors translated the codon TCG for residue 33 as Trp
R:Khurshed, B.; Rogers, J.C.
J. Biol. Chem. 263, 18953-18960, 1988
A:Title: Barley alpha amylase genes. Quantitative comparison of steady-state mRNA levels
A:Reference number: A92700; MUID:89066591; PMID:3264283
A:Accession: B31960
A:Status: not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-51 <KHD>
A:Experimental source: strain Himalaya gene Amy46 for alpha-amylase B precursor
R:Huang, J.K.; Sweigle, M.; Dandekar, A.M.; Muthukrishnan, S.
J. Mol. Appl. Genet. 2, 579-588, 1984
A:Reference number: A92837; MUID:85159405; PMID:6335720
A:Accession: B21826
A:Molecule type: mRNA
A:Residues: 379-389,'T',391-392,'D',394-429 <HUA>
A:Cross-references: GB:K02636; NID:g166992; PIDN:AAA32932.1; PID:g166993
A:Experimental source: cv. Himalaya aleurone cell mRNA (clone 96 for alpha-amylase B)
C:Genetics: <A56>
A:Gene: Amy56
A:Introns: 29/3; 346/3
C:Genetics: <A46>
A:Gene: Amy46
C:Genetics: <AA1>
A:Gene: Amy1
A:Map position: 6
A:Introns: 29/3; 346/3
C:Function:
A:Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
A:Pathway: glycogen/starch degradation
C:Superfamily: wheat alpha-amylase; alpha-amylase core homology
C:Keywords: aleurone cell; germination; glycosidase; hydrolase; polysaccharide degradati
F:173-318/Domain: alpha-amylase core homology <AMY>

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F:205,230,315/Active site: Asp, Glu, Asp #status predicted
Query Match 79.5%; Score 58; DB 1; Length 429;
Best Local Similarity 86.7%; Pred. No. 0.0062;
Matches 13; Conservativity 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 IDRLVSIRTRGQIHS 15
DB 360 IDRLVSIRTRGQIHS 374

RESULT 2
A21826
alpha-amylase (EC 3.2.1.1) (clone 103) - barley (fragment)
N:Alternate names: 1,4-alpha-D-glucan glucanohydrolase
C:Species: Hordeum vulgare (barley)
C>Date: 05-Jun-1987 #sequence_revision 05-Jun-1987 #text_change 22-Jun-1999
C:Accession: A21826
R:Huang, J.K.; Sweigle, M.; Dandekar, A.M.; Muthukrishnan, S.
J. Mol. Appl. Genet. 2, 579-588, 1984
A:Reference number: A92837; MUID:85159405; PMID:6335720
A:Accession: A21826
A:Molecule type: mRNA
A:Residues: 1-153 <HUA>
A:Cross-references: GB:M10056; NID:g166988; PIDN:AAA32930.1; PID:g166989
C:Function:
A:Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
A:Pathway: glycogen/starch degradation
C:Superfamily: wheat alpha-amylase; alpha-amylase core homology
C:Keywords: aleurone cell; carbohydrate metabolism; germination; glycosidase; hydrola

Query Match 74.0%; Score 54; DB 2; Length 153;
Best Local Similarity 73.3%; Pred. No. 0.011;
Matches 11; Conservativity 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 IDRLVSIRTRGQIHS 15
DB 84 IDRLVSIRTRGQIHS 98

RESULT 3
ALBHB
alpha-amylase (EC 3.2.1.1) B precursor 6-4 - barley
N:Alternate names: 1,4-alpha-D-glucan glucanohydrolase; alpha-amylase 2
C:Species: Hordeum vulgare (barley)
C>Date: 30-Jun-1987 #sequence_revision 01-Sep-1995 #text_change 18-Jun-1999
C:Accession: A31960; A00847; JE0405; A26267; A24457; A30759
R:Khurshed, B.; Rogers, J.C.
J. Biol. Chem. 263, 18953-18960, 1988
A:Title: Barley alpha-amylase genes. Quantitative comparison of steady-state mRNA lev
A:Reference number: A92700; MUID:89066591; PMID:3264283
A:Accession: A31960
A:Molecule type: DNA
A:Residues: 1-427 <KHD>
A:Cross-references: GB:J04202
A:Experimental source: cv. Himalaya; gene Amy6-4
R:Rogers, J.C.
J. Biol. Chem. 260, 3731-3738, 1985
A:Title: Two barley alpha-amylase gene families are regulated differently in aleurone
A:Reference number: A00847; MUID:85131184; PMID:3871776
A:Accession: A00847
A:Molecule type: mRNA
A:Residues: 1-133,'D',135-194,'HRL',198-424,'Q',426-427 <ROG>
A:Experimental source: seed
R:Rahmatullah, R.J.; Huang, J.K.; Clark, K.L.; Reeck, G.R.; Chandra, G.R.; Muthukrish
Plant Mol. Biol. 12, 119-121, 1989
A:Title: Nucleotide and predicted amino acid sequences of two different genes for hig
A:Reference number: JE0405
A:Accession: JE0405
A:Molecule type: DNA
A:Residues: 1-133,'D',135-424,'Q',426-427 <RAH>
A:Cross-references: EMBL:X15226; NID:g18894; PIDN:CAA33298.1; PID:g295804
A:Experimental source: gene Amy152

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R.Chandler, P.M.; Zwar, J.A.; Jacobsen, J.V.; Higgins, T.J.V.; Inglis, A.S.
 Plant Mol. Biol. 3, 407-418, 1984
 A>Title: The effects of gibberellic acid and abscisic acid on alpha-amylase mRNA levels
 A:Reference number: A26267
 A:Accession: A26267
 A:Molecule type: mRNA
 A:Residues: 1-133, 'V', 135-184, 'A', 186-366, 'GA' <GMA>
 A:Experimental source: cv. Himalaya
 A:Note: The authors translated the codon GTC for residue 134 as Gly
 R.Svensson, B.; Mundy, J.; Gibson, R.M.; Svendsen, I.
 Carlsberg Res. Commun. 50, 15-22, 1985
 A>Title: Partial amino acid sequences of alpha-amylase isozymes from barley malt.
 A:Reference number: A24457
 A:Accession: A24457
 A:Molecule type: Protein
 A:Residues: 25-59, 'X', 61-67, 'HX', 70-85, 'X', 87-92, 'E', 94, 146-165; 228-251; 297-303, 'X', 305-310
 A:Comment: The mRNA of this isozyme (B) is present at very low levels in unstimulated and by the embryo during germination.
 C:Genetics:
 A:Gene: Amy2-2
 A:Map position: 6
 A:Introns: 29/3, 344/3
 A:Note: multigene family on chromosome 6 encodes type B alpha-amylases; type A alpha-amylase encodes type A alpha-amylases
 C:Function:
 A:Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
 A:Pathway: glycogen/starch degradation
 C:Superfamily: wheat alpha-amylase; alpha-amylase core homology
 C:Keywords: aleurone cell; blocked amino end; calcium binding; germination; glycosidase; F:1-24/Domain: signal sequence #status predicted <SIG>
 F:1-24/Domain: signal sequence #status predicted <SIG>
 F:25-427/Product: alpha-amylase core homology <AMY>
 F:170-316/Domain: alpha-amylase core homology <AMY>
 F:25/Modified site: blocked amino end (Gln) (in mature form) (probably pyrrolidone carbonyl)
 F:203,228,313/Active site: Asp, Glu, Asp #status predicted

Query Match 74.0%; Score 54; DB 1; Length 427;
 Best Local Similarity 73.3%; Pred. No. 0.035;
 Matches 11; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 1 IDRLVSIRTRGQHS 15
 |||||:||||
 DB 358 IDRLVSIRTRGQHS 372

RESULT 4
 C21826
 alpha-amylase (EC 3.2.1.1) (clone 168) - barley (fragment)
 N:Alternate names: 1,4-alpha-D-glucan glucanohydrolase
 C:Species: Hordeum vulgare (barley)
 C>Date: 05-Jun-1997 #sequence_revision 05-Jun-1997 #text_change 22-Jun-1999
 C:Accession: C21826
 R:huang, J.K.; Sweigle, M.; Dandekar, A.M.; Muthukrishnan, S.
 J. Mol. Appl. Genet. 2, 579-588, 1984
 A:Reference number: A92837; MUID:85159405; PMID:6335720
 A:Accession: C21826
 A:Molecule type: mRNA
 A:Residues: 1-135 <HDA>
 A:Cross-references: GB:K02635; NID:g166990; PIDN:MAA32931.1; PID:g166991
 C:Comment: The authors translated the codon CAA for residue 47 as Pro and the codon GGG as Gly
 C:Function:
 A:Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
 A:Pathway: glycogen/starch degradation
 C:Superfamily: wheat alpha-amylase; alpha-amylase core homology
 C:Keywords: aleurone cell; carbohydrate metabolism; germination; glycosidase; hydrolyase;

- Query Match 69.9%; Score 51; DB 2; Length 135;
 Best Local Similarity 73.3%; Pred. No. 0.035;
 Matches 11; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 1 IDRLVSIRTRGQHS 15
 |||||:||||
 DB 66 IDRLVSIRTRGQHS 80

RESULT 5
 A69593
 naringenin-chalcone synthase bcsa - Bacillus subtilis
 C:Species: Bacillus subtilis
 C>Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 20-Jun-2000
 C:Accession: A69593
 R:Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Ber
 A: Bron, S.; Brouillet, S.; Brusch, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.;
 A: Ehrlich, S.D.; Emerson, P.T.; Entlian, K.D.; Errington, J.; Fajret, C.; Ferrati,
 Nature 390, 249-256, 1997
 A:Authors: Follmer, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Gallizzi, A.; Gal
 lech, J.; Harwood, C.R.; Henuat, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M
 Koester, P.; Konungstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapius, A.; Lardino
 Y, M.; Ogawa, K.; Ogawa, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portele
 A:Authors: Schleich, S.; Schroeter, R.; Scottone, F.; Sekiguchi, J.; Sekowska, A.; Se
 akauchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchida
 T.; Winters, P.; Wipet, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida
 A:Authors: Yoshikawa, H.F.; Zumbstein, E.; Yoshikawa, H.; Danchin, A.
 A>Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis
 A:Reference number: A69580; MUID:98044033; PMID:9384377
 A:Accession: A69593
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-365 <NUN>
 A:Cross-references: GB:299115; GB:AL009126; NID:g2634478; PIDN:CAB14122.1; PID:g26346
 A:Experimental source: strain 168
 C:Genetics:
 A:Gene: bcsa
 C:Superfamily: chalcone synthase

Query Match 61.6%; Score 45; DB 2; Length 365;
 Best Local Similarity 66.7%; Pred. No. 1.5;
 Matches 10; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

OY 1 IDRLVSIRTRGQHS 15
 |||||:||||
 DB 36 IDRLVSIRTRGQHS 50

RESULT 6
 S10013
 alpha-amylase (EC 3.2.1.1) 1 precursor (clone lambda-Osg2) - rice
 C:Species: Oryza sativa (rice)
 C>Date: 21-Nov-1993 #sequence_revision 17-Nov-1995 #text_change 22-Jun-1999
 C:Accession: S10013
 R:huang, J.K.; Sweigle, M.; Dandekar, A.M.; Muthukrishnan, S.
 Plant Mol. Biol. 14, 655-668, 1990
 A>Title: Classification and characterization of the rice alpha-amylase multigene fami
 A:Reference number: S10013; MUID:9134657; PMID:2102847
 A:Accession: S10013
 A:Molecule type: DNA
 A:Residues: 1-428 <HDA>
 A:Cross-references: EMBL:X16509; NID:g20166; PIDN:CAA34516.1; PID:g20167
 A:Experimental source: var. M202
 C:Genetics:
 A:Introns: 30/3; 75/1; 345/3
 C:Function:
 A:Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
 A:Pathway: glycogen/starch degradation
 C:Superfamily: wheat alpha-amylase; alpha-amylase core homology
 C:Keywords: glycosidase; hydrolyase; polysaccharide degradation
 F:170-317/Domain: alpha-amylase core homology <AMY>

Query Match 61.6%; Score 45; DB 2; Length 428;
 Best Local Similarity 71.4%; Pred. No. 1.8;
 Matches 10; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 1 IDRLVSIRTRGQHS 14
 |||||:||||
 DB 359 IDRLVSIRTRGQHS 372

```
RESULT 7
S12775
alpha-amylase (EC 3.2.1.1) precursor (clone pos103) - rice
C:Species: Oryza sativa (rice)
C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 22-Jun-1999
C:Accession: S12775
R:O'Neill, S.D.; Kumagai, M.H.; Majumdar, A.; Huang, N.; Sutcliffe, T.D.; Rodriguez, R.L.
Mol. Gen. Genet. 221, 235-244, 1990
A:Title: The alpha-amylase genes in Oryza sativa: characterization of cDNA clones and m
A:Reference number: S12775; MUID:90318322; PMID:2370848
A:Accession: S12775
A:Molecule type: mRNA
A:Residues: 1-434 <ONE>
A:Cross-references: EMBL:M24286; NID:9169752; PIDN:AAA33885.1; PID:9169753
C:Function:
A:Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
A:Pathway: glycogen/starch degradation
C:Superfamily: wheat alpha-amylase; alpha-amylase core homology
C:Keywords: glycosidase; hydrolase; polysaccharide degradation
F:176-333/domain: alpha-amylase core homology <AMY>
F:209,234,320/Active site: Asp, Glu, Asp #status predicted

Query Match 61.6%; Score 45; DB 2; Length 434;
Best Local Similarity 71.4%; Pred. No. 1.8;
Matches 10; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 IDRLVSIRTRGOIH 14
|:|||||:|
Db 365 IERLVSIRTRNGI 378

RESULT 8
G86601
coproporphyrinogen III oxidase [imported] - Chlamydomonadales (strain J138)
C:Species: Chlamydomonadales (strain J138)
C>Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 23-Mar-2001
C:Accession: G86601
R:Shirai, M.; Hirakawa, H.; Kimoto, M.; Tabuchi, M.; Kishi, F.; Ouchi, K.; Shiba, T.; I
Nucleic Acids Res. 28, 2311-2314, 2000
A:Title: Comparison of whole genome sequences of Chlamydomonadales J138.
A:Reference number: A86491; MUID:20330349; PMID:10871362
A:Accession: G86601
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-458 <STO>
A:Cross-references: GB:BA000008; NID:98979263; PIDN:BA09097.1; GSPDB:GN00142
A:Experimental source: strain J138
C:Genetics:
A:Gene: hemm_2
C:Superfamily: oxygen-independent coproporphyrinogen oxidase

Query Match 60.3%; Score 44; DB 2; Length 458;
Best Local Similarity 57.1%; Pred. No. 3;
Matches 8; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 2 DRLVSIRTRGOIHS 15
|:|:|:|:|
Db 405 DRLISMETGTLIHN 418

RESULT 9
E72023
oxygen-independent coproporphyrinogen III oxidase CP0977 [imported] - Chlamydomonadales pneu
C:Species: Chlamydomonadales pneumoniae, Chlamydomonadales pneumoniae
C>Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 11-May-2000
C:Accession: E72023; H81517
R:Kaltman, S.; Mitchell, W.; Marathe, R.; Lammel, C.; Fan, J.; Olinger, L.; Grimwood, J.;
Nature Genet. 21, 385-389, 1999
A:Title: Comparative genomes of Chlamydomonadales pneumoniae and C. trachomatis.
A:Reference number: A72000; MUID:99206606; PMID:10192388
A:Accession: E72023
A>Status: preliminary
```

```
A:Molecule type: DNA
A:Residues: 1-458 <ARN>
A:Cross-references: GB:AE001669; GB:AE001363; NID:94377199; PIDN:AAD19027.1; PID:9437
A:Experimental source: strain CMT029
R:Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hicke
C.; Dodson, R.; Gilm, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzbe
Nucleic Acids Res. 28, 1397-1406, 2000
A:Title: Genome sequences of Chlamydomonadales trachomatis Morn and Chlamydomonadales AR39
A:Reference number: A81500; MUID:20150255; PMID:10684935
A:Accession: H81517
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-458 <REA>
A:Cross-references: GB:AE002256; GB:AE002161; NID:97189893; PIDN:AAF38757.1; PID:9718
A:Experimental source: strain AR39, HL cells
C:Genetics:
A:Gene: hemm_2; CP0977
C:Superfamily: oxygen-independent coproporphyrinogen oxidase

Query Match 60.3%; Score 44; DB 2; Length 458;
Best Local Similarity 57.1%; Pred. No. 3;
Matches 8; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 2 DRLVSIRTRGOIHS 15
|:|:|:|:|
Db 405 DRLISMETGTLIHN 418

RESULT 10
D87683
conserved hypothetical protein CC3502 [imported] - Caulobacter crescentus
C:Species: Caulobacter crescentus
C>Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 20-Apr-2001
C:Accession: D87683
R:Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg,
B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gilm, M.L.; Haft, D.H.; Ko
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A:Title: Complete Genome Sequence of Caulobacter crescentus.
A:Reference number: A87249; MUID:21173698; PMID:11259647
A:Accession: D87683
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-151 <STO>
A:Cross-references: GB:AE005673; NID:913425228; PIDN:AAK25464.1; GSPDB:GN00148
C:Genetics:
A:Gene: CC3502

Query Match 57.5%; Score 42; DB 2; Length 151;
Best Local Similarity 50.0%; Pred. No. 2.1;
Matches 9; Conservative 4; Mismatches 1; Indels 4; Gaps 1;

QY 2 DRLVSIRTRTRGOIHS 15
|:|:|:|:|
Db 54 DRLVAVETTAARAGEIHT 71

RESULT 11
C90464
hypothetical protein acsa-9 [imported] - Sulfolobus solfataricus
C:Species: Sulfolobus solfataricus
C>Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 15-Jun-2001
C:Accession: C90464
R:She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Ch
Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder
submitted to Genbank, April 2001
A:Description: Sulfolobus solfataricus complete genome.
A:Accession: C90464
A:Reference number: A99139
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-666 <KOR>
```

```
A:Cross-references: GB:AE006641; NID:g13816221; PID:AAK42970.1; GSPDB:GN00155
C:Genetics:
A:Gene: acsA-9
C:Superfamily: acetate-CoA ligase; acetate-CoA ligase homology

Query Match          57.5%; Score 42; DB 2; Length 666;
Best Local Similarity 60.0%; Pred. No. 11;
Matches 9; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 IDRLVSIRTRGQIHS 15
DB 19 LMRVLTGKRQDLHA 33

RESULT 12
AH2812
50S ribosomal protein L17 [imported] - Agrobacterium tumefaciens (strain C58, Dupont)
C:Species: Agrobacterium tumefaciens
C:Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 18-Nov-2002
C:Accession: AH2812
R:Wood, D.W.; Sedulal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I.;
  erage, G.; Gallet, W.; Grant, C.; Guenther, D.; Kutayavin, T.; Levy, R.; Li, M.; McClell
  ; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
R:Authors: Yoo, H.; Tao, Y.; Bidde, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
  ster, E.W.
A:Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A:Reference number: AB2577; MUID:21608550; PMID:11743193
A:Accession: AH2812
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-141 <KUR>
A:Cross-references: GB:AE008688; PID:AAU42918.1; PID:g17740374; GSPDB:GN00186
A:Experimental source: strain C58 (Dupont)
C:Genetics:
A:Gene: rplO
A:Map position: circular chromosome
C:Superfamily: Escherichia coli ribosomal protein L17

Query Match          54.8%; Score 40; DB 2; Length 141;
Best Local Similarity 40.0%; Pred. No. 4; 6;
Matches 6; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

QY 1 IDRLVSIRTRGQIHS 15
DB 48 VERLVTLGKRQDLHA 62

RESULT 13
B97591
50S ribosomal protein L17 nma0102 [imported] - Agrobacterium tumefaciens (strain C58, Ce
C:Species: Agrobacterium tumefaciens
C:Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 18-Nov-2002
C:Accession: B97591
R:Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Quirillo, B.; Goldman,
  A.; Liu, F.; Wolim, C.; Allinger, M.; Doughly, D.; Scott, C.; Lappas, C.; Markelz, B.;
  Science 294, 2323-2328, 2001
A:Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum
  A:Reference number: AB7359; MUID:21608551; PMID:11743194
A:Accession: B97591
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-141 <KUR>
A:Cross-references: GB:AE007869; PID:AAK87683.1; PID:g15157042; GSPDB:GN00169
C:Genetics:
A:Gene: ACR_C_3516
A:Map position: circular chromosome
C:Superfamily: Escherichia coli ribosomal protein L17

Query Match          54.8%; Score 40; DB 2; Length 141;
Best Local Similarity 40.0%; Pred. No. 4; 6;
Matches 6; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

QY 1 IDRLVSIRTRGQIHS 15
DB 48 VERLVTLGKRQDLHA 62

RESULT 14
E75481
RNA methyltransferase, TrmH family - Deinococcus radiodurans (strain RI)
C:Species: Deinococcus radiodurans
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 17-Mar-2000
C:Accession: E75481
R:White, O.; Eissen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;
  M.; Shen, M.; Vamathevan, J.; Lam, P.; McDonald, D.; Uitterback, T.; Zalewski, C.;
  Science 266, 1571-1577, 1995; Fraser, C.M.
A:Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans RI
  A:Reference number: A75250; MUID:20036896; PMID:10567266
A:Accession: E75481
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-246 <MHL>
A:Cross-references: GB:AE001930; GB:AE000513; NID:g6458450; PID:AAF10325.1; PID:g6445
  A:Experimental source: strain RI
C:Genetics:
A:Gene: DR0748
A:Map position: 1
C:Superfamily: conserved hypothetical protein H10860

Query Match          54.8%; Score 40; DB 2; Length 246;
Best Local Similarity 64.3%; Pred. No. 8; 5;
Matches 9; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 2 DRLVSIRTRGQIHS 15
DB 208 DVLVSIPVRGQVOS 221

RESULT 15
S59771
hypothetical protein YPR106w - Yeast (Saccharomyces cerevisiae)
N:Alternate names: hypothetical protein P8283.9
C:Species: Saccharomyces cerevisiae
C:Date: 13-Jan-1996 #sequence_revision 01-Mar-1996 #text_change 06-Feb-1998
C:Accession: S59771
R:Nelson, J.
Submitted to the EMBL Data Library, July 1995
A:Description: The sequence of S. cerevisiae cosmid 8283.
A:Reference number: S59764
A:Accession: S59771
A:Molecule type: DNA
A:Residues: 1-443 <NEL>
A:Cross-references: EMBL:U32445; NID:g914969; PID:g914977; MIPS:YPR106w
C:Genetics:
A:Gene: SGD:ISR1
A:Cross-references: SGD:S0006310; MIPS:YPR106w
A:Map position: 16R

Query Match          53.4%; Score 39; DB 2; Length 443;
Best Local Similarity 57.1%; Pred. No. 25;
Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 IDRLVSIRTRGQIHS 14
DB 265 IDALKSLKTKNGIHH 278

RESULT 16
A56043
steroid hormone receptor-like protein RLD-1 - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 01-Dec-1995 #sequence_revision 01-Dec-1995 #text_change 24-Sep-1999
C:Accession: A56043
R:Apfel, R.; Bendbrook, D.; Bernhardt, E.; Ortliz, M.A.; Salbert, G.; Pfahl, M.
```

Mol. Cell. Biol. 14, 7025-7035, 1994
 A:Title: A novel orphan receptor specific for a subset of thyroid hormone-responsive elements
 A:Reference number: A56043; MUID:95021230; PMID:7935418
 A:Accession: A56043
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-445 <RES>
 A:Cross-references: GB:011685; NID:9555751; PIDN:AAA53633.1; PID:9555752
 A:Note: authors translated the codon GAG for residue 73 as Ser
 C:Superfamily: unassigned erba-related proteins; erba transforming protein homology
 C:Keywords: steroid hormone receptor; zinc finger
 F:94-365/Domain: erba transforming protein homology <ERBA>

Query Match 53.4%; Score 39; DB 2; Length 445;
 Best Local Similarity 53.8%; Pred. No. 25;
 Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

OY 3 RLVSIRTRGOIHS 15
 Db 408 KLVSLRTLSSVHS 420
 :|||:|:|:|

RESULT 17
 149021
 retinoid X receptor interacting protein No.15 - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 24-Sep-1999
 C:Accession: 149021
 R:Seol, W.; Choi, H.S.; Moore, D.D.
 Mol. Endocrinol. 9, 72-85, 1995
 A:Title: Isolation of proteins that interact specifically with the retinoid X receptor:
 A:Reference number: A57664; MUID:95280959; PMID:7760852
 A:Accession: 149021
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-446 <RES>
 A:Cross-references: EMBL:U09419; NID:9691713; PIDN:AAC52164.1; PID:9691714
 C:Genetics:
 A:Gene: R1P15
 C:Superfamily: unassigned erba-related proteins; erba transforming protein homology
 C:Keywords: zinc finger
 F:76-366/Domain: erba transforming protein homology <ERBA>

Query Match 53.4%; Score 39; DB 2; Length 446;
 Best Local Similarity 53.8%; Pred. No. 25;
 Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

OY 3 RLVSIRTRGOIHS 15
 Db 409 KLVSLRTLSSVHS 421
 :|||:|:|:|

RESULT 18
 159354
 orphan nuclear receptor OR-1 - rat
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 24-Sep-1999
 C:Accession: 159354; 159264
 R:Tepon, M.; Enmark, E.; Li, Q.; Wikstrom, A.C.; Peltto-Huikko, M.; Gustafsson, J.A.
 Proc. Natl. Acad. Sci. U.S.A. 92, 2096-2100, 1995
 A:Title: OR-1, a member of the nuclear receptor superfamily that interacts with the 9-cis
 A:Reference number: 159354; MUID:95199298; PMID:7892230
 A:Accession: 159354
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-446 <RES>
 A:Cross-references: EMBL:U20389; NID:9665941; PIDN:AAA69522.1; PID:9665942
 A:Experimental source: Sprague-Dawley, hepatic
 R:Song, C.; Kokontis, J.M.; Hilpakra, R.A.; Liao, S.
 Proc. Natl. Acad. Sci. U.S.A. 91, 10809-10813, 1994
 A:Title: Ubiquitous receptor: a receptor that modulates gene activation by retinoic acid
 A:Reference number: 159264; MUID:95062154; PMID:7971966
 A:Accession: 159264

A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-32, 'V', 34-51, 55-218, 'V', 220-446 <RES2>
 A:Cross-references: EMBL:U14533; NID:9565661; PIDN:AAA52361.1; PID:9565662
 A:Experimental source: vagina
 C:Superfamily: unassigned erba-related proteins; erba transforming protein homology
 C:Keywords: DNA binding; zinc finger
 F:76-366/Domain: erba transforming protein homology <ERBA>

Query Match 53.4%; Score 39; DB 2; Length 446;
 Best Local Similarity 53.8%; Pred. No. 25;
 Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

OY 3 RLVSIRTRGOIHS 15
 Db 409 KLVSLRTLSSVHS 421
 :|||:|:|:|

RESULT 19
 138975
 nuclear orphan receptor LXR-alpha - human
 C:Species: Homo sapiens (man)
 C:Date: 16-Feb-1996 #sequence_revision 16-Feb-1996 #text_change 20-Sep-1999
 C:Accession: 138975
 R:Killy, P.J.; Umesono, K.; Ong, E.S.; Evans, R.M.; Heyman, R.A.; Mangelsdorf, D.J.
 Genes Dev. 9, 1033-1045, 1995
 A:Title: LXR, a nuclear receptor that defines a distinct retinoid response pathway.
 A:Reference number: 138975; MUID:95262897; PMID:7744246
 A:Accession: 138975
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-447 <RES>
 A:Cross-references: EMBL:U22662; NID:9726512; PIDN:AA85856.1; PID:9726513
 C:Superfamily: unassigned erba-related proteins; erba transforming protein homology
 C:Keywords: zinc finger
 F:96-367/Domain: erba transforming protein homology <ERBA>

Query Match 53.4%; Score 39; DB 2; Length 447;
 Best Local Similarity 53.8%; Pred. No. 26;
 Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

OY 3 RLVSIRTRGOIHS 15
 Db 410 KLVSLRTLSSVHS 422
 :|||:|:|:|

RESULT 20
 JC4014
 steroid hormone-nuclear receptor NER - human
 C:Species: Homo sapiens (man)
 C:Date: 13-Jun-1995 #sequence_revision 14-Jul-1995 #text_change 24-Sep-1999
 C:Accession: JC4014
 R:Shinar, D.M.; Endo, N.; Rutledge, S.T.; Vogel, R.; Rodan, G.A.; Schmidt, A.
 Gene 147, 273-276, 1994
 A:Title: NER, a new member of the gene family encoding the human steroid hormone nucl
 A:Reference number: JC4014; MUID:95011628; PMID:7926214
 A:Accession: JC4014
 A:Molecule type: mRNA
 A:Residues: 1-461 <SHI>
 A:Cross-references: GB:U07132; NID:9641961; PIDN:AAA61783.1; PID:9641962
 A:Experimental source: osteosarcoma cells SACS-2/810
 C:Genetics:
 A:Gene: GDB:UNR
 A:Cross-references: GDB:389570; OMIM:600380
 A:Map position: 19q13.3-19q13.3
 C:Superfamily: unassigned erba-related proteins; erba transforming protein homology
 C:Keywords: steroid hormone receptor
 F:85-381/Domain: erba transforming protein homology <ERBA>
 F:87-134/Domain: DNA binding; status predicted <BIN>

Query Match 53.4%; Score 39; DB 2; Length 461;
 Best Local Similarity 53.8%; Pred. No. 26;
 Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

OY 3 RLVSIRTRGOIHS 15
:||||:|:|
DB 424 KLVSLRILSSVHS 436

RESULT 21

S46034
Hypothetical protein YBR163w - yeast (Saccharomyces cerevisiae)
N:Alternate names: hypothetical protein YBR1215
C:Species: Saccharomyces cerevisiae
C>Date: 26-Aug-1994 #sequence_revision 09-Sep-1994 #text_change 19-Apr-2002
C:Accession: S46034
R:Enliam, K.D.; Koeltter, P.; Rose, M.; Becker, J.; Grey, M.; Li, Z.; Niegemann, E.; Sche
S.; Gruenheid, R.; Helges, D.; Klesau, P.; Korol, S.; Krems, B.; Proft, M.; Slegers, K.
submitted to the Protein Sequence Database, August 1994
A:Reference number: S46034
A:Accession: S46034
A:Molecule type: DNA
A:Residues: 1-585 <ENT>
A:Cross-references: EMBL:Z36032; NID:G536499; PID:G536500; GSPDB:GN00002; MIPS:YBR163w
A:Experimental source: strain S288C
C:Gene: SCD1; DML1; MIPS:YBR163w
A:Gene: SCD1; DML1; MIPS:YBR163w
A:Cross-references: SGD:S0000367
A:Map position: 2R
C:Superfamily: saccharomyces cerevisiae hypothetical protein YBR163w

Query Match 53.4%; Score 39; DB 2; Length 585;
Best Local Similarity 53.3%; Pred. No. 34;
Matches 8; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

OY 1 IDRLVSIRTRGOIHS 15
:||||:|:|
DB 218 INRLVSLFTKGDGHA 232

RESULT 22

S57596
Ribosomal RNA processing protein RRP5 - yeast (Saccharomyces cerevisiae)
N:Alternate names: protein YM9959.11c; protein YMR229c
C:Species: Saccharomyces cerevisiae
C>Date: 19-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 24-Sep-1999
C:Accession: S57596; S72446
R:Skellton, J.; Churcher, C.M.
submitted to the EMBL Data Library, June 1995
A:Reference number: S57587
A:Accession: S57596
A:Molecule type: DNA
A:Residues: 1-1729 <SME>
A:Cross-references: EMBL:Z49939; NID:G887599; PIDN:CAA90200.1; PID:G887610; MIPS:YMR229c
A:Experimental source: strain AB972
R:Venema, J.; Tollervey, D.
EMBO J. 15, 5701-5714, 1996
A:Title: RRP5 is required for formation of both 18S and 5.8S rRNA in yeast.
A:Reference number: S72446; MUID:97051828; PMID:8896463
A:Accession: S72446
A:Molecule type: DNA
A:Status: nucleic acid sequence not shown
A:Residues: 1-1729 <VEN>
A:Cross-references: EMBL:Z49939; NID:G887599; PIDN:CAA90200.1; PID:G887610
C:Gene: SCD1; RRP5
A:Cross-references: SGD:S0004842; MIPS:YMR229c
A:Map position: 13R
C:Function:
A:Description: required for pre-rRNA processing
C:Superfamily: ribosomal RNA processing protein RRP5
C:Keywords: nucleus; RNA binding

Query Match 53.4%; Score 39; DB 2; Length 1729;
Best Local Similarity 41.7%; Pred. No. 11e+02;
Matches 5; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

OY 3 RLVSIRTRGOIHS 14
:||||:|:|
DB 565 RLVSINRGNVH 576

RESULT 23

B87407
ribosomal protein L17 [imported] - Caulobacter crescentus
C:Species: Caulobacter crescentus
C>Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 10-May-2001
C:Accession: B87407
R:Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, R.; Nierman, W.C.; Debay, R.T.; Dodson, R.J.; Durkin, A.S.; Gwin, M.L.; Haft, D.H.; Ko
n, J.; Ermolaeva, M.; White, O.; S.A. 98 9136-4141, 2001
Proc. Natl. Acad. Sci. U.S.A.
A:Title: Complete genome sequence of Caulobacter crescentus.
A:Reference number: B87407; MUID:21173698; PMID:11259647
A:Accession: B87407
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-137 <SNC>
A:Cross-references: GB:AE005673; NID:G1342606; PIDN:AAK23254.1; GSPDB:GN00148
C:Gene: CCL1273
A:Gene: CCL1273
C:Superfamily: Escherichia coli ribosomal protein L17

Query Match 52.1%; Score 38; DB 2; Length 137;
Best Local Similarity 33.3%; Pred. No. 11;
Matches 5; Conservative 7; Mismatches 3; Indels 0; Gaps 0;

OY 1 IDRLVSIRTRGOIHS 15
:||||:|:|
DB 48 VKKVTIAKRGDHA 62

RESULT 24

S48937
Hypothetical protein YHL031c - yeast (Saccharomyces cerevisiae)
C:Species: Saccharomyces cerevisiae
C>Date: 02-Dec-1994 #sequence_revision 02-Dec-1994 #text_change 29-Oct-1999
C:Accession: S48937
R:Avellio, T.
submitted to the EMBL Data Library, June 1994
A:Description: The sequence of S. cerevisiae cosmid 9196.
A:Reference number: S46794
A:Accession: S48937
A:Molecule type: DNA
A:Residues: 1-223 <FAV>
A:Cross-references: EMBL:U11583; NID:G2289854; PIDN:ANB5043.1; PID:G2289860; MIPS:YH
C:Gene: SCD1
A:Cross-references: SGD:S0001023; MIPS:YHL031c
A:Map position: 8L

Query Match 52.1%; Score 38; DB 2; Length 223;
Best Local Similarity 52.9%; Pred. No. 18;
Matches 9; Conservative 2; Mismatches 4; Indels 2; Gaps 1;

OY 1 IDRLVSIRTRGOIHS 15
:||||:|:|
DB 152 VDRLISQAMRISQPHS 168

RESULT 25

H36792
Hypothetical protein ORP61 - Ictalurid herpesvirus 1 (strain Auburn 1)
C:Species: Ictalurid herpesvirus 1
A:Note: host Ictalurus punctatus (channel catfish)
C>Date: 17-Aug-1992 #sequence_revision 17-Aug-1992 #text_change 08-Oct-1999
C:Accession: H36792
R:Davidson, A.J.
submitted to Genbank, January 1992

A:Description: Channel catfish virus: a new type of herpesvirus.
A:Reference number: A36804
A:Accession: H36792
A:Molecule type: DNA
A:Residues: 1-319 <DNV>
A:Cross-references: GB:M75136; NID:g331209; PIDN:AAA88164.1; PID:g331271
R:Davidson, A.U.
Virology 186, 9-14, 1992
A:Title: Channel catfish virus: a new type of herpesvirus.
A:Reference number: A39447; MUID:92087490; PMID:1727613
A:Contents: annotation
A:Note: neither protein nor nucleic acid sequence is given
C:Genetics:
A:Gene: 61

Query Match 52.1%; Score 38; DB 2; Length 319;
Best Local Similarity 46.2%; Pred. No. 27;
Matches 6; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

OY 1 IDRLVSIPTRGQI 13
:|||:|:|:|:
Db 213 VDRLGKLRAGEV 225

RESULT 26
S50409
hypothetical protein YMR152w - yeast (Saccharomyces cerevisiae)
N:Alternate names: hypothetical protein YMR520.01; hypothetical protein YMR375.22
C:Species: Saccharomyces cerevisiae
C>Date: 27-Jan-1995 #sequence_revision 12-Jul-1996 #text_change 19-Apr-2002
C:Accession: S50409; S16819; S54510; S54597
R:Badcock, K.; Churcher, C.
submitted to the EMBL Data Library, December 1994
A:Reference number: S50388
A:Accession: S50409
A:Molecule type: DNA
A:Residues: 1-316 <BAD>
A:Cross-references: EMBL:Z47071; NID:9606429; PIDN:CAA87367.1; PID:9606451; MIPS:YMR152w
R:Behrens, M.; Michaelis, G.; Pratlje, E.
Mol. Gen. Genet. 228, 167-176, 1991
A:Title: Mitochondrial inner membrane protease 1 of Saccharomyces cerevisiae shows sequence
A:Reference number: S16817; MUID:91360060; PMID:1886606
A:Accession: S16819
A:Status: not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-120, 'T', 122-233, 'T', 235-279, 'N', 281-295, 'S', 297-365 <BEH>
R:Hunt, S.; Bowman, S.
submitted to the EMBL Data Library, May 1995
A:Reference number: S54510
A:Accession: S54510
A:Molecule type: DNA
A:Residues: 196-365 <HUN>
A:Cross-references: GB:Z49705; EMBL:Z49700; NID:9825556; PIDN:CAA89788.1; PID:9825557; F
A:Experimental source: strain AB972
C:Genetics:
A:Gene: SGD:YIM1
A:Cross-references: SGD:S0004760
A:Map position: 13R
C:Keywords: transmembrane protein
F:170-186/Domain: transmembrane #status predicted <TMM>

Query Match 52.1%; Score 38; DB 2; Length 365;
Best Local Similarity 53.8%; Pred. No. 32;
Matches 7; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

OY 1 IDRLVSIPTRGQI 13
:|||:|:|:|:
Db 348 IDRLMSNRAGKV 360

RESULT 27
JF0398
ribosomal protein L17 - Thermus aquaticus (strain HB8)

C:Species: Thermus aquaticus
C>Date: 23-Jul-1999 #sequence_revision 23-Jul-1999 #text_change 11-May-2000
C:Accession: JF0398
R:Wada, T.; Yamazaki, T.; Kuramitsu, S.; Kyogoku, Y.
J. Biochem. 125, 143-150, 1999
A:Title: Cloning of the rRNA polymerase alpha subunit gene from Thermus thermophilus H
A:Reference number: JF0397; MUID:99098837; PMID:9880810
A:Accession: JF0398
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-118 <WAD>
C:Genetics:
A:Gene: rpl17
C:Superfamily: Escherichia coli ribosomal protein L17

Query Match 50.7%; Score 37; DB 2; Length 118;
Best Local Similarity 33.3%; Pred. No. 14;
Matches 5; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

OY 1 IDRLVSIPTRGQIHS 15
:|||:|:|:|:
Db 48 VDHLIHLAKRGDLHA 62

RESULT 28
S77863
ribosomal protein L17 - Mycoplasma capricolum (fragment)
N:Alternate names: protein MC060
C:Species: Mycoplasma capricolum
C>Date: 09-Oct-1997 #sequence_revision 24-Oct-1997 #text_change 21-Jul-2000
C:Accession: S77863; S48596
R:Bork, P.; Ouzounis, C.; Casari, G.; Schneider, R.; Sander, C.; Dolan, M.; Gilbert, M.
Mol. Microbiol. 16, 955-967, 1995
A:Title: Exploring the Mycoplasma capricolum genome: a minimal cell reveals its physi
A:Reference number: S77739; MUID:96059641; PMID:7476192
A:Accession: S77863
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-119 <BOR>
A:Cross-references: EMBL:Z33050; NID:9541697; PIDN:CAA83721.1; PID:94379134
A:Experimental source: ATCC 27343
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, July 1994
C:Genetics:
A:Genetic code: SGC3
C:Superfamily: Escherichia coli ribosomal protein L17
C:Keywords: protein biosynthesis; ribosome

Query Match 50.7%; Score 37; DB 2; Length 119;
Best Local Similarity 35.7%; Pred. No. 14;
Matches 5; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

OY 2 DRLVSIPTRGQIHS 15
:|||:|:|:|:
Db 46 DHMITLAKRGDLHS 59

RESULT 29
AH3349
LSU ribosomal protein L17P [imported] - Brucella melitensis (strain 16M)
C:Species: Brucella melitensis
C>Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 15-Feb-2002
C:Accession: AH3349
R:DelVecchio, V.G.; Kapatal, V.; Redkar, R.J.; Patra, G.; Mufer, C.; Los, T.; Ivanov
.; Mazur, M.; Goldsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Let
Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A:Title: The genome sequence of the facultative intracellular pathogen Brucella melit
A:Reference number: AD3252; PMID:11756688
A:Accession: AH3349
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-142 <KUR>
A:Cross-references: GB:AE008917; PIDN:AAL51963.1; PID:917982722; GSPDB:GN00190
A:Experimental source: strain 16M

C:Genetics:
A:Gene: BME10782
A:Map position: I
C:Superfamily: Escherichia coli ribosomal protein L17

Query Match 50.7%; Score 37; DB 2; Length 142;
Best Local Similarity 33.3%; Pred. No. 17;
Matches 5; Conservative 7; Mismatches 3; Indels 0; Gaps 0;

OY 1 IDRLVSIIRGQIHS 15
:::|::|::|:
Db 48 VEKLVTLGKRGLHA 62

RESULT 30

JQ1722
3b: protein - canine coronavirus
C:Species: canine coronavirus
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999
C:Accession: JQ1722
R: Horsburgh, B.C.; Brerley, I.; Brown, T.D.K.
J. Gen. Virol. 73, 2849-2862, 1992
A:Title: Analysis of a 9.6 kb sequence from the 3' end of canine coronavirus genomic RNA
A:Reference number: PQ0481; MUID:93057357; PMID:1431811
A:Accession: JQ1722
A:Molecule type: mRNA
A:Residues: 1-251 <HOR>
A:Cross-references: DDBJ:DJ3096
A:Experimental source: strain insavc-1

Query Match 50.7%; Score 37; DB 2; Length 251;
Best Local Similarity 66.7%; Pred. No. 32;
Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 4 LVSIIRGQIHS 15
||| ||| |:
Db 179 LVSIIRGLHA 190

Search completed: August 29, 2003, 18:48:28
Job time : 17.4286 secs

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GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: August 29, 2003, 18:39:11 ; Search time 9.85714 Seconds

(without alignments)
71.562 Million cell updates/sec

Title: US-09-830-876-1

Perfect score: 73

Sequence: 1 IDRLVSRIRGQIHS 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 127863 segs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	58	79.5	429	1	AMT6_HORVU
2	54	74.0	153	1	AMT4_HORVU
3	54	74.0	427	1	AMT2_HORVU
4	51	69.9	135	1	AMT5_HORVU
5	45	61.6	365	1	BCSA_BACSU
6	45	61.6	428	1	AMT1_ORYSA
7	40	54.8	368	1	AMT3_HORVU
8	39	53.4	445	1	NRH3_MOUSE
9	39	53.4	445	1	NRH2_MOUSE
10	39	53.4	446	1	NRH2_MOUSE
11	39	53.4	446	1	NRH2_MOUSE
12	39	53.4	447	1	NRH2_MOUSE
13	39	53.4	461	1	NRH2_HUMAN
14	39	53.4	585	1	VRB3_YEAST
15	39	53.4	1729	1	RRP5_YEAST
16	38	52.1	223	1	VRH1_YEAST
17	38	52.1	319	1	VRG1_HSV1
18	38	52.1	365	1	VRG1_HSV1
19	37	50.7	118	1	RLI7_THEH
20	37	50.7	119	1	RLI7_MYCCA
21	37	50.7	141	1	RLI7_RHME
22	37	50.7	250	1	VNS3_CVCAI
23	37	50.7	258	1	TRC2_STRCO
24	37	50.7	282	1	T4HR_MAGGR
25	37	50.7	311	1	ISPE_CORGL
26	37	50.7	336	1	FLIP_SHEEP
27	37	50.7	337	1	FLIP_PIG
28	37	50.7	362	1	FLIP_PIG
29	37	50.7	383	1	AMC1_ORYSA
30	37	50.7	475	1	YMA8_YEAST
31	37	50.7	566	1	YMA3_YEAST
32	37	50.7	1804	1	YMA3_YEAST
33	36.5	50.0	230	1	RS1_CAUCK

34	36	49.3	253	1	TPR5_ORYSA
35	36	49.3	257	1	TPR5_ORYSA
36	36	49.3	267	1	TPR5_ORYSA
37	36	49.3	274	1	TPR5_ORYSA
38	36	49.3	319	1	TPR5_ORYSA
39	36	49.3	319	1	TPR5_ORYSA
40	36	49.3	319	1	TPR5_ORYSA
41	36	49.3	319	1	TPR5_ORYSA
42	36	49.3	353	1	TPR5_ORYSA
43	36	49.3	353	1	TPR5_ORYSA
44	36	49.3	521	1	TPR5_ORYSA
45	36	49.3	521	1	TPR5_ORYSA
46	36	49.3	639	1	TPR5_ORYSA
47	36	49.3	639	1	TPR5_ORYSA
48	35	47.9	119	1	TPR5_ORYSA
49	35	47.9	119	1	TPR5_ORYSA
50	35	47.9	119	1	TPR5_ORYSA
51	35	47.9	119	1	TPR5_ORYSA
52	35	47.9	119	1	TPR5_ORYSA
53	35	47.9	119	1	TPR5_ORYSA
54	35	47.9	119	1	TPR5_ORYSA
55	35	47.9	119	1	TPR5_ORYSA
56	35	47.9	119	1	TPR5_ORYSA
57	35	47.9	119	1	TPR5_ORYSA
58	35	47.9	119	1	TPR5_ORYSA
59	35	47.9	119	1	TPR5_ORYSA
60	35	47.9	119	1	TPR5_ORYSA
61	35	47.9	119	1	TPR5_ORYSA
62	35	47.9	119	1	TPR5_ORYSA
63	35	47.9	119	1	TPR5_ORYSA
64	35	47.9	119	1	TPR5_ORYSA
65	35	47.9	119	1	TPR5_ORYSA
66	35	47.9	119	1	TPR5_ORYSA
67	35	47.9	119	1	TPR5_ORYSA
68	35	47.9	119	1	TPR5_ORYSA
69	35	47.9	119	1	TPR5_ORYSA
70	35	47.9	119	1	TPR5_ORYSA
71	35	47.9	119	1	TPR5_ORYSA
72	35	47.9	119	1	TPR5_ORYSA
73	35	47.9	119	1	TPR5_ORYSA
74	35	47.9	119	1	TPR5_ORYSA
75	35	47.9	119	1	TPR5_ORYSA
76	35	47.9	119	1	TPR5_ORYSA
77	35	47.9	119	1	TPR5_ORYSA
78	35	47.9	119	1	TPR5_ORYSA
79	35	47.9	119	1	TPR5_ORYSA
80	35	47.9	119	1	TPR5_ORYSA
81	35	47.9	119	1	TPR5_ORYSA
82	35	47.9	119	1	TPR5_ORYSA
83	35	47.9	119	1	TPR5_ORYSA
84	35	47.9	119	1	TPR5_ORYSA
85	35	47.9	119	1	TPR5_ORYSA
86	35	47.9	119	1	TPR5_ORYSA
87	35	47.9	119	1	TPR5_ORYSA
88	35	47.9	119	1	TPR5_ORYSA
89	35	47.9	119	1	TPR5_ORYSA
90	35	47.9	119	1	TPR5_ORYSA
91	35	47.9	119	1	TPR5_ORYSA
92	35	47.9	119	1	TPR5_ORYSA
93	35	47.9	119	1	TPR5_ORYSA
94	35	47.9	119	1	TPR5_ORYSA
95	35	47.9	119	1	TPR5_ORYSA
96	35	47.9	119	1	TPR5_ORYSA
97	35	47.9	119	1	TPR5_ORYSA
98	35	47.9	119	1	TPR5_ORYSA
99	35	47.9	119	1	TPR5_ORYSA
100	35	47.9	119	1	TPR5_ORYSA

ALIGNMENTS

RESULT 1

AMY6_HORVU STANDARD; PRT; 429 AA.
 ID AMY6_HORVU PRT; 429 AA.
 AC P04750;
 DT 13-AUG-1987 (Rel. 05, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE Alpha-amylase type B isozyme precursor (EC 3.2.1.1) (1,4-alpha-D-glucan glucanohydrolase) (Clones GRAMY56 and 963).
 GN AMY1.6.
 OS Hordeum vulgare (Barley).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae; CC Triticeae; Hordeum.
 OK NCBI_TaxID=4513;
 RN [1]
 RP SEQUENCE FROM N.A. (CLONE GRAMY56).
 RA Rasmussen R.J., Huang J.-K., Clark K.L., Reek G.R.,
 RA Chandra G.R., Muthukrishnan S.;
 RT "Nucleotide and predicted amino acid sequences of two different genes for high-pi alpha-amylases from barley.";
 RT Plant Mol. Biol. 12:119-121(1989).
 RN [2]
 RP SEQUENCE OF 380-429 FROM N.A. (CLONE 963).
 RX MEDLINE=85159405; PubMed=6335720;
 RA Huang J.-K., Swegle M., Dandekar A.M., Muthukrishnan S.;
 RT "Expression and regulation of alpha-amylase gene family in barley aleurones.";
 RL J. Mol. Appl. Genet. 2:579-588(1984).
 CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic linkages in oligosaccharides and polysaccharides.
 CC -1- COFACTOR: BINDS A CALCIUM ION REQUIRED FOR ITS ACTIVITY.
 CC -1- DEVELOPMENTAL STAGE: PRODUCTION OF ALPHA-AMYLASE IS HORMONALLY REGULATED. GERMINATING EMBRYOS PRODUCE THE HORMONE GIBBERELIC ACID, WHICH WITHIN 10 HOURS STIMULATES THE ALEURONE CELLS COVERING THE ENDOSPERM OF THE SEED TO PRODUCE ALPHA-AMYLASE. THE ENZYME THEN DEGRADES THE STARCH WITHIN THE ENDOSPERM FOR USE BY THE DEVELOPING PLANT EMBRYO.
 CC -1- MISCELLANEOUS: THERE ARE AT LEAST 4 TYPES OF ALPHA-AMYLASE IN BARLEY.
 CC -1- MISCELLANEOUS: TYPE B ISOZYME MRNA IS UNDETECTABLE IN UNSTIMULATED CELLS AND INCREASES A HUNDRED-FOLD AFTER STIMULATION WITH GIBBERELIC ACID.
 CC -1- SIMILARITY: BELONGS TO FAMILY 13 OF GLYCOSYL HYDROLASES, ALSO KNOWN AS THE ALPHA-AMYLASE FAMILY.
 CC -----
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 CC -----
 DR EMBL: X15227; CAA33299.1; -;
 DR EMBL: K02636; AAA32932.1; -;
 DR PIR: JE0406; JE0406.
 DR HSSP: P04063; JAV4.
 DR InterPro: IPR006589; Alp_amy1_cat_sub.
 DR InterPro: IPR006047; Alpha_amy1_cat.
 DR Pfam: PF00128; alpha-amylase; 1.
 DR SMART: SM00642; Amy; 1.
 KW Hydroxylase; Glycosidase; Carbohydrate metabolism; Seed; Germination;
 KW Calcium; Multigene family; Signal.
 FT SIGNAL 1 24
 FT CHAIN 25 429 ALPHA-AMYLASE TYPE B ISOZYME.
 FT ACT_SITE 205 205 BY SIMILARITY.
 FT ACT_SITE 315 315 BY SIMILARITY.
 SQ SEQUENCE 429 AA; 47937 MW; 1C924CA6319D5262 CRC64;

QY 1 IDRLVSVTRRGQIHS 15
 Db 360 IDRLVSVTRRGQIHS 374
 ID AMY4_HORVU STANDARD; PRT; 153 AA.
 AC P04748;
 DT 13-AUG-1987 (Rel. 05, Created)
 DT 13-AUG-1987 (Rel. 05, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE Alpha-amylase type B isozyme (EC 3.2.1.1) (1,4-alpha-D-glucan glucanohydrolase) (Clone 103) (Fragment).
 GN AMY1.4.
 OS Hordeum vulgare (Barley).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae; CC Triticeae; Hordeum.
 OK NCBI_TaxID=4513;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=85159405; PubMed=6335720;
 RA Huang J.-K., Swegle M., Dandekar A.M., Muthukrishnan S.;
 RT "Expression and regulation of alpha-amylase gene family in barley aleurones.";
 RL J. Mol. Appl. Genet. 2:579-588(1984).
 CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic linkages in oligosaccharides and polysaccharides.
 CC -1- COFACTOR: BINDS A CALCIUM ION REQUIRED FOR ITS ACTIVITY.
 CC -1- DEVELOPMENTAL STAGE: PRODUCTION OF ALPHA-AMYLASE IS HORMONALLY REGULATED. GERMINATING EMBRYOS PRODUCE THE HORMONE GIBBERELIC ACID, WHICH WITHIN 10 HOURS STIMULATES THE ALEURONE CELLS COVERING THE ENDOSPERM OF THE SEED TO PRODUCE ALPHA-AMYLASE. THE ENZYME THEN DEGRADES THE STARCH WITHIN THE ENDOSPERM FOR USE BY THE DEVELOPING PLANT EMBRYO.
 CC -1- MISCELLANEOUS: THERE ARE AT LEAST 4 TYPES OF ALPHA-AMYLASE IN BARLEY.
 CC -1- MISCELLANEOUS: TYPE B ISOZYME MRNA IS UNDETECTABLE IN UNSTIMULATED CELLS AND INCREASES A HUNDRED-FOLD AFTER STIMULATION WITH GIBBERELIC ACID.
 CC -1- SIMILARITY: BELONGS TO FAMILY 13 OF GLYCOSYL HYDROLASES, ALSO KNOWN AS THE ALPHA-AMYLASE FAMILY.
 CC -----
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 CC -----
 DR EMBL: M10056; AAA32930.1; -;
 DR PIR: A21826; A21826.
 DR HSSP: P04063; JAV4.
 DR InterPro: IPR006047; Alpha_amy1_cat.
 DR Pfam: PF00128; alpha-amylase; 1.
 KW Hydroxylase; Glycosidase; Carbohydrate metabolism; Seed; Germination;
 KW Calcium; Multigene family.
 FT NON_TER 1 1
 FT ACT_SITE 39 39 BY SIMILARITY.
 SQ SEQUENCE 153 AA; 17275 MW; BE5233AE1D65F72 CRC64;

Query Match 74.0%; Score 54; DB 1; Length 153;
 Best Local Similarity 73.3%; Pred. No. 0.0034;
 Matches 11; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 IDRLVSVTRRGQIHS 15
 Db 84 IDRLVSVTRRGQIHS 98

RESULT 3

AMV2	HORVU	STANDARD;	PRR:	427 AA.
ID	AMV2.HORVU	STANDARD;	PRR:	427 AA.
AC	PO4063:			
DT	01-NOV-1986 (Rel. 03, Created)			
DT	15-JUL-1998 (Rel. 36, Last sequence update)			
DT	15-SEP-2003 (Rel. 42, Last annotation update)			
DE	Alpha amylase type B isozyme precursor (EC 3.2.1.1) (1.4-alpha-D-glucan glucanohydrolase) (AMV2-2) (High pI alpha-amylase).			
GN	AMV1.2			
OC	hordeum vulgare (Barley).			
OC	Eukaryota: Viridiplantae: Streptophyta: Embryophyta: Tracheophyta: Spermatophyta: Magnoliophyta: Liliopsida: Poales: Poaceae: Pooidae: Triticeae; Hordeum.			
ON	NCBI_TaxID=4513;			
OX	1)			
RA	SEQUENCE FROM N.A.			
RA	Rahmatullah R.J., Huang J.K., Clark K.L., Reek G.R., Chandra G.R., Muthukrishnan S.;			
RT	"Nucleotide and predicted amino acid sequences of two different genes for high-pI alpha-amylases from barley.";			
RT	Plant Mol. Biol. 12:119-121(1989).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=85111184; PubMed=3871776;			
RX	Rogers J.C.;			
RL	"Two barley alpha-amylase gene families are regulated differently in aleurone cells.";			
RL	J. Biol. Chem. 260: 3731-3738(1985).			
RN	[3]			
RP	X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS).			
RX	MEDLINE=94254083; PubMed=8196040.			
RA	Kadziola A., Abe J.-I., Svensson B., Haser R.;			
RT	"Crystal and molecular structure of barley alpha-amylase.";			
RT	J. Mol. Biol. 239:104-121(1994).			
RL	[4]			
RP	X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS) OF COMPLEX WITH BAST.			
RP	STRAN-98; Menet.			
RX	MEDLINE=98298441; PubMed=9644702;			
RA	Wallée F., Kadziola A., Bourne Y., Juy M., Rodenburg K.W., Svensson B., Haser R.;			
RT	"Barley alpha-amylase bound to its endogenous protein inhibitor BAST: crystal structure of the complex at 1.9-A resolution.";			
RT	Structure 6:649-659(1998).			
RL	-1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic linkages in oligosaccharides and polysaccharides.			
CC	-1- COFACTOR: BINDS A CALCIUM ION REQUIRED FOR ITS ACTIVITY.			
CC	-1- DEVELOPMENTAL STAGE: PRODUCTION OF ALPHA-AMYLASE IS HORMONALLY REGULATED. GERMINATING EMBRYOS PRODUCE THE HORMONE GIBBERELLIC ACID, WHICH WITHIN 10 HOURS STIMULATES THE ALEURONE CELLS COVERING THE ENDOSPERM OF THE SEED TO PRODUCE ALPHA-AMYLASE. THE ENZYME THEN DEGRADES THE STARCH WITHIN THE ENDOSPERM FOR USE BY THE DEVELOPING PLANT EMBRYO.			
CC	-1- INDUCTION: TYPE B ISOZYME MRNA IS UNDETECTABLE IN UNSTIMULATED CELLS AND INCREASES A HUNDRED-FOLD AFTER STIMULATION WITH GIBBERELLIC ACID.			
CC	-1- MISCELLANEOUS: THERE ARE AT LEAST 4 TYPES OF ALPHA-AMYLASE IN BARLEY.			
CC	-1- SIMILARITY: BELONGS TO FAMILY 13 OF GLYCOSYL HYDROLASES, ALSO KNOWN AS THE ALPHA-AMYLASE FAMILY.			
CC	-----			
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CC	-----			
DR	EMBL; X15226; CAA33298.1; -			
DR	EMBL; K02637; AAA98790.1; -			
DR	PIR; A31960; ALBHB.			
DR	PDB; 1AMY; 13-MAY-95.			
DR	PDB; 1AV4; 16-MAR-99.			

DR	PDB: 1BG9, 15-JUN-89.	Alp, amyl_cat, sub.
DR	InterPro: IPR006589.	Alp, amyl_cat, sub.
DR	InterPro: IPR006047; Alpha_Amyl_cat.	
DR	InterPro: IPR006046; Glyco_hydro_13.	
DR	Pfam: PF00128; alpha-amylase_1.	
DR	PRINTS: PR00110; ALPHAMYLASE.	
DR	SMART: SM00542; Amy_1.	
DR	Hydrolase; Glycosidase; Carbohydrate metabolism; Seed; Germination;	
KM	Calcium; Multigene family; Signal; 3D-structure.	
KM	Signal.	
FT	CHAIN	25 427 24
FT	ACT_SITE	203 203
FT	ACT_SITE	228 228
FT	ACT_SITE	313 313
FT	CONFLICT	134 134
FT	CONFLICT	195 197
FT	CONFLICT	425 425
FT	STRAND	27 29
FT	TURN	33 34
FT	HELIX	35 37
FT	TURN	39 40
FT	HELIX	42 47
FT	TURN	48 49
FT	HELIX	50 56
FT	TURN	57 57
FT	STRAND	60 63
FT	STRAND	69 69
FT	TURN	72 73
FT	STRAND	77 77
FT	TURN	80 81
FT	TURN	84 85
FT	TURN	87 88
FT	HELIX	91 104
FT	TURN	105 105
FT	STRAND	107 112
FT	STRAND	116 116
FT	STRAND	121 122
FT	TURN	124 125
FT	STRAND	128 130
FT	TURN	139 140
FT	HELIX	144 146
FT	STRAND	147 147
FT	TURN	149 150
FT	TURN	152 154
FT	STRAND	165 165
FT	TURN	168 169
FT	STRAND	172 173
FT	TURN	175 176
FT	HELIX	178 193
FT	TURN	194 195
FT	STRAND	199 202
FT	TURN	203 204
FT	HELIX	205 207
FT	HELIX	210 220
FT	STRAND	224 227
FT	STRAND	235 235
FT	TURN	237 238
FT	STRAND	241 241
FT	HELIX	246 260
FT	TURN	261 262
FT	STRAND	265 268
FT	HELIX	270 279
FT	TURN	280 282
FT	HELIX	284 287
FT	TURN	290 291
FT	HELIX	297 299
FT	TURN	300 300
FT	HELIX	302 304
FT	STRAND	305 308
FT	TURN	312 314
FT	TURN	316 318
FT	HELIX	325 327
FT	HELIX	328 337

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FT STRAND 341 345
FT HELIX 346 350
FT TURN 351 351
FT HELIX 355 367
FT TURN 368 369
FT TURN 372 373
FT STRAND 376 382
FT TURN 383 384
FT STRAND 385 390
FT TURN 391 393
FT STRAND 394 398
FT HELIX 405 407
FT STRAND 412 418
FT TURN 419 420
FT STRAND 421 427
SQ SEQUENCE 427 AA; 47355 MM; 957C0B16621BF748 CRC64;

Query Match 74.0%; Score 54; DB 1; Length 427;
Best Local Similarity 73.3%; Pred. No. 0.011;
Matches 11; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 IDRLVSIRTRGQIHS 15
DB 358 IDRLVSIRTRGQIHS 372

RESULT 4
AMY5_HORVU STANDARD; PRT: 135 AA.
ID AMY5_HORVU
AC P04749;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Alpha-amylase type B isozyme (EC 3.2.1.1) (1,4-alpha-D-glucan
DE glucanohydrolase) (Clone 168) (Fragment).
GN AMY1.5
OS Hordeum vulgare (Barley).
OC Euarystida; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
OC Triticeae; Hordeum.
OC NCBI_TaxID=4513;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85159405; PubMed=6335720;
RA Huang J.-K., Sweigle M., Dandekar A.M., Muthukrishnan S.;
RT "Expression and regulation of alpha-amylase gene family in barley
RT aleurones."
RL J. Mol. Appl. Genet. 2:579-588(1984).
CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic
CC linkages in oligosaccharides and polysaccharides.
CC -1- COFACTOR: BINDS A CALCIUM ION REQUIRED FOR ITS ACTIVITY.
CC -1- DEVELOPMENTAL STAGE: PRODUCTION OF ALPHA-AMYLASE IS HORMONALLY
CC REGULATED. GERMINATING EMBRYOS PRODUCE THE HORMONE GIBBERELLIC
CC ACID, WHICH WITHIN 10 HOURS STIMULATES THE ALEURONE CELLS COVERING
CC THE ENDOSPERM OF THE SEED TO PRODUCE ALPHA-AMYLASE. THE ENZYME
CC THEN DEGRADES THE STARCH WITHIN THE ENDOSPERM FOR USE BY THE
CC DEVELOPING PLANT EMBRYO.
CC -1- MISCELLANEOUS: THERE ARE AT LEAST 4 TYPES OF ALPHA-AMYLASE IN
CC BARLEY.
CC -1- MISCELLANEOUS: TYPE B ISOZYME MRNA IS UNDETECTABLE IN UNSTIMULATED
CC CELLS AND INCREASES A HUNDRED-FOLD AFTER STIMULATION WITH
CC GIBBERELLIC ACID.
CC -1- SIMILARITY: BELONGS TO FAMILY 13 OF GLYCOSYL HYDROLASES, ALSO
CC KNOWN AS THE ALPHA-AMYLASE FAMILY.
CC -----
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CC -----

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DR EMBL: K02635; AAA32931.1; -.
DR PIR: C21826; C21826.
DR HSSP: P04063; IAVA.
DR InterPro: IPR006047; Alpha.amyl.cat.
DR Pfam: PF00128; alpha-amylase; 1.
KW Hydrolase; Glycosidase; Carbohydrate metabolism; Seed; Germination;
KW Calcium; Multigene family.
FT ACT_SITE 21 21 BY SIMILARITY.
FT NON_TER 1
SQ SEQUENCE 135 AA; 15140 MM; 947E71F5E13DD2A6 CRC64;

Query Match 69.9%; Score 51; DB 1; Length 135;
Best Local Similarity 73.3%; Pred. No. 0.011;
Matches 11; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 IDRLVSIRTRGQIHS 15
DB 66 IDRLVSIRTRGQIHS 80

RESULT 5
BCSA_BACSU STANDARD; PRT: 365 AA.
ID BCSA_BACSU
AC P54157;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Putative chalcone synthase (EC 2.3.1.74) (Naringenin-chalcone
DE synthase).
GN BCSA
OS Bacillus subtilis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OC NCBI_TaxID=1423;
RN [1]
RP SEQUENCE FROM N.A.
RX SPRAIN-168 / Marburg;
RX MEDLINE=96349105; PubMed=8760912;
RA Sorokin A.V., Azevedo V., Zumbstein E., Galleron N., Ehrlich S.D.,
RA Serior P.;
RT "Sequence analysis of the Bacillus subtilis chromosome region between
RT the sera and kgd loci cloned in a yeast artificial chromosome."
RL Microbiology 142:2005-2016(1996).
RN [2]
RP SEQUENCE FROM N.A.
RX SPRAIN-168;
RX MEDLINE=98044033; PubMed=9384377;
RA Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,
RA Azevedo V., Bertorello M.G., Bessieres P., Bolotin A., Borchert S.,
RA Borriss R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
RA Brouillet S., Brusch C.V., Caldwell B., Capuano V., Carter N.M.,
RA Choi S.K., Codani J.J., Connerion I.F., Cummings N.J., Daniel R.A.,
RA Danilot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emerson P.T.,
RA Eutling K.D., Errington J., Fabret C., Ferrari E., Fougere D.,
RA Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
RA Ghim S.Y., Glaeser P., Goffeau A., Golligly E.J., Grandi G.,
RA Giuseppe G., Guy B.J., Haga K., Halech J., Harwood C.R., Henaut A.,
RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
RA Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C.,
RA Kobayashi Y., Koetter P., Koningsstein G., Krogh S., Kumano M.,
RA Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
RA Lee S.M., Levine A., Liu H., Masuda S., Manuel C., Medigue C.,
RA Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,
RA Noone D., O'Reilly M., Ogawa K., Ogihara A., Oudega B., Park S.H.,
RA Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,
RA Presecan E., Pujic P., Purnelle B., Rapoport G., Ray M., Reynolds S.,
RA Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadaie Y.,
RA Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,
RA Sekiguchi J., Sekowska A., Seror S.J., Seror P., Shin B.S., Soldo B.,
RA Sorokini M., Taccioni E., Takagi T., Takahashi H., Takemaru K.,
RA Takenuchi M., Takamochi A., Tanaka T., Terpstra P., Tognoni A.,
RA Tosato V., Uchiyama S., Vandenbol M., Vannier F., Vassarotti A.,
RA Viari A., Wambutt R., Wedler E., Wedler H., Welzenegger T.,
RA Winters P., Wipet A., Yamamoto H., Yamane K., Yasunoto K., Yata K.,

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RA Yoshida K., Yoshikawa H.F., Zumbstein E., Yoshikawa H., Danchin A.;
RT "The complete genome sequence of the Gram-positive bacterium Bacillus
RT subtilis."
RL Nature 390:249-256(1997).
RN [3]
RP SEQUENCE OF 1-27 FROM N.A.
RC STRAIN-168;
RA Saxild H.H., Christensen L., Nygaard P., Schou S.;
RL Submitted (JUN-1995) to the EMBL/GenBank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: 3 malonyl-CoA + 4 coumaroyl-CoA = 4 CoA +
CC naringenin-chalcone + 3 CO(2)
CC
CC -1- SIMILARITY: BELONGS TO THE CHALCONE/STILBENE SYNTHASES FAMILY.
CC
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CC -----
CC EMBL: L77246; AAA96613.1; -
CC EMBL: Z99115; CAB14122.1; -
CC EMBL: X83878; -; NOT_ANNOTATED_CDS.
CC PIR: A69593; A69593.
CC Subtilist; BG11523; bcsA.
CC InterPro: IPR001099; N-C-synthase.
CC Pfam: PF00195; Chal_stil_synth; 1.
CC Pfam: PF02797; Chal_stil_synth; 1.
CC PRODOM: PD000453; N-C-synthase; 1.
CC PROSITE: PS00441; CHALCONE_SYNTM; 1.
CC Transferrase: Acyltransferase; Complete proteome.
CC ACT SITE 144 BY SIMILARITY.
CC SEQUENCE 365 AA; 40713 MW; 2c8779BD648925A4 CRC64;

Query Match 61.6%; Score 45; DB 1; Length 365;
Best Local Similarity 66.7%; Pred. No. 0.5;
Matches 10; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

OY 1 IDRLVSIRTRGOIHS 15
DB 36 IDRLVSIRTRGOIHS 50

RESULT 6
AMYLORISA STANDARD: PRT; 428 AA.
AC P17654;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Alpha-amylase precursor (EC 3.2.1.1) (1,4-alpha-D-glucan
DE glucanohydrolase) (Isozyme 1b).
GN AMY1.1 OR AMY1A.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-CV. Japonica M202;
RL MEDLINE-91346657; PubMed-2102847;
RA Huang N., Sutliff T.D., Lits J.C., Rodriguez R.L.;
RT "Classification and characterization of the rice alpha-amylase
RT multigene family."
RT Plant Mol. Biol. 14:655-668(1990).
RN [2]
RP SEQUENCE FROM N.A. (CLONE POS103).
RC STRAIN-CV. Japonica M202;
RL MEDLINE-90318322; PubMed-2370848;
RA O'Neill S.D., Kunagai M.H., Majumdar A., Huang N., Sutliff T.D.,
Rodriguez R.L.;

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RT "The alpha-amylase genes in Oryza sativa: characterization of cDNA
RT clones and mRNA expression during seed germination."
RL Mol. Gen. Genet. 221:235-244(1990).
CC -1- FUNCTION: IMPORTANT FOR BREAKDOWN OF ENDOSPERM STARCH DURING
CC GERMINATION.
CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic
CC linkages in oligosaccharides and polysaccharides.
CC -1- COFACTOR: BINDS A CALCIUM ION REQUIRED FOR ITS ACTIVITY.
CC -1- SUBUNIT: Monomer.
CC -1- TISSUE SPECIFICITY: MORE ABUNDANT IN GERMINATING SEEDS, THAN IN
CC CALDUS, YOUNG ROOTS AND LEAVES.
CC -1- DEVELOPMENTAL STAGE: EXPRESSED AT A HIGH LEVEL DURING GERMINATION
CC IN THE ALEURONES CELLS UNDER THE CONTROL OF THE PLANT HORMONE
CC GIBBERELIC ACID AND IN THE DEVELOPING GRAINS AT A LOW LEVEL.
CC -1- PTM: ONLY CEREAL AMYLASE KNOWN TO BE GLYCOSYLATED.
CC -1- SIMILARITY: BELONGS TO FAMILY 13 OF GLYCOSYL HYDROLASES, ALSO
CC KNOWN AS THE ALPHA-AMYLASE FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: X16509; CAA34516.1; -
CC EMBL: M24286; AAA33885.1; ALT_INIT.
CC PIR: S10013; S10013.
CC HSSP: P04063; IAVA.
CC Gramene: P17654; -
CC InterPro: IPR006589; Alp_amy1_cat_sub.
CC InterPro: IPR006047; Alpha_amy1_cat.
CC InterPro: IPR006046; Glyco_hydro_13.
CC Pfam: PF00128; alpha-amylase; 1.
CC PRINTS: PR00110; ALPHAMYLASE.
CC SMART: SM00542; Amy1; 1.
CC K01 Hydroxylase; Glycosidase; Carbohydrate metabolism; Calcium; Signal;
KM Glycoprotein; Multigene family.
FT SIGNAL 1 25 PROBABLE.
FT CHAIN 26 428 ALPHA-AMYLASE.
FT ACT_SITE 203 203 BY SIMILARITY.
FT ACT_SITE 314 314 BY SIMILARITY.
FT METAL 116 116 CALCIUM (BY SIMILARITY).
FT METAL 174 174 CALCIUM (BY SIMILARITY).
FT CARBOHYD 265 265 N-LINKED (GLCNAC. . .) (PROBABLE).
SQ SEQUENCE 428 AA; 47755 MW; 3B71403AACFEC6A6 CRC64;

Query Match 61.6%; Score 45; DB 1; Length 428;
Best Local Similarity 71.4%; Pred. No. 0.6;
Matches 10; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 1 IDRLVSIRTRGOIH 14
DB 359 IDRLVSIRTRGOIH 372

RESULT 7
AMY3_HORVU STANDARD: PRT; 368 AA.
ID AMY3_HORVU
AC P04747;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 15-JUN-1999 (Rel. 38, Last annotation update)
DE Alpha-amylase type B isozyme precursor (EC 3.2.1.1) (1,4-alpha-D-
DE glucan glucanohydrolase) (Clone PHV19) (Fragment).
GN AMY1.3
OS Hordeum vulgare (Barley).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Triticeae; Hordeum.
OX NCBI_TaxID=4513;
RN [1]

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RP SEQUENCE FROM N.A.
RA Chandler P.M., Zwar J.A., Jacobsen J.V., Higgins T.J.V., Inglis A.S.;
RT "The effects of gibberellic acid and abscisic acid on alpha-amylase
RT mRNA levels in barley aleurone layers studies using an alpha amylase
RT cDNA clone."
RL Plant Mol. Biol. 3:407-418(1984).
CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic
CC linkages in oligosaccharides and polysaccharides.
CC -1- COFACTOR: BINDS A CALCIUM ION REQUIRED FOR ITS ACTIVITY.
CC -1- DEVELOPMENTAL STAGE: PRODUCTION OF ALPHA-AMYLASE IS NORMALLY
CC REGULATED. GERMINATING EMBRYOS PRODUCE THE HORMONE GIBBERELIC
CC ACID, WHICH WITHIN 10 HOURS STIMULATES THE ALEURONE CELLS COVERING
CC THE ENDOSPERM OF THE SEED TO PRODUCE ALPHA-AMYLASE. THE ENZYME
CC THEN DEGRADS THE STARCH WITHIN THE ENDOSPERM FOR USE BY THE
CC DEVELOPING PLANT EMBRYO.
CC -1- MISCELLANEOUS: THERE ARE AT LEAST 4 TYPES OF ALPHA-AMYLASE IN
CC BARLEY.
CC -1- MISCELLANEOUS: TYPE B ISOZYME MRNA IS UNDETECTABLE IN UNSTIMULATED
CC CELLS AND INCREASES A HUNDRED-FOLD AFTER STIMULATION WITH
CC GIBBERELIC ACID.
CC -1- SIMILARITY: BELONGS TO FAMILY 13 OF GLYCOSYL HYDROLASES, ALSO
CC KNOWN AS THE ALPHA-AMYLASE FAMILY.
CC -----
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CC -----
DR EMBL: K02638; AAA32933.1; -.
DR HSSP: P04063; IAVA.
DR InterPro: IPR006589; Alp_amy1_cat_sub.
DR InterPro: IPR006047; Alpha_amy1_cat.
DR Pfam: PF00128; alpha-amylase; 1.
DR SMART: SM00642; Amy; 1.
DR SMART: Glycosidase; Carbohydrate metabolism; Seed; Germination;
KW Calcium; Multigene family; Signal.
FT SIGNAL 1 24
FT CHAIN 25 >368 ALPHA-AMYLASE TYPE B ISOZYME.
FT ACT_SITE 203 203 BY SIMILARITY.
FT ACT_SITE 228 228 BY SIMILARITY.
FT ACT_SITE 313 313 BY SIMILARITY.
FT NON_TER 368 368
SQ SEQUENCE 368 AA; 40787 MW; A237EF55793BA93B CRC64;

Query Match 54.8%; Score 40; DB 1; Length 368;
Best Local Similarity 88.9%; Pred. No. 4.7;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 IDRLVSIRT 9
DB 358 IDRLVSIRT 366

RESULT 8
NRH3_MOUSE STANDARD; PRT; 445 AA.
ID NRH3_MOUSE
AC Q9Z0Y9; G9Q0U7;
DT 30-MAY-2000 (Rel. 39, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Oxyterol receptor LXR-alpha (Liver X receptor alpha) (Nuclear orphan
DE receptor LXR-alpha).
GN NR1H3 OR LXR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCB1_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=129/SvJ; TISSUE=Liver;

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RX MEDLINE=20156373; PubMed=10675617;
RA Alberti S., Steffensen K.R., Gustafsson J.-A.;
RT "Structural characterisation of the mouse nuclear oxysterol receptor
RT gene LXRalpha and LXRbeta."
RL Gene 243:93-103(2000).
RN [2]
RP SEQUENCE FROM N.A.
RA Chen Y.E., Horiuchi M., Dzau V.J.;
RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: ORPHAN RECEPTOR. INTERACTION WITH RXR SHIFTS RXR FROM
CC ITS ROLE AS A SILENT DNA-BINDING PARTNER TO AN ACTIVE LIGAND-
CC BINDING SUBUNIT IN MEDIATING RETINOID RESPONSES THROUGH TARGET
CC GENES DEFINED BY LXRES. LXRES ARE DR-1-TYPE RESPONSE ELEMENTS
CC CHARACTERIZED BY DIRECT REPEATS OF TWO SIMILAR HEXANUCLEOTIDE HALF-
CC SITES SPACED BY FOUR NUCLEOTIDES. LXRA PLAYS AN IMPORTANT ROLE IN
CC THE REGULATION OF CHOLESTEROL HOMEOSTASIS.
CC -1- SUBUNIT: HETERODIMER OF LXRA AND RXR.
CC -1- SUBCELLULAR LOCATION: Nuclear (Potential).
CC -1- SIMILARITY: Belongs to the nuclear hormone receptor family. NR1
CC subfamily.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: AJ132599; CAB51952.1; -.
DR EMBL: AJ132600; CAB51952.1; JOINED.
DR EMBL: AJ132601; CAB51923.1; -.
DR EMBL: AF085745; AAD16050.1; -.
DR HSSP: P03372; IHCO.
DR TRANSFAC: T04430; -.
DR MGD: MGI:1352462; Nr1h3.
DR InterPro: IPR000536; Hormone_rec_1lg.
DR InterPro: IPR001723; Steroidm_receptor.
DR InterPro: IPR001628; Znfc4steroid.
DR Pfam: PF00104; hormone_rec; 1.
DR PRINTS: PR00398; STRODHOMONER.
DR PRINTS: PR00047; STRODFINGER.
DR PRODOM: PD000035; Znfc4steroid; 1.
DR SMART: SM00430; HO1; 1.
DR SMART: SM00399; Znfc4; 1.
DR PROSITE: PS00031; NUCLEAR_RECEPTOR; 1.
KW Receptor; Transcription regulation; DNA-binding; Nuclear protein;
KW Zinc-finger.
FT DNA_BIND 96 161 NUCLEAR RECEPTOR-TYPE.
FT ZN_FING 96 116 C4-TYPE.
FT ZN_FING 132 156 C4-TYPE.
FT DOMAIN 213 432 LIGAND-BINDING (POTENTIAL).
FT CONFLICT 399 399 R -> P (IN REF. 2).
SQ SEQUENCE 445 AA; 50476 MW; CC9A8DF3BD935593 CRC64;

Query Match 53.4%; Score 39; DB 1; Length 445;
Best Local Similarity 53.8%; Pred. No. 9.1;
Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 3 RLVSIRTRQIHS 15
DB 408 KLVSRLTSSVHS 420

RESULT 9
NRH3_RAT STANDARD; PRT; 445 AA.
ID NRH3_RAT
AC O62685;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Oxyterol receptor LXR-alpha (Liver X receptor alpha) (Nuclear orphan
DE receptor LXR-alpha).

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DE receptor LXR-alpha) (RLD-1).
GN NRH3 OR LXRA.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_Taxid=10116.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver.
RA MEDLINE=95021230; PubMed=7935418;
RA Apfel R.H., Bendrook D., Lernerhart E., Ottiz M.A., Salbert G.,
RA Pahl M.;
RT "A novel orphan receptor specific for a subset of thyroid hormone-
RT responsive elements and its interaction with the retinoid/thyroid
RT hormone receptor subfamily."
RL Mol. Cell. Biol. 14:7025-7035(1994).
CC -1- FUNCTION: ORPHAN RECEPTOR. INTERACTION WITH RXR SHIFTS RXR FROM
CC ITS ROLE AS A SILENT DNA-BINDING PARTNER TO AN ACTIVE LIGAND-
CC BINDING SUBUNIT IN MEDIATING RETINOID RESPONSES THROUGH TARGET
CC GENES DEFINED BY LXRES. LXRES ARE DR4-TYPE RESPONSE ELEMENTS
CC CHARACTERIZED BY DIRECT REPEATS OF TWO SIMILAR HEXANUCLEOTIDE HALF-
CC SITES SPACED BY FOUR NUCLEOTIDES. LXRA PLAYS AN IMPORTANT ROLE IN
CC THE REGULATION OF CHOLESTEROL HOMEOSTASIS (BY SIMILARITY).
CC -1- SUBUNIT: HETERODIMER OF LXRA AND RXR (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Nuclear (potential).
CC -1- TISSUE SPECIFICITY: IN ADULTS IT IS EXPRESSED IN SPLEEN,
CC PITUITARY, LUNG, LIVER, AND FAT. WEAKER EXPRESSION IS OBSERVED IN
CC SEVERAL OTHER TISSUES.
CC -1- SIMILARITY: Belongs to the nuclear hormone receptor family. NRI
CC subfamily.
CC -----
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CC -----
CC EMBL: U01685; AAC53633.1;
CC PIR: A56043; A56043.
CC DR HSSP: P03372; IHCO.
CC DR TRANSFAC: T04434.
CC DR InterPro: IPR000536; Hormone_rec_1lg.
CC DR InterPro: IPR001723; Sterhmr_receptor.
CC DR InterPro: IPR001628; Znfc4steroid.
CC DR Pfam: PF00105; zf-C4; 1.
CC DR PRINTS: PR00398; STROHOMNER.
CC DR PRINTS: PR00047; STROIDFINGER.
CC DR ProDom: PD000035; Znfc4steroid; 1.
CC DR SMART: SM00430; HOL1; 1.
CC DR SMART: SM00399; ZnF_C4; 1.
CC DR PROSITE: PS00031; NUCLEAR_RECEPTOR; 1.
CC DR Receptor; Transcription regulation; DNA-binding; Nuclear protein;
CC Zinc-finger.
CC KW DNA_BIND 96 161 NUCLEAR RECEPTOR-TYPE.
CC FT ZN_FING 96 116 C4-TYPE.
CC FT ZN_FING 132 156 C4-TYPE.
CC FT DOMAIN 213 432 LIGAND-BINDING (POTENTIAL).
CC SO SEQUENCE 445 AA; 50554 MW; 131A84AB12A8B2 CRC64;

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Query Match 53.4%; Score 39; DB 1; Length 445;
 Best Local Similarity 53.8%; Pred. No. 9.1;
 Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

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ID NRH2 MOUSE STANDARD; PRT: 446 AA.
AC O06644.
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Oxytetracycline receptor LXR-beta (liver X receptor beta) (Nuclear orphan
DE receptor LXR-beta) (ubiquitously-expressed nuclear receptor) (Retinoid
DE X receptor interacting protein No.15).
GN NRH2 OR LXRB OR UNR2 OR UNR OR RIP15.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RC MEDLINE=95280959; PubMed=7760852;
RA Seol W., Choi H.S., Moore D.D.;
RT "Isolation of proteins that interact specifically with the retinoid X
RT receptor: two novel orphan receptors."
RL Mol. Endocrinol. 9:72-85(1995).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=129/SvJ; TISSUE=Liver;
RC MEDLINE=20156373; PubMed=10675617;
RA Alberti S., Steffensen K.R., Gustafsson J.-A.;
RA "Structural characterisation of the mouse nuclear oxytetracycline receptor
RT genes LXRAalpha and LXRBeta."
RL Gene 243:93-103(2000)
CC -1- FUNCTION: ORPHAN RECEPTOR. BINDS PREFERENTIALLY TO DOUBLE-STRANDED
CC OLIGONUCLEOTIDE DIRECT REPEATS HAVING THE CONSENSUS HALF-SITE
CC SEQUENCE 5'-ACGCA-3' AND A-NT SPACING (DR-4).
CC -1- SUBUNIT: FORMS A HETERODIMER WITH RXR.
CC -1- SUBCELLULAR LOCATION: Nuclear (potential).
CC -1- TISSUE SPECIFICITY: Ubiquitous.
CC -1- SIMILARITY: Belongs to the nuclear hormone receptor family. NRI
CC subfamily.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: U09419; AAC52164.1;
CC PIR: A132602; CAB51924.1;
CC DR HSSP: P03372; IHCO.
CC DR TRANSFAC: T04467;
CC DR InterPro: IPR000536; Hormone_rec_1lg.
CC DR InterPro: IPR001723; Sterhmr_receptor.
CC DR InterPro: IPR001628; Znfc4steroid.
CC DR Pfam: PF00105; zf-C4; 1.
CC DR PRINTS: PR00398; STROHOMNER.
CC DR PRINTS: PR00047; STROIDFINGER.
CC DR ProDom: PD000035; Znfc4steroid; 1.
CC DR SMART: SM00430; HOL1; 1.
CC DR SMART: SM00399; ZnF_C4; 1.
CC DR PROSITE: PS00031; NUCLEAR_RECEPTOR; 1.
CC DR Receptor; Transcription regulation; DNA-binding; Nuclear protein;
CC Zinc-finger.
CC KW DNA_BIND 78 145 NUCLEAR RECEPTOR-TYPE.
CC FT ZN_FING 78 98 C4-TYPE.
CC FT ZN_FING 116 140 C4-TYPE.
CC FT DOMAIN 216 446 LIGAND-BINDING (POTENTIAL).
CC FT DOMAIN 162 168 POLY-GLN.
CC FT DOMAIN 169 172 POLY-PRO.
CC SO SEQUENCE 446 AA; 49719 MW; 73153B635302C9DF CRC64;

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RESULT 10
 NRH2_MOUSE

Query Match 53.4%; Score 39; DB 1; Length 446;
 Best Local Similarity 53.8%; Pred. No. 9.1;
 Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

3 RLVSTRTGQIHS 15
 :|||:|:|:|
 Db 409 KLVSLRTLSVHS 421

RESULT 11
 NRH2_RAT STANDARD; PRT; 446 AA.
 ID 062755: 062694;
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Oxytocin receptor LXR-beta (Liver X receptor beta) (Nuclear orphan
 DE receptor LXR-beta) (Ubiquitously-expressed nuclear receptor) (UR
 DE (Orphan nuclear receptor OR-1).
 GN NR1H2 OR LXRb.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus;
 OC NCBI_TaxID=10116;
 [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-Sprague-Dawley; TISSUE=Liver;
 RX MEDLINE=95199298; PubMed=7892230;
 RA Teboul M., Enmark E., Li Q., Wikstrom A.C., Peltto-Huikko M.,
 RA Gustafsson J.-A.;
 RT "OR-1, a member of the nuclear receptor superfamily that interacts
 RT with the 9-cis-retinoic acid receptor."
 RL Proc. Natl. Acad. Sci. U.S.A. 92:2096-2100(1995).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-Sprague-Dawley; TISSUE=Vagina;
 RX MEDLINE=95062154; PubMed=7971966;
 RA Song C., Kokontis J.M., Hlipakka R.A., Liao S.;
 RT "Ubiquitous receptor: a receptor that modulates gene activation by
 RT retinoic acid and thyroid hormone receptors."
 RL Proc. Natl. Acad. Sci. U.S.A. 91:10809-10813(1994).
 CC -1- FUNCTION: ORPHAN RECEPTOR. BINDS PREFERENTIALLY TO DOUBLE-STRANDED
 CC OLIGONUCLEOTIDE DIRECT REPEATS HAVING THE CONSENSUS HALF-SITE
 CC SEQUENCE 5'-AGGTCA-3' AND 4'-NT SPACING (DR-4).
 CC -1- SUBUNIT: FORMS A HETERODIMER WITH RXR.
 CC -1- SUBCELLULAR LOCATION: Nuclear (Potential).
 CC -1- SIMILARITY: Belongs to the nuclear hormone receptor family. NR1
 CC subfamily.
 CC -----
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 CC -----
 CC EMBL: U20389; AAA69522.1; -;
 CC EMBL: U14533; AAA52361.1; -;
 CC PIR: I59354; I59354.
 CC HSSP: P03372; IHCO.
 CC TRANSFAC: T04451; -;
 CC InterPro: IPR000536; Hormone_rec_119.
 CC InterPro: IPR001723; Steroid_receptor.
 CC InterPro: IPR001628; znf_C4steroid.
 CC Pfam: PF00104; hormone_rec.1.
 CC Pfam: PF00105; znf-C4.1.
 CC PRINTS: PR00398; STRDHOMONER.
 CC PRINTS: PR00047; STRODIFINGER.
 CC PRODOM: PD000035; znf_C4steroid.1.
 CC SMART: SM00430; HOLT.1.
 CC SMART: SM00399; znf-C4.1.
 CC PROSITE: PS00031; NUCLEAR_RECEPTOR.1.

KW Receptor; Transcription regulation; DNA-binding; Nuclear protein;
 DT Zinc-finger. 78 145
 FT ZN_FING 78 98
 FT ZN_FING 116 140
 FT DOMAIN 216 446
 FT DOMAIN 162 168
 FT DOMAIN 169 172
 FT CONFLICT 33 33
 FT CONFLICT 52 54
 FT CONFLICT 219 219
 SQ SEQUENCE 446 AA; 49735 MW; 13DF6DC2F0F5FA4D CRC64;

Query Match 53.4%; Score 39; DB 1; Length 446;
 Best Local Similarity 53.8%; Pred. No. 9.1;
 Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

3 RLVSTRTGQIHS 15
 :|||:|:|:|
 Db 409 KLVSLRTLSVHS 421

RESULT 12
 NRH3_HUMAN STANDARD; PRT; 447 AA.
 ID 013133; 096h87.
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Oxytocin receptor LXR-alpha (Liver X receptor alpha) (Nuclear orphan
 DE receptor LXR-alpha).
 GN NR1H3 OR LXRa.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OC NCBI_TaxID=9606;
 [1]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC TISSUE=Liver;
 RX MEDLINE=95262897; PubMed=7744246;
 RA Willy P.J., Umesono K., Ong E.S., Evans R.M., Heyman R.A.,
 RA Mangelsdorf D.J.;
 RT "LXR, a nuclear receptor that defines a distinct retinoid response
 RT pathway."
 RL Genes Dev. 9:1033-1045(1995).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORM 2).
 RC TISSUE=Placenta;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altshul S.F., Zeeberg B., Buetow K.H., Scheffer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin J.M., Hong L.,
 RA Straplenko M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullan S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gnaratine P.H.,
 RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butlerfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences."
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 CC -1- FUNCTION: ORPHAN RECEPTOR. INTERACTION WITH RXR SHIFTS RXR FROM
 CC ITS ROLE AS A SILENT DNA-BINDING PARTNER TO AN ACTIVE LIGAND-
 CC BINDING SUBUNIT IN MEDIATING RETINOID RESPONSES THROUGH TARGET
 CC GENES DEFINED BY LXRES. LXRES ARE DR4-TYPE RESPONSE ELEMENTS

CC CHARACTERIZED BY DIRECT REPEATS OF TWO SIMILAR HEXANUCLEOTIDE HALF-
 CC STES SPACED BY FOUR NUCLEOTIDES. LXXA PLAYS AN IMPORTANT ROLE IN
 CC THE REGULATION OF CHOLESTEROL HOMEOSTASIS.
 CC -1- SUBUNIT: HETERODIMER OF LXXA AND RXR.
 CC -1- SUBCELLULAR LOCATION: Nuclear (Potential).
 CC -1- ALTERNATIVE PRODUCTS:
 CC Name=1;
 CC Name=2;
 CC IsoId-Q13133-1; Sequence=Displayed;
 CC Name=2;
 CC IsoId-Q13133-2; Sequence=VSP_003664;
 CC Note=No experimental confirmation available:
 CC -1- TISSUE SPECIFICITY: VISCERAL ORGANS SPECIFIC EXPRESSION. STRONG
 CC EXPRESSION WAS FOUND IN LIVER, KIDNEY AND INTESTINE FOLLOWED BY
 CC SPLEEN AND TO A LESSER EXTENT THE ADRENALS.
 CC -1- INDUCTION: BY 9-CIS RETINOIC ACID (9CRA).
 CC -1- SIMILARITY: Belongs to the nuclear hormone receptor family. NR1
 CC subfamily.
 CC -----
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 CC -----
 CC EMBL: U22662; AAA85856.1; -.
 CC DR EMBL: BC008819; AAH08919.1; -.
 CC DR PIR: I38975; I38975.
 CC DR HSSP: P03372; IHCO.
 CC DR TRANSFAC: T02752; -.
 CC DR Genew: HGNC:7966; NR1H3.
 CC DR MIM: 602423; -.
 CC DR GO: GO:0005634; C:nucleus; TAS.
 CC DR GO: GO:0007213; F:transcription co-activator activity; TAS.
 CC DR InterPro: IPR000535; Hormone_rec.Lig.
 CC DR InterPro: IPR001723; Steroid_receptor.
 CC DR InterPro: IPR001628; ZnF_C4steroid.
 CC DR Pfam: PF00104; hormone_rec.1.
 CC DR Pfam: PF00105; zf-C4; 1.
 CC DR PRINTS: PR00398; STERODRMONER.
 CC DR PRINTS: PR00047; STERODPTRNGR.
 CC DR PRODOM: PD000035; ZnF_C4steroid; 1.
 CC DR SMART: SM00430; HOL1; 1.
 CC DR SMART: SM00390; ZnF_C4; 1.
 CC DR PROSITE: PS00031; NUCLEAR_RECEPTOR; 1.
 CC DR PROSITE: PS00031; NUCLEAR_RECEPTOR; DNA-binding; Nuclear protein;
 CC KW Zinc-finger; Alternative splicing.
 CC FT Dna_Bind 98 163 NUCLEAR RECEPTOR-TYPE.
 CC FT ZN_FING 98 118 C4-TYPE.
 CC FT ZN_FING 134 158 C4-TYPE.
 CC FT DOMAIN 215 434 LIGAND-BINDING (POTENTIAL).
 CC FT VARSPLIC 237 296 MISSING (in isoform 2).
 CC FT CONFLICT 196 196 A -> R (in REF. 1).
 CC FT SEQUENCE 447 AA; 50395 MW; 0D27B37440FB9C CRC64;
 CC
 CC Query Match 53.4%; Score 39; DB 1; Length 447;
 CC Best Local Similarity 53.8%; Pred. No. 9.1;
 CC Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
 CC
 CC OY 3 RLVSIRTGQHS 15
 CC DB 410 KLVSLRTLSVHS 422
 CC
 CC RESULT 13
 CC NR12_HUMAN STANDARD; PRT: 461 AA.
 CC AC P55055: Q12970:
 CC DT 01-OCT-1996 (Ref. 34, Created)
 CC DT 01-OCT-1996 (Ref. 34, Last sequence update)

DT 15-SEP-2003 (Ref. 42, Last annotation update)
 DE Oxytocin receptor LXR-beta (Liver X receptor beta) (Nuclear orphan
 DE receptor LXR-beta) (ubiquitously-expressed nuclear receptor) (Nuclear
 DE receptor NER)
 GN NR1H2 OR LXRβ OR UNR OR NER.
 OS Homo sapiens (human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Euteleostomi; Primates; Carnivora; Hominoidea; Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Osteosarcoma;
 RX MEDLINE=95011628; PubMed=7926814;
 RA Shinar D.M., Endo N., Rutledge S.J., Vogel R., Rodan G.A., Schmidt A.;
 RT "NER, a new member of the gene family encoding the human steroid
 RT hormone nuclear receptor."
 RL gene 147:273-276(1994).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Placenta;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feilgenfeldt E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Hopkins R.F., Zeeberg B., Buettow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stachleiron M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mulhally S.J.,
 RA Bosak S.A., McGowan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Huliyil S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Vahedi J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shychenko Y., Bouffard G.C.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Kravinsky M.I., Skalska U., Smalls D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Maitra M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences".
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [3]
 RP SEQUENCE OF 7-461 FROM N.A.
 RA Song C., Konkolis J.M., Hlipakka R.A., Liao S.,
 RA "Ubiquitous receptor: a novel receptor that modulates gene activation
 RA by retinoic acid and thyroid hormone receptors."
 RL Submitted (SEP-1994) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: ORPHAN RECEPTOR. BINDS PREFERENTIALLY TO DOUBLE-STRANDED
 CC OLIGONUCLEOTIDE DIRECT REPEATS HAVING THE CONSENSUS HALF-SITE
 CC SEQUENCE 5'-AGGTCA-3' AND 4-NT SPACING (DR-4).
 CC -1- SUBUNIT: FORMS A HETERODIMER WITH RXR.
 CC -1- SUBCELLULAR LOCATION: Nuclear (Potential).
 CC -1- TISSUE SPECIFICITY: Ubiquitous.
 CC -1- SIMILARITY: Belongs to the nuclear hormone receptor family. NR1
 CC subfamily.
 CC -----
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 CC -----
 CC EMBL: U07132; AAA61783.1; -.
 CC DR EMBL: BC007790; AAH07790.1; -.
 CC DR EMBL: U14534; AAA58594.1; -.
 CC DR PIR: JC4014; JC4014.
 CC DR HSSP: P03372; IHCO.
 CC DR TRANSFAC: T04453; -.
 CC DR Genew: HGNC:7965; NR1H2.
 CC DR MIM: 600380; -.
 CC DR GO: GO:0005634; C:nucleus; TAS.


```

FT REPEAT 1455 1487 HAT 1.
FT REPEAT 1561 1594 HAT 2.
FT REPEAT 1632 1664 HAT 3.
FT REPEAT 1666 1701 HAT 4.
SQ SEQUENCE 1729 AA; 193133 MW; 39BF46E5587B3B0A CRC64;

Query Match 53.4%; Score 39; DB 1; Length 1729;
Best Local Similarity 41.7%; Pred. No. 42;
Matches 5; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

OY 3 RUVSIFTRGQIH 14
DB 565 RUVSINSGNVH 576

RESULT 16
YHDL_YEAST STANDARD; PRT; 223 AA.
AC P38736;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 01-FEB-1996 (Rel. 33, Last annotation update)
DE Hypothetical 25.4 kDa protein in GUT1-RIM1 intergenic region.
GN YH031C.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=5288C / AB972;
RX MEDLINE=94378003; PubMed=8091229;
RA Johnston M., Andrews S., Brinkman R., Cooper J., Ding H., Dwyer J.,
RA Du Z., Favali A., Fulton L., Gattung S., Gelsel C., Kirsten J.,
RA Kucaba T., Hillier L., Jier M., Johnston L., Langston Y.,
RA Latreille P., Louis E.J., Macri C., Mandis E., Menezes S., Mouser L.,
RA Nham M., Rifkin L., Riles L., St Peter H., Trevasakis E., Vaughan K.,
RA Vignati D., Wilcox L., Wohlman P., Waterston R., Wilson R.,
RA Vandin M.;
RT "Complete nucleotide sequence of Saccharomyces cerevisiae chromosome
RT VIII."
RL Science 265:2077-2082(1994).
CC -!- SIMILARITY: TO S.FOMBE SPAC4G8.10.
CC -----
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CC -----
DR EMBL; U11583; AAB65043.1; -.
DR PIR; S48937; S48937.
DR SGD; S0001023; GOSL.
DR GO; GO:0016021; C:Integral to membrane; NAS.
DR Pfam; PF05008; V-SNARE; 1.
KM Hypothetical protein.
SQ SEQUENCE 223 AA; 25394 MW; 1E833249CC306C2 CRC64;

Query Match 52.1%; Score 38; DB 1; Length 223;
Best Local Similarity 52.9%; Pred. No. 6;
Matches 9; Conservative 2; Mismatches 4; Indels 2; Gaps 1;

OY 1 IDRLVSI--ITRGOIHS 15
DB 152 VDRLSQAMETRSQFHS 168

RESULT 17
VG61_HSV11 STANDARD; PRT; 319 AA.
AC 000122;

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DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 01-DEC-1992 (Rel. 24, Last annotation update)
DE Hypothetical gene 61 protein.
GN 61
OS Ictalurid herpesvirus 1 (channel catfish virus) (CCV).
OC viruses; dsDNA viruses, no RNA stage; Herpesviridae.
OC Ictalurid Herpes-like viruses.
OX NCBI_TaxID=10401;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Adorn 1;
RX MEDLINE=92087490; PubMed=1727613;
RA Davison A.J.;
RT "Channel catfish virus: a new type of herpesvirus.";
RL Virology 186:9-14(1992).
CC -----
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CC -----
DR EMBL; M75136; AAB8164.1; -.
DR PIR; H36792; H36792.
KM Hypothetical protein.
SQ SEQUENCE 319 AA; 36909 MW; 253E93AE41815143 CRC64;

Query Match 52.1%; Score 38; DB 1; Length 319;
Best Local Similarity 46.2%; Pred. No. 9;
Matches 6; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

OY 1 IDRLVSI--ITRGOI 13
DB 213 VDRLGKLRARGEV 225

RESULT 18
YH27_YEAST STANDARD; PRT; 365 AA.
AC P28625;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Hypothetical 41.6 kDa protein in IMPI-HLJ1 intergenic region (RF1095).
GN YMR152W OR YM9375.22 OR YM8520.01.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91360060; PubMed=1886606;
RA Behrens M., Michaelis G., Pralte E.;
RT "Mitochondrial inner membrane protease 1 of Saccharomyces cerevisiae
RT shows sequence similarity to the Escherichia coli leader peptidase.";
RL Mol. Gen. Genet. 228:167-176(1991).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=5288C / AB972;
RX PubMed=9169872;
RA Bowman S., Churcher C.M., Badcock K., Brown D., Chillingworth T.,
RA Connor R., Dedman K., Devlin K., Gentles S., Hamlin N., Hunt S.,
RA Jagels K., Lye G., Moule S., Odell C., Pearson D., Rajadream M.A.,
RA Rice R., Skelton J., Walsh S., Whitehead S., Barrett B.G.;
RT "The nucleotide sequence of Saccharomyces cerevisiae chromosome
RT XII."
RL Nature 387:90-93(1997).
CC -!- SIMILARITY: SOME: TO YEAST AST1/AST2.
CC -----
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 CC -----
 DR EMBL: S55518; AAB19702.1; -
 DR EMBL: Z47071; CAA87367.1; -
 DR EMBL: Z49705; CAA89788.1; -
 DR PIR: S50409; S50409.
 DR SGD: S0004760; YIM1.
 DR GO: GO:0005811; C:lipid particle; IDA.
 DR GO: GO:0005743; C:mitochondrial inner membrane; IDA.
 DR GO: GO:0008233; F:peptidase activity; IMP.
 DR GO: GO:0006627; P:mitochondrial processing; IMP.
 DR InterPro: IPR002085; Adh_zn_family.
 DR Pfam: PF00107; ADH_zinc_N; 1.
 DR KW Hypothetical protein; Transmembrane.
 FT TRANSMEM 140 158 POTENTIAL.
 FT CONFLICT 121 121 V -> I (IN REF. 1).
 FT CONFLICT 234 234 S -> I (IN REF. 1).
 FT CONFLICT 280 280 D -> N (IN REF. 1).
 FT CONFLICT 296 296 L -> S (IN REF. 1).
 SQ SEQUENCE 365 AA; 41637 MW; 88F6453D9E918A16 CRC64;
 Query Match 52.1%; Score 38; DB 1; Length 365;
 Best Local Similarity 53.8%; Pred. No. 11;
 Matches 7; Conservative 4; Mismatches 2; Indels 0; Gaps 0;
 QY 1 IDRLVSIRTRGOI 13
 Db 348 IDRLMSNRKGV 360
 Db 348 IDRLMSNRKGV 360
 RESULT 19
 RL17_THETH STANDARD: PRT; 118 AA.
 AC Q929H5;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE 50S ribosomal protein L17.
 GN RPLQ OR RPL17.
 OS Thermus thermophilus.
 OC Bacteria; Deinococcus-Thermus; Deinococci; Thermales; Thermaceae;
 OC Thermus.
 OX NCBI_TaxID=274;
 RP [1]
 RC STRAIN=HB8 / ATCC 27634;
 RX MEDLINE=99098837; PubMed=980810;
 RA Wada T., Yamazaki T., Kuramitsu S., Kyogoku Y.;
 RT "Cloning of the RNA polymerase alpha subunit gene from Thermus
 RT thermophilus HB8 and characterization of the protein.";
 RL J. Biochem. 125:143-150(1999).
 CC -1- SIMILARITY: BELONGS TO THE L17P FAMILY OF RIBOSOMAL PROTEINS.
 CC -----
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 CC -----
 DR EMBL: AB024328; BAA75550.1; -
 DR PDB: 1GD8; 28-JAN-03.
 DR InterPro: IPR000456; Ribosomal_L17.
 DR Pfam: PF01196; Ribosomal_L17; 1.
 DR ProDom: PD004277; Ribosomal_L17; 1.
 DR TIGRfams: TIGR00059; L17; 1.
 DR PROSITE: PS01167; RIBOSOMAL_L17; FALSE_NEG.
 DR PROSITE: PS01167; RIBOSOMAL_L17; FALSE_NEG.

KW Ribosomal protein; 3D-structure.
 SQ SEQUENCE 118 AA; 13715 MW; C98BD552F6C42AF CRC64;
 Query Match 50.7%; Score 37; DB 1; Length 118;
 Best Local Similarity 33.3%; Pred. No. 5;
 Matches 5; Conservative 5; Mismatches 5; Indels 0; Gaps 0;
 QY 1 IDRLVSIRTRGOIHS 15
 Db 48 VDHLIHLAKRGDLHA 62
 Db 48 VDHLIHLAKRGDLHA 62
 RESULT 20
 RL17_MYCCA STANDARD: PRT; 119 AA.
 ID IDRLVSIRTRGOIHS 15
 AC Q48980;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE 50S ribosomal protein (Fragment).
 GN RPLQ.
 OS Mycoplasma capricolum.
 OC Bacteria; Firmicutes; Mollicutes; Entomoplasmatales;
 OC Entomoplasmataceae.
 OX NCBI_TaxID=2095;
 RP [1]
 RC STRAIN=ATCC 27343 / Kid;
 RX MEDLINE=96059641; PubMed=7476192;
 RA Bork P., Ouzounis C., Casari G., Schneider R., Sander C., Dolan M.,
 RA Gilbert W., Gillet P.M.;
 RT "Exploring the Mycoplasma capricolum genome: a minimal cell reveals
 RT its physiology.";
 RL Mol. Microbiol. 16:955-967(1995).
 CC -1- SIMILARITY: BELONGS TO THE L17P FAMILY OF RIBOSOMAL PROTEINS.
 CC -----
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 CC -----
 DR EMBL: Z33050; CAA83721.1; -
 DR PIR: S77863; S77863.
 DR InterPro: IPR000456; Ribosomal_L17.
 DR Pfam: PF01196; Ribosomal_L17; 1.
 DR ProDom: PD004277; Ribosomal_L17; 1.
 DR TIGRfams: TIGR00059; L17; 1.
 DR PROSITE: PS01167; RIBOSOMAL_L17; FALSE_NEG.
 KW Ribosomal protein.
 FT NON_TER 119 119
 SQ SEQUENCE 119 AA; 13896 MW; 420CEADA708A9FEB CRC64;
 Query Match 50.7%; Score 37; DB 1; Length 119;
 Best Local Similarity 35.7%; Pred. No. 5;
 Matches 5; Conservative 5; Mismatches 4; Indels 0; Gaps 0;
 QY 2 DRLVSIRTRGOIHS 15
 Db 46 DHMITLAKRGDLHS 59
 Db 46 DHMITLAKRGDLHS 59
 RESULT 21
 RL17_RHIME STANDARD: PRT; 141 AA.
 ID IDRLVSIRTRGOIHS 15
 AC Q926A5;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE 50S ribosomal protein L17.
 GN RPLQ OR R01381 OR SMC01283.


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OC Rhizobium meliloti (Sinorhizobium meliloti).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Rhizobiales; Sinorhizobium/Ensifer group; Sinorhizobium.
OX NCBI_TaxID=382;
RM [1]
RM SEQUENCE FROM N.A.
RC STRAIN=1021;
RA Peck M.C., Fisher R.F., Long S.R.;
RT "Isolation and characterization of RpoA from Rhizobium meliloti.";
RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
RM [2]
RM SEQUENCE FROM N.A.
RC STRAIN=1021;
RC MEDLINE=21396507; PubMed=11481430;
RA Capela D., Barloy-Hubler F., Gouzy J., Bothe G., Ampe F., Batut J.,
RA Bolstad P., Becker A., Boutry M., Cadieu E., Dreano S., Gloux S.,
RA Goffie T., Goffeau A., Kahn D., Kiss E., Lelaure V., Maury S.,
RA Pohl T., Portetle D., Puehler A., Punnett B., Ramseger U.,
RA Renard C., Thebault P., Vandenbol M., Weidner S., Gallibert F.;
RT "Analysis of the chromosome sequence of the legume symbiont
RT Sinorhizobium meliloti strain 1021.";
RL Proc Natl Acad Sci U S A. 98:9877-9882(2001).
CC -1- SIMILARITY: BELONGS TO THE L17P FAMILY OF RIBOSOMAL PROTEINS.
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CC -----
CC EMBL: AF317474; AL26902.1; -
CC EMBL: AL591787; CAC45960.1; -
CC DR Interpro: IPR000456; Ribosomal_L17.
CC DR Pfam: PF01196; Ribosomal_L17.1.
CC DR ProDom: PD004277; Ribosomal_L17.1.
CC DR TIGRFAMs: TIGR00059; L17.1.
CC DR PROSITE: PS01167; RIBOSOMAL_L17.1.
CC DR Ribosomal protein; Complete proteome.
CC SQ SEQUENCE 141 AA; 15492 MW; 351EB47A113C14D8 CRC64;

Query Match 50.7%; Score 37; DB 1; Length 141;
Best Local Similarity 33.3%; Pred. No. 6.1;
Matches 5; Conservative 7; Mismatches 3; Indels 0; Gaps 0;

OY 1 IDRLVSTRFGQIHS 15
DB 48 VKELVTGKRGDLHA 62

RESULT 22
VNS3_CVCAI STANDARD: PRT: 250 AA.
ID VNS3_CVCAI
DC P36693;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Nonstructural protein 3-B (ORF 3B).
OS Canine enteric coronavirus (strain Insauc-1) (CCOV) (CCV).
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
OC Coronaviridae; Coronavirus.
OX NCBI_TaxID=36391;
RM [1]
RM SEQUENCE FROM N.A.
RC MEDLINE=93057357; PubMed=1431811;
RA Horsburgh B.C., Brierley I., Brown T.D.K.;
RT "Analysis of a 9.6 kb sequence from the 3' end of canine coronavirus
RT genomic RNA.";
RL J. Gen. Virol. 73:2849-2862(1992).
CC -1- SIMILARITY: Belongs to the coronavirus NS3b protein family.
CC -----
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CC -----
CC EMBL: D13096; BAA02411.1; ALT-TERM.
CC DR Interpro: IPR004293; Corona_NS3b.
CC DR Pfam: PF03053; Corona_NS3b.1.
CC Nonstructural protein.
CC SQ SEQUENCE 250 AA; 28426 MW; FCB7ABFD83DD9CPE CRC64;

Query Match 50.7%; Score 37; DB 1; Length 250;
Best Local Similarity 66.7%; Pred. No. 12;
Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 4 LVSTRFGQIHS 15
DB 178 LVSTRFGIATAH 189

RESULT 23
TRC2_STRCO STANDARD: PRT: 258 AA.
ID TRC2_STRCO
DC Q924X0;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Indole-3-glycerol phosphate synthase 2 (EC 4.1.1.48) (IGPS 2).
GN TRP2 OR SCO3211 OR SCEB.04C.
OS Streptomyces coelicolor.
OC Bacteria; Actinobacteria; Actinomycetales;
OC Streptomycetales; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1902;
RM [1]
RM SEQUENCE FROM N.A.
RC STRAIN=A3(2) / M145;
RC MEDLINE=21996410; PubMed=12000953;
RA Bentley S.D., Chater K.F., Cerdeno-Terraga A.-M., Challis G.L.,
RA Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
RA Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
RA Cronin A., Fraser A., Goble A., Hidaigo J., Horsby T., Howarth S.,
RA Huang C.-H., Krieser T., Larke L., Murphy L., Oliver K., O'Neill S.,
RA Rabinowitsch E., Rajandream M.A., Rutherford K., Rutter S.,
RA Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
RA Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
RA Hopwood D.A.;
RT "Complete genome sequence of the model actinomycete Streptomyces
RT coelicolor A3(2).";
RL Nature 417:141-147(2002).
CC -1- FUNCTION: THE FUNCTION OF THE SECOND TRP OPERON IN S. COELICOLOR IS
CC TO PRODUCE TRP FOR THE BIOSYNTHESIS OF CALCIUM-DEPENDENT
CC ANTI-BIOTIC (CDA).
CC CC -1- CATALYTIC ACTIVITY: 1-(2-carboxyphenylamino)-1-deoxy-D-ribose 5-
CC phosphate - 1-(indol-3-yl)glycerol 3-phosphate + CO(2) + H(2)O.
CC CC -1- PATHWAY: Tryptophan biosynthesis; fourth step.
CC CC -1- SIMILARITY: BELONGS TO THE TRP2 FAMILY.
CC -----
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CC -----
CC EMBL: AL035654; CAB38582.1; -
CC DR PIR: T36303; T36303.
CC DR HSSP: P00909; IPTI.
CC DR HAMAP: MF_00134; -.1.
CC DR Interpro: IPR003009; FMN_enzyme.
CC DR Interpro: IPR001468; IGPS.

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DR Pfam; PF00218; IGPS; 1.
DR PRODOM; PD001511; IGPS; 1.
DR PROSITE; PS00614; IGPS; 1.
DR Tryptophan biosynthesis; Lyase; Decarboxylase;
KW Antibiotic biosynthesis; Complete proteome.
SO SEQUENCE 258 AA; 26815 MW; BZA3JBF4B5C642A CRC64;

Query Match 50.7%; Score 37; DB 1; Length 258;
Best Local Similarity 53.8%; Pred. No. 12;
Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

OY 1 IDRLVSIRTRGOI 13
Db 196 IDRLTSLARLGRV 208

RESULT 24
T4HR_MAGGR STANDARD; PRT; 282 AA.
AC Q12634;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Tetrahydroxynaphthalene reductase (EC 1.1.1.252) (T4HN reductase)
DE (THNR).
OS Magnaporthe grisea (Rice blast fungus) (Pyricularia grisea).
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariomycetes; Incertae sedis; Magnaportheaceae; Magnaporthe.
OX NCBI_TaxID=148305;
RN [1]
RP SEQUENCE FROM N.A., PARTIAL SEQUENCE, AND CHARACTERIZATION.
RC STRAIN=Guyane 11;
RX MEDLINE=94155906; PubMed=8112349;
RA Vidal-Cros A., Viviani F., Labesse G., Boccard M., Gaudy M.;
RT "Polyhydroxynaphthalene reductase involved in melanin biosynthesis in
RL Magnaporthe grisea. Purification, cDNA cloning and sequencing.";
RN Euk. J. Biochem. 219:985-992(1994).
RN [2]
RP X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS).
RC STRAIN=4091-5-8;
RX MEDLINE=97094973; PubMed=8939741;
RA Andersson A., Jordan D., Schneider G., Lindqvist Y.;
RT "Crystal structure of the ternary complex of
RL 1,3,8-trihydroxynaphthalene reductase from Magnaporthe grisea with
RT NADPH and an active-site inhibitor.";
RT Structure 4:1161-1170(1996).
CC -1- FUNCTION: CATALYZES THE NADPH-DEPENDENT REDUCTION OF 1,3,6,8-
CC TETRAHYDROXYNAPHTHALENE (T4HN) INTO (+)-SCYTALONE AND 1,3,8-
CC TRIHYDROXYNAPHTHALENE INTO (-)-VERMELONE. THIS ENZYME IS THE
CC BIOCHEMICAL TARGET OF SEVERAL COMMERCIALY IMPORTANT FUNGICIDES
CC WHICH ARE USED TO PREVENT BLAST DISEASE IN RICE PLANTS.
CC -1- CATALYTIC ACTIVITY: scytalone + NADP(+) -> 1,3,6,8-
CC tetrahydroxynaphthalene + NADPH.
CC -1- PATHWAY: Fungal melanin biosynthesis.
CC -1- SUBUNIT: Homotetramer.
CC -1- SIMILARITY: Belongs to the short-chain dehydrogenases/reductases
CC (SDR) family.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; L22309; AA19514.1; -.
DR PIR; S41412; S41412.
DR PDB; 1YBV; 15-OCT-97.
DR PDB; 1DOH; 06-JUN-01.
DR PDB; 1G0N; 06-JUN-01.
DR PDB; 1G0O; 06-JUN-01.
DR InterPro; IPR002198; ADH_short.

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DR Pfam; PF00106; adh_short; 1.
DR PRINTS; PR00080; SDRFAMILY.
DR PROSITE; PS00061; ADH_SHORT; 1.
DR Oxidoreductase; NADP; Melanin biosynthesis; 3D-structure.
KW INIT_MER 0 0
FT NP_BIND 32 56 NADP (BY SIMILARITY).
FT ACT_SITE 177 177
FT HELIX 21 24
FT TURN 27 28
FT STRAND 29 33
FT TURN 34 35
FT HELIX 39 50
FT TURN 51 52
FT STRAND 53 59
FT HELIX 63 75
FT TURN 76 77
FT STRAND 80 84
FT TURN 87 88
FT HELIX 90 104
FT STRAND 109 112
FT HELIX 122 124
FT HELIX 127 137
FT TURN 138 138
FT HELIX 139 151
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FT TURN 222 222
FT TURN 224 225
FT TURN 227 228
FT HELIX 231 241
FT TURN 244 245
FT STRAND 249 249
FT HELIX 251 262
FT TURN 264 268
FT STRAND 272 276
SO SEQUENCE 282 AA; 29922 MW; 2520709137763087 CRC64;

Query Match 50.7%; Score 37; DB 1; Length 282;
Best Local Similarity 63.6%; Pred. No. 13;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 2 DRLVSIIRTRGO 12
Db 131 DRVFTIRTRGO 141

RESULT 25
ISPE_CORGL STANDARD; PRT; 311 AA.
ID ISPE_CORGL
AC Q8NRV0;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE 4-diphosphocytidyl-2-C-methyl-D-erythritol kinase (EC 2.7.1.148) (CMK)
DE (4-(cytidine-5'-diphospho)-2-C-methyl-D-erythritol kinase).
GN ISPE OR CGL0911.
OS Corynebacterium glutamicum (Brevibacterium flavum).
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Corynebacteriaceae; Corynebacterium.
OX NCBI_TaxID=1718;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 13032 / DSM 20300 / NCIB 10025;
RA Nakagawa S.;

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RT "Complete genomic sequence of *Corynebacterium glutamicum* ATCC 13032.";
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Catalyzes the phosphorylation of the position 2 hydroxy
CC group of 4-diphosphocytidylyl-2C-methyl-D-erythritol (By
CC similarity).
CC -1- CATALYTIC ACTIVITY: ATP + 4-(cytidine 5'-diphospho)-2-C-methyl-D-
CC erythritol = ADP + 2-phospho-4-(cytidine 5'-diphospho)-2-C-
CC methyl-D-erythritol.
CC -1- PATHWAY: Nonmevalonate terpenoid biosynthesis pathway; fourth
CC step.
CC -1- SIMILARITY: BELONGS TO THE ISPE FAMILY.
CC -----
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CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: AP005276; BAB98304.1; -.
DR HAMAP: MF_00061; -; 1.
DR InterPro: IPR006204; GHMP_Kinase.
DR InterPro: IPR004424; ISPE.
DR Pfam: PF00288; GHMP_Kinases; 1.
DR TIGRFAMs: TIGR00154; ispe; 1.
DR Transferase: Kinase; Isoprene biosynthesis; ATP-Binding;
KM Complete proteome.
FT NP_BIND 105 115 ATP (POTENTIAL).
SQ SEQUENCE 311 AA; 32630 MW; 392FD92100D040F8 CRC64;

Query Match 50.7%; Score 37; DB 1; Length 311;
Best Local Similarity 46.2%; Pred. No. 15;
Matches 6; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

OY 2 DRUYSIRTRGQIH 14
DB 163 EQLVDMLTRGKLIH 175

RESULT 26
F16P-SHEEP STANDARD; PRT; 336 AA.
ID F16P-SHEEP
AC P09199;
DT 01-MAR-1989 (Rel. 10, Created)
DT 01-MAR-1989 (Rel. 10, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Fructose-1,6-bisphosphatase (EC 3.1.3.11) (D-fructose-1,6-bisphosphate
DE 1-phosphohydroxylase) (FBPase).
GN FBP1 OR FBP.
OS Ovis aries (Sheep).
OC Chordata; Craniata; Vertebrata; Euteleostomi;
OC Eukaryota; Metazoa; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Ovis.
OC NCBI_TaxID=9940;
OX NCBI_TaxID=9940;
RN [1]
RP SEQUENCE.
RX MEDLINE=84079343; PubMed=6316885;
RA Fisher W.K., Thompson E.O.P.;
RT "Amino acid sequence studies on sheep liver fructose-bisphosphatase.
RT II. The complete sequence.";
RL Aust. J. Biol. Sci. 36:235-250(1983).
RN [2]
RP SEQUENCE OF 1-60.
RX MEDLINE=81232062; PubMed=6264908;
RA Fisher W.K., Thompson E.O.P.;
RT "Amino acid sequence studies on sheep liver fructose-bisphosphatase.
RT I. The S-peptide.";
RL Aust. J. Biol. Sci. 33:665-674(1980).
CC -1- CATALYTIC ACTIVITY: D-fructose 1,6-bisphosphate + H2O = D-
CC fructose 6-phosphate + phosphate.
CC -1- ENZYME REGULATION: INHIBITED BY AMP, WHICH AFFECTS THE TURNOVER
CC OF BOUND SUBSTRATE AND NOT THE AFFINITY FOR SUBSTRATE.

CC -1- PATHWAY: NECESSARY FOR, AND SPECIFIC TO, GLUCONEOGENESIS.
CC -1- SUBUNIT: HOMODIMER, WITH FOUR BINDING SITES
CC EACH FOR THE SUBSTRATE FOR AMP, AND FOR DIVALENT METAL CATION
CC (THE GREATEST AFFINITY IS FOR ZINC).
CC -1- SIMILARITY: BELONGS TO THE FBPA FAMILY.
DR PIR: A05316; A05316.
DR HSSP: P00636; FBPA.
DR InterPro: IPR00046; In_FBP_phphatase.
DR Pfam: PF00316; FBPA; 1.
DR PRINTS: PR00177; INFBPHPTASE.
DR ProDom: PD00191; In_FBP_phphatase; 1.
DR PROSITE: PS00124; FBPA; 1.
KM Hydroxylase; carbonylate metabolism; Gluconeogenesis; Acetylation;
KM Phosphorylation; Zinc 0 Allosteric enzyme.
FT INT_MET 0 1 ACETYLATION.
FT MOD_RES 141 141 ALLOSTERIC REGULATION BY AMP.
FT BIND_RES 207 207 PHOSPHORYLATION (BY PKA).
FT MOD_RES 274 274 BY SIMILARITY.
FT ACT_SITE 274 274 BY SIMILARITY.
SQ SEQUENCE 336 AA; 36544 MW; 2E9826BA50EC925E CRC64;

Query Match 50.7%; Score 37; DB 1; Length 336;
Best Local Similarity 46.7%; Pred. No. 16;
Matches 7; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

OY 1 IDUYSIRTRGQIHS 15
DB 196 VDRVKKIKKGSIS 210

RESULT 27
F16P-PIG STANDARD; PRT; 337 AA.
ID F16P-PIG
AC P00636;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Fructose-1,6-bisphosphatase (EC 3.1.3.11) (D-fructose-1,6-bisphosphate
DE 1-phosphohydroxylase) (FBPase).
GN FBP1 OR FBP.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OC NCBI_TaxID=9823;
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92212971; PubMed=1313579;
RA Williams M.K., Kantrowitz E.R.;
RT "Isolation and sequence analysis of the cDNA for pig kidney fructose
RT 1,6-bisphosphatase.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:3080-3082(1992).
RN [2]
RP SEQUENCE OF 1-335.
RX MEDLINE=83117639; PubMed=6296821;
RA Marcus F., Edelstein I., Reardon I., Heinrichson R.L.;
RT "Complete amino acid sequence of pig kidney
RT fructose-1,6-bisphosphatase.";
RL Proc. Natl. Acad. Sci. U.S.A. 79:7161-7165(1982).
RN [3]
RP SEQUENCE OF 1-23 AND 43-60.
RX MEDLINE=83047209; PubMed=6291465;
RA McGregor J.S., Hannappel E., Xu G.-J., Pontremoli S., Horecker B.L.;
RT "Conservation of primary structure at the proteinase-sensitive site
RT of fructose 1,6-bisphosphatases.";
RL Arch. Biochem. Biophys. 217:652-664(1982).
RN [4]
RP SUBSTRATE-BINDING SITE, LIGANDS, AND REVIEW.
RX MEDLINE=82132308; PubMed=62771165;
RA Benkovic S.J., Demaine M.M.;
RT "Mechanism of action of fructose 1,6-bisphosphatase."

RL Adv. Enzymol. Relat. Areas Mol. Biol. 53:45-82(1982).
 RN [3] X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS), AND REVISIONS.
 RX MEDLINE=90219022; PubMed=2157849;
 RA Ke H.M., Thorpe C.M., Seaton B.A., Lipscomb W.N., Marcus F.;
 RT "Structure refinement of fructose-1,6-bisphosphatase and its fructose
 2,6-bisphosphate complex at 2.8-A resolution.";
 RL J. Mol. Biol. 212:513-539(1990).
 RN [6] X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).
 RX MEDLINE=90319088; PubMed=2164670;
 RA Ke H.M., Zhang Y.P., Lipscomb W.N.;
 RT "Crystal structure of fructose-1,6-bisphosphatase complexed with
 fructose 6-phosphate, AMP, and magnesium.";
 RL Proc. Natl. Acad. Sci. U.S.A. 87:5243-5247(1990).
 RN [7] X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS).
 RX MEDLINE=9195276; PubMed=1849642;
 RA Ke H.M., Zhang Y.P., Liang J.-Y., Lipscomb W.N.;
 RT "Crystal structure of the neutral form of fructose-1,6-bisphosphatase
 complexed with the product fructose 6-phosphate at 2.1-A
 resolution.";
 RL Proc. Natl. Acad. Sci. U.S.A. 88:2989-2993(1991).
 RN [8] X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS).
 RX MEDLINE=92196126; PubMed=1312721;
 RA Liang J.-Y., Huang S., Zhang Y.P., Ke H.M., Lipscomb W.N.;
 RT "Crystal structure of the neutral form of fructose 1,6-bisphosphatase
 complexed with regulatory inhibitor fructose 2,6-bisphosphate at
 2.6-A resolution.";
 RL Proc. Natl. Acad. Sci. U.S.A. 89:2404-2408(1992).
 RN [9] X-RAY CRYSTALLOGRAPHY (2.27 ANGSTROMS).
 RX MEDLINE=98376425; PubMed=9708979;
 RA Choe J.Y., Poland B.W., Fromm H.J., Honzatko R.B.;
 RT "Role of a dynamic loop in cation activation and allosteric
 regulation of recombinant porcine fructose-1,6-bisphosphatase.";
 RL Biochemistry 37:11441-11450(1998).
 RN [10] X-RAY CRYSTALLOGRAPHY (2.23 ANGSTROMS).
 RX MEDLINE=20374531; PubMed=10913263;
 RA Choe J.Y., Fromm H.J., Honzatko R.B.;
 RT "Crystal structures of fructose 1,6-bisphosphatase: mechanism of
 catalysis and allosteric inhibition revealed in product complexes.";
 RL Biochemistry 39:8565-8574(2000).
 CC -1- CATALYTIC ACTIVITY: D-fructose 1,6-bisphosphate + H(2)O = D-
 fructose 6-phosphate + phosphate.
 CC -1- ENZYME REGULATION: INHIBITED BY AMP, WHICH AFFECTS THE TURNOVER OF
 BOUND SUBSTRATE AND NOT THE AFFINITY FOR SUBSTRATE.
 CC -1- PATHWAY: NECESSARY FOR, AND SPECIFIC TO, GLUCONEOGENESIS.
 CC -1- SUBUNIT: HOMOTETRAMER, WITH FOUR BINDING SITES
 EACH FOR THE SUBSTRATE, FOR AMP, AND FOR DIVALENT METAL CATION
 (THE GREATEST AFFINITY IS FOR ZINC).
 CC -1- MISCELLANEOUS: THE MOLECULE HAS A HIGHLY REACTIVE CYSTEINE RESIDUE
 (CYS-116 OR CYS-128), WHICH TENDS TO FORM MIXED DISULFIDES (E.G.,
 WITH HOMOCYSTEINE) BUT IS NOT ESSENTIAL FOR ENZYME ACTIVITY.
 CC -1- SIMILARITY: BELONGS TO THE FBPAE FAMILY.
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: M86347; AAA31035.1; -
 CC PIR: S37696; PAPF.
 DR PDB: 1FBP; 15-APR-92.
 DR PDB: 1FBP; 15-APR-92.
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DR PDB: 1FBC; 31-OCT-93.
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FT HELIX 213 218
FT HELIX 221 231
FT TURN 234 235
FT STRAND 241 242
FT STRAND 244 244
FT HELIX 248 258
FT STRAND 261 264
FT STRAND 267 267
FT TURN 268 269
FT STRAND 270 270
FT TURN 271 272
FT STRAND 276 276
FT TURN 277 280

Query Match 50.7%; Score 37; DB 1; Length 337;
Best Local Similarity 46.7%; Pred. No. 16;
Matches 7; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Oy 1 IDRLVSIIRFGQHS 15
DB 196 VDRDVKKKKGNYS 210

RESULT 28
F16P-RAT STANDARD: PRT: 362 AA.
AC P19112; 064594;
DT 01-NOV-1990 (Rel. 16, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DE Fructose-1,6-bisphosphatase (EC 3.1.3.11) (D-fructose-1,6-bisphosphate
  1-phosphohydrolyase) (FBPase).
GN FBP1 OR FBP.
OS Rattus norvegicus (Rat).
OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_Taxid=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA MEDLINE=89042197; PubMed=2847161;
RA El-Maghrabi M.R., Plikis J., Marker A.J., Colosia A.D., D'Angelo G.,
RA Fraser B.A., Plikis S.J.;
RT "cDNA sequence of rat liver fructose-1,6-bisphosphatase and evidence
  for down-regulation of its mRNA by insulin."
RL Proc. Natl. Acad. Sci. U.S.A. 85:8430-8434(1988).
RN [2]
RP SEQUENCE FROM N.A.
RA MEDLINE=96078844; PubMed=7589895;
RA Bettelot R., Amruster L., Okayama H.;
RT Liver fructose-1,6-bisphosphatase cDNA: trans-complementation of
  flission yeast and characterization of two human transcripts."
RL Differentiation 59:51-60(1995).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley;
RA MEDLINE=9115820; PubMed=1846613;
RA El-Maghrabi M.R., Lange A.J., Kummel L., Plikis S.J.;
RT "The rat fructose-1,6-bisphosphatase gene. Structure and regulation
  of expression."
RL J. Biol. Chem. 266:2115-2120(1991).
RN [4]
RP SEQUENCE OF 319-361.
RC TISSUE=Liver;
RA MEDLINE=8338340; PubMed=6305949;
RA Rittenhouse J., Chatterjee T., Marcus F., Reardon I., Heinrichson R.L.;
RT "Amino acid sequence of the COOH-terminal region of fructose-1,6-
  bisphosphatases in relation to cyclic AMP-dependent
  phosphorylation."
RL J. Biol. Chem. 258:7648-7653(1983).
CC -1- CATALYTIC ACTIVITY: D-fructose 1,6-bisphosphate + H(2)O = D-
  fructose 6-phosphate + phosphate.
CC -1- ENZYME REGULATION: INHIBITED BY AMP, WHICH AFFECTS THE TURNOVER

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CC OF BOUND SUBSTRATE AND NOT THE AFFINITY FOR SUBSTRATE.
CC -1- PATHWAY: NECESSARY FOR, AND SPECIFIC TO, GLUCONEOGENESIS.
CC -1- SUBUNIT: HOMOTETRAMER, WITH FOUR BINDING SITES
CC EACH FOR THE SUBSTRATE, FOR AMP, AND FOR DIVALENT METAL CATION
CC (THE GREATEST AFFINITY IS FOR ZINC).
CC -1- SIMILARITY: BELONGS TO THE FBPAE FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@sib-sib.ch).
CC -----
DR EMBL; J04112; AAA60739.1; -
DR EMBL; M86240; AAA86425.1; -
DR EMBL; M57284; AAA41131.1; -
DR EMBL; M57274; AAA41131.1; JOINED.
DR EMBL; M57279; AAA41131.1; JOINED.
DR EMBL; M57278; AAA41131.1; JOINED.
DR EMBL; M57282; AAA41131.1; JOINED.
DR EMBL; M57281; AAA41131.1; JOINED.
DR PIR; A1342; A1342.
DR HSSE; P00636; IEU.
DR InterPro; IPR000146; In_FB_phphatase.
DR Pfam; PF00316; FBPAE; 1.
DR PRINTS; PR00377; INFBNPHATASE.
DR ProDom; PD001491; In_FB_phphatase; 1.
DR PROSITE; PS00124; FBPAE; 1.
KW Hydrolyase; Carbohydrate metabolism; Gluconeogenesis; Zinc;
KW Allosteric enzyme.
FT INIT_MET 0
FT BINDING 141 141
FT FT ALLOSTERIC REGULATION BY AMP (BY
FT ACT_SITE 274 274 SIMILARITY).
FT CONFLICT 147 147 BY SIMILARITY.
FT P -> A (IN REF. 3).
SQ SEQUENCE 362 AA; 39478 MW; B07F061CDDC1CF2D CRC64;

Query Match 50.7%; Score 37; DB 1; Length 362;
Best Local Similarity 46.7%; Pred. No. 18;
Matches 7; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Oy 1 IDRLVSIIRFGQHS 15
DB 196 VDRDVKKKKGNYS 210

RESULT 29
AMCL_ORYZA /
ID AMCL_ORYZA STANDARD: PRT: 383 AA.
AC P27940;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Alpha-amylase isozyme C precursor (EC 3.2.1.1) (1,4-alpha-D-glucan
  glucanohydrolase) (Isozyme 1B).
GN AMYC OR AMY1B.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliopsida; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_Taxid=4530;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Indica-IR26; TISSUE=Leaf;
RA MEDLINE=92119260; PubMed=1731997;
RA Kim J.-K., Wu R.;
RT "Nucleotide sequence of a high-pI rice (Oryza sativa) -amylase gene."
RL Plant Mol. Biol. 18:399-402(1992).
RN [2]
RP SEQUENCE OF 1-50 FROM N.A.
RC STRAIN=cv. Japonica M202; TISSUE=Etolated leaf;

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RX MEDLINE-91088278; PubMed-2263460;
RA Huang N., Kozlumi N., Reini S., Kodriguez R.L.;
RT "Structural organization and differential expression of rice alpha-
RT amylose genes."
RL Nucleic Acids Res. 18:7007-7014(1990).
CC -I- FUNCTION: IMPORTANT FOR BREAKDOWN OF ENDOSPERM STARCH DURING
CC GERMINATION.
CC -I- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic
CC linkages in oligosaccharides and polysaccharides.
CC -I- COFACTOR: BINDS A CALCIUM ION REQUIRED FOR ITS ACTIVITY.
CC -I- SUBUNIT: Monomer.
CC -I- TISSUE SPECIFICITY: IN CALLUS, WEAKLY EXPRESSED.
CC -I- DEVELOPMENTAL STAGE: EXPRESSED AT A HIGH LEVEL DURING GERMINATION
CC IN THE ALEURONE CELLS UNDER THE CONTROL OF THE PLANT HORMONE
CC GIBBERELLIC ACID AND IN THE DEVELOPING GRAINS AT A LOW LEVEL.
CC -I- SIMILARITY: BELONGS TO FAMILY 13 OF GLYCOSYL HYDROLASES, ALSO
CC KNOWN AS THE ALPHA-AMYLASE FAMILY.
CC -I- CAUTION: ALL THE CATALYTIC RESIDUES ARE HIDDEN BY WHAT SEEMS TO BE
CC FRAMESHIFT ERRORS FROM THE ORIGINAL NUCLEOTIDE REFERENCE.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC use by non-profit institutions as long as its content is in no way
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@sib-sib.ch).
CC -----
DR EMBL: X52240; CAA36485.1; -
DR EMBL: M59350; AAA33893.1; -
DR PIR: S19142; ALR2OC.
DR HSP: P04063; IAVA.
DR Gramene; P27940; -
KW Hydrolase; Glycosidase; Carbohydrate metabolism; Calcium; signal;
KW Multigene family.
FT SIGNAL 1 31 POTENTIAL.
FT CHAIN 32 383 ALPHA-AMYLASE ISOZYME C.
SQ SEQUENCE 383 AA; 43254 MW; 7426BFE7C411B54 CRC64;

Query Match 50.7%; Score 37; DB 1; Length 383;
Best Local Similarity 64.3%; Pred. No. 19;
Matches 9; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 IDRLVSIRTRGOIH 14
DB 327 IECLVSRIRNRGOIH 340

RESULT 30
YME8_YEAST
ID YME8_YEAST STANDARD; PRT; 475 AA.
AC Q03790;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Hypothetical 52.6 kDa protein in IMP1-HL01 Intergenic region.
GN YMR15W OR YMR520.02.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=S288C / AB972;
RX PubMed=9169872;
RA Bowman S., Churcher C.M., Badcock K., Brown D., Chillingworth T.,
RA Connor R., Dedman K., Devlin K., Gentles S., Hamlin N., Hunt S.,
RA Jagels K., Lye G., Moule G., Odell C., Pearson D., Rajandream M.A.,
RA Rice P., Skelton J., Walsh S., Whitehead S., Barrell B.G.;
RT "The nucleotide sequence of Saccharomyces cerevisiae chromosome
RT XIII."
RL Nature 387:90-93(1997).
CC -I- SIMILARITY: TO YEAST ASMA.

```

```

CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC -----
DR EMBL: 249705; CAA89789.1; -
DR PIR: S54511; S54511.
DR SGD: S0004762; NRP53.
DR GO: GO:0005643; C:nuclear pore, IDA.
DR GO: GO:0000059; P:protein-nucleus import, docking; IPI.
DR Pfam: PF05172; MPN: 1.
KW Hypothetical protein.
SQ SEQUENCE 475 AA; 52618 MW; 2E0E0C561D27E523 CRC64;

Query Match 50.7%; Score 37; DB 1; Length 475;
Best Local Similarity 53.8%; Pred. No. 24;
Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 3 RLVSIRTRGOIHS 15
DB 426 RSLFIRNRKGIHS 438

Search completed: August 29, 2003, 18:45:10
Job time : 11.8571 secs

```

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 29, 2003, 18:40:26 ; Search time 36.8571 Seconds

(without alignments)
105.021 Million cell updates/sec

Title: US-09-830-876-1

Perfect score: 73
Sequence: 1 IDRVSIRTRQIHS 15Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 100 summaries

Database :

1: SP archaea:*
2: SP bacteria:*
3: SP fungi:*
4: SP human:*
5: SP invertebrate:*
6: SP mammal:*
7: SP mhc:*
8: SP organelle:*
9: SP phage:*
10: SP plant:*
11: SP rodent:*
12: SP virus:*
13: SP vertebrate:*
14: SP unclassified:*
15: SP_virus:*
16: SP_bacteriap:*
17: SP_archaeap:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	60	82.2	429	10	Q40016
2	58	79.5	427	10	Q03651
3	54	74.0	427	10	Q40015
4	44	60.3	458	16	Q40015
5	43	58.9	416	10	Q92717
6	43	58.9	429	13	Q8LJ06
7	43	58.9	544	17	Q8AYB0
8	42	57.5	151	16	Q974R6
9	42	57.5	345	4	Q9NRA1
10	42	57.5	345	4	Q9NRA1
11	42	57.5	666	17	Q97UX8
12	40.5	55.5	343	16	Q8KXC4
13	40	54.8	141	16	Q8UR41
14	40	54.8	246	16	Q9PWC1
15	40	54.8	416	10	Q8GUR0
16	40	54.8	906	10	Q8L0K4

17	39.5	54.1	506	11	Q9PA04	Q9d4 mus musculu
18	39	53.4	245	10	Q94Ar6	Q94Ar6 arabidopsis
19	39	53.4	272	10	Q9S0R2	Q9S0R2 arabidopsis
20	39	53.4	284	3	Q9C425	Q9C425 ophiostoma
21	39	53.4	402	4	Q8IM13	Q8IM13 homo sapien
22	39	53.4	409	13	Q8AHU1	Q8AHU1 gallus gall
23	39	53.4	443	3	Q06098	Q06098 saccharomyc
24	39	53.4	443	11	Q08P65	Q08P65 mus musculu
25	39	53.4	445	11	Q9IX41	Q9IX41 mus musculu
26	39	53.4	467	16	Q9KX13	Q9KX13 streptomyce
27	39	53.4	647	2	Q9AR08	Q9AR08 salmonella
28	38	52.1	137	16	Q9A6S8	Q9A6S8 caulobacter
29	38	52.1	166	13	Q91B05	Q91B05 gallus gall
30	38	52.1	177	16	Q8G3Z2	Q8G3Z2 birdobacte
31	38	52.1	212	2	Q69215	Q69215 agrobacteri
32	38	52.1	245	2	Q9RIQ2	Q9RIQ2 streptomyce
33	38	52.1	270	3	Q93874	Q93874 curvularia
34	38	52.1	737	10	Q8S700	Q8S700 oryza sativ
35	38	52.1	1194	10	Q9PKY7	Q9PKY7 arabidopsis
36	37	50.7	142	16	Q8YHL5	Q8YHL5 bruceella me
37	37	50.7	142	16	Q8G095	Q8G095 rhizobium su
38	37	50.7	143	16	Q98N32	Q98N32 rhizobium l
39	37	50.7	155	17	Q8TK54	Q8TK54 methanosarc
40	37	50.7	168	13	Q91BD4	Q91BD4 gallus gall
41	37	50.7	213	12	Q8JUQ2	Q8JUQ2 foot-and-mo
42	37	50.7	223	3	Q9C496	Q9C496 bipolaris s
43	37	50.7	250	3	Q74141	Q74141 bipolaris c
44	37	50.7	250	3	Q74150	Q74150 bipolaris p
45	37	50.7	250	3	Q74157	Q74157 bipolaris y
46	37	50.7	250	3	Q74159	Q74159 bipolaris b
47	37	50.7	250	3	Q74153	Q74153 bipolaris s
48	37	50.7	250	3	Q9UR11	Q9UR11 bipolaris s
49	37	50.7	250	3	Q74145	Q74145 bipolaris h
50	37	50.7	250	3	Q74155	Q74155 bipolaris s
51	37	50.7	250	3	Q74156	Q74156 bipolaris v
52	37	50.7	250	3	Q74143	Q74143 cochllobolu
53	37	50.7	250	3	Q74149	Q74149 bipolaris l
54	37	50.7	250	3	Q74142	Q74142 bipolaris c
55	37	50.7	250	3	Q9UPK8	Q9UPK8 bipolaris s
56	37	50.7	250	3	Q74160	Q74160 bipolaris s
57	37	50.7	250	3	Q74138	Q74138 bipolaris s
58	37	50.7	250	3	Q74152	Q74152 bipolaris s
59	37	50.7	250	3	Q74152	Q74152 bipolaris s
60	37	50.7	250	3	Q74146	Q74146 curvularia
61	37	50.7	250	3	Q74144	Q74144 bipolaris k
62	37	50.7	250	3	Q74151	Q74151 cochllobolu
63	37	50.7	250	3	Q74158	Q74158 bipolaris p
64	37	50.7	250	3	Q74148	Q74148 bipolaris z
65	37	50.7	250	3	Q74140	Q74140 bipolaris n
66	37	50.7	250	3	Q74154	Q74154 bipolaris c
67	37	50.7	250	3	Q74147	Q74147 bipolaris s
68	37	50.7	256	5	Q9NCB5	Q9NCB5 trllobolum c
69	37	50.7	267	3	Q93802	Q93802 altermaria
70	37	50.7	267	3	Q42693	Q42693 cochllobolu
71	37	50.7	267	3	Q8J2T3	Q8J2T3 bipolaris o
72	37	50.7	267	3	Q8J2N1	Q8J2N1 curvularia
73	37	50.7	271	3	Q87025	Q87025 colletothic
74	37	50.7	277	5	Q950G7	Q950G7 caenorhabdi
75	37	50.7	328	15	Q9E670	Q9E670 human immun
76	37	50.7	329	15	Q8E122	Q8E122 human immun
77	37	50.7	337	6	Q77657	Q77657 sus scrofa
78	37	50.7	412	10	Q9G6S0	Q9G6S0 arabidopsis
79	37	50.7	413	10	Q8LXK1	Q8LXK1 arabidopsis
80	37	50.7	413	10	Q9M6R9	Q9M6R9 malus domes
81	37	50.7	437	11	Q9IX45	Q9IX45 mus musculu
82	37	50.7	444	2	Q9Y4K6	Q9Y4K6 pseudomonas
83	37	50.7	456	16	Q93236	Q93236 mycobacteri
84	37	50.7	496	10	Q9P4T6	Q9P4T6 oryza sativ
85	37	50.7	570	36	Q9S5Z9	Q9S5Z9 neurospora
86	37	50.7	610	6	Q9HX20	Q9HX20 pseudomonas
87	37	50.7	710	6	Q9K162	Q9K162 ceratoplinec
88	37	50.7	743	5	Q8VPJ5	Q8VPJ5 clostridium
89	37	50.7	989	5	Q8ML20	Q8ML20 drosophila

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90      37      50.7      2514      5      Q9Y061      caenorhabdi
91      37      50.7      2531      5      Q22258      caenorhabdi
92      37      50.7      4753      16      Q8P113      xanthomonas
93      36.5      50.0      441      5      Q9VW38      drosophila
94      36.5      50.0      441      5      Q8SYU7      drosophila
95      36      49.3      83      16      Q9A931      caulibacter
96      36      49.3      156      2      Q8RS47      uncultured
97      36      49.3      159      2      Q9JMY7      listeria mo
98      36      49.3      161      13      Q9JMF2      esox lucius
99      36      49.3      165      2      Q9JMW0      listeria mo
100     36      49.3      168      2      Q9JMY9      listeria mo

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ALIGNMENTS

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RESULT 1
Q40016      PRELIMINARY;      PRT;      429 AA.
AC      Q40016
DT      01-NOV-1996 (TREMBLrel. 01, Created)
DT      01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DE      01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE      Barley (H. vulgare) alpha-amylase 1.
OS      Hordeum vulgare (Barley).
OC      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC      Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
OC      Triticeae; Hordeum.
OX      NCBI_TaxID=4513;
RN      [1]
RP      SEQUENCE FROM N.A.
RA      Knox C.A.P., Sonthayanon B., Chandra G.R., Muthukrishnan S.;
RT      "Structure and organization of two divergent alpha-amylase genes from
RT      barley."
RL      Plant Mol. Biol. 9:3-17(1987).
RN      [2]
RP      SEQUENCE FROM N.A.
RA      Muthukrishnan S.;
RL      Submitted (JUL-1988) to the EMBL/GenBank/DBJ databases.
DR      EMBL; M17125; AAA32926.1; -.
DR      HSSP; P04063; IAVA.
DR      InterPro: IPR006047; Alpha_aml1_cat.
DR      InterPro: IPR006589; Alp_aml1_cat_sub.
DR      Pfam; PF00128; alpha-amylase; 1.
DR      SMART; SM00642; Amy; 1.
SQ      SEQUENCE 429 AA: 47970 MW: 4E7B8B741C944095 CRC64;

Query Match      82.2%; Score 60; DB 10; Length 429;
Best Local Similarity 86.7%; Pred. No. 0.0081;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 IDRLVSIRTRGOIHS 15
Db      360 IDRLVSIRTRGOIHS 374

RESULT 2
Q03651      PRELIMINARY;      PRT;      427 AA.
AC      Q03651
DT      01-NOV-1996 (TREMBLrel. 01, Created)
DT      01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DE      01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE      Alpha-amylase precursor (Ec 3.2.1.1).
GN      AMY46.
OS      Hordeum vulgare (Barley).
OC      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC      Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
OC      Triticeae; Hordeum.
OX      NCBI_TaxID=4513;
RN      [1]
RP      SEQUENCE FROM N.A.
RA      STRAIN-Himalaya;
RC

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RX      MEDLINE=89066691; PubMed=3264283;
RA      Knutshed B., Rogers J.C.;
RT      "Barley alpha-amylase genes. Quantitative comparison of steady-state
RT      mRNA levels from individual members of the two different families
RT      expressed in aleurone cells."
RL      J. Biol. Chem. 263:18953-18960(1988).
DR      EMBL; J04202; AAA98615.1; -.
DR      HSSP; P04063; IAVA.
DR      InterPro: IPR006047; Alpha_aml1_cat.
DR      InterPro: IPR006589; Alp_aml1_cat_sub.
DR      InterPro: IPR006046; Glyco_hydro_13.
DR      Pfam; PF00128; alpha-amylase; 1.
DR      PRINTS; PR00110; ALPHAMYLASE.
DR      SMART; SM00642; Amy; 1.
KW      Glycosidase; Hydrolase; Signal.
FT      SIGNAL
FT      CHAIN 26 427
SQ      SEQUENCE 427 AA: 47456 MW: 5A7496B9B6643824 CRC64;

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Query Match 79.5%; Score 58; DB 10; Length 427;

Best Local Similarity 86.7%; Pred. No. 0.019; Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 IDRLVSIRTRGOIHS 15

Db 358 IDRLVSIRTRGOIHS 372

RESULT 3

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Q40015      PRELIMINARY;      PRT;      427 AA.
AC      Q40015
DT      01-NOV-1996 (TREMBLrel. 01, Created)
DT      01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DE      01-OCT-2002 (TREMBLrel. 22, Last annotation update)
DE      Barley (H. vulgare) alpha-amylase 1.
OS      Hordeum vulgare (Barley).
OC      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC      Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
OC      Triticeae; Hordeum.
OX      NCBI_TaxID=4513;
RN      [1]
RP      SEQUENCE FROM N.A.
RA      Knox C.A.P., Sonthayanon B., Chandra G.R., Muthukrishnan S.;
RT      "Structure and organization of two divergent alpha-amylase genes from
RT      barley."
RL      Plant Mol. Biol. 9:3-17(1987).
RN      [2]
RP      SEQUENCE FROM N.A.
RA      Muthukrishnan S.;
RL      Submitted (JUL-1988) to the EMBL/GenBank/DBJ databases.
DR      EMBL; M17126; AAA32925.1; -.
DR      HSSP; P04063; IAVA.
DR      InterPro: IPR006047; Alpha_aml1_cat.
DR      InterPro: IPR006046; Glyco_hydro_13.
DR      Pfam; PF00128; alpha-amylase; 1.
DR      PRINTS; PR00110; ALPHAMYLASE.
SQ      SEQUENCE 427 AA: 47402 MW: D21BA12EAB5F3534 CRC64;

Query Match      74.0%; Score 54; DB 10; Length 427;
Best Local Similarity 73.3%; Pred. No. 0.11;
Matches 11; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY      1 IDRLVSIRTRGOIHS 15
Db      358 IDRLVSIRTRGOIHS 372

RESULT 4
Q92717      PRELIMINARY;      PRT;      458 AA.
AC      Q92717
DT      01-MAY-1999 (TREMBLrel. 10, Created)

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RP SEQUENCE FROM N.A.
RX MEDLINE-2134763; PubMed-11297552;
RA Gilbertson D.G., Duff M.E., West J.W., Kelly J.D., Sheppard P.O.,
RA Hofstrand P.D., Gao Z., Shoemaker K., Bukowski T.R., Moore M.,
RA Feldhaus A.L., Humes J.M., Palmer T.E., Hart C.E.;
RT "Platelet-derived Growth Factor C (PDGF-C), a Novel Growth Factor That
RT Binds to PDGF alpha and beta Receptor."
RT J Biol Chem 276:27406-27414(2001).
CC -1- SIMILARITY: CONTAINS 1 CUB DOMAIN.
DR EMBL: AF091434; AF000491; -.
DR EMBL: AF033831; BAB03266.1; -.
DR EMBL: AF60738; AAKS1637.1; -.
DR InterPro: IPR000859; CUB_dommain.
DR Pfam: PF00431; CUB; 1.
DR SMART: SM00042; PDGF; 1.
DR SMART: SM00141; PDGF; 1.
DR PROSITE: PS01180; CUB; 1.
DR PROSITE: PS50278; PDGF_2; 1.
SQ SEQUENCE 345 AA; 39029 MW; CDE9E51F40633E78 CRC64;

Query Match 57.5%; Score 42; DB 4; Length 345;
Best Local Similarity 42.9%; Pred. No. 16;
Matches 6; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

OY 2 DRLVLSIRTRGOIHS 15
DB 47 ERLTVSTNGSIHS 60
:|:::|::|

RESULT 11
O97UX8 PRELIMINARY; PRT; 666 AA.
ID O97UX8;
DT 01-OCT-2001 (TREMBLrel. 18, Created)
DT 01-OCT-2001 (TREMBLrel. 18, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Acetyl-CoA synthetase (Acetate CoA ligase) (acsa-9) (EC 6.2.1.1).
GN ACSA9 OR SSO2863.
OS Sulfolobus solfataricus.
OC Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;
OC Sulfolobus;
OC NCBI_Taxid-2287;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN-ATCC 35092 / DSM 1617 / P2;
MEDLINE-21332296; PubMed-11427726;
RA She Q., Singh R.K., Confalonieri F., Zivanovic Y., Allard G.,
RA Awaiez M.J., Chan-Welher C.C.-Y., Clausen I.G., Curtis B.A.,
RA De Moers A., Erasuo G., Fletcher C., Gordon P.M.K.,
RA Helkamp-de Jong I., Jeffries A.C., Kozera C.J., Medina N., Peng X.,
RA Thi-Ngoc H.P., Redder P., Schenk M.E., Theriault C., Tolstrup N.,
RA Charlebois R.L., Doolittle W.F., Duguet M., Gaasterland T.,
RA Garrett R.A., Ragan M.A., Sensen C.W., Van der Oost J.;
RT "The complete genome of the crenarchaeon Sulfolobus solfataricus P2."
RT Proc. Natl. Acad. Sci. U.S.A. 98:7835-7840(2001).
RL EMBL: AE006879; AAK42970.1; -.
DR InterPro: IPR000873; AMP-bind.
DR Pfam: PF00501; AMP-binding; 1.
DR PRINTS: PR00154; AMP-BINDING.
DR PROSITE: PS00455; AMP-BINDING; 1.
SQ SEQUENCE Complete proteome.
KW Ligase; Complete proteome.
E2779A7118B7C2C5 CRC64;

Query Match 57.5%; Score 42; DB 17; Length 666;
Best Local Similarity 60.0%; Pred. No. 32;
Matches 9; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

OY 1 DRLVLSIRTRGOIHS 15
DB 19 LRLVLSITTKKSIHS 33
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RESULT 12
O8KDC4 PRELIMINARY; PRT; 343 AA.
ID O8KDC4;
DT 01-OCT-2002 (TREMBLrel. 22, Created)
DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Hypothetical protein CT1130.
GN CT1130.
OS Chlorobium tepidum.
OC Bacteria; Chlorobi; Chlorobia; Chlorobiales; Chlorobiaceae;
OC Chlorobium;
OC NCBI_Taxid-1097;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN-TLS / ATCC 49652 / DSM 12025;
MEDLINE-22103685; PubMed-12093901;
RA Eidsen J.A., Nelson K.E., Paulsen I.T., Heidelberg J.F., Wu M.,
RA Dodson R.J., Deboy R., Gwin M.L., Nelson W.C., Haft D.H.,
RA Hickey E.K., Peterson J.D., Durkin A.S., Kolonay J.L., Yang F.,
RA Holt I., Umayam L.A., Mason T., Brenner M., Shea T.P., Parksey D.,
RA Nierman W.C., Feldblyum T.V., Hansen C.L., Craven M.B., Radune D.,
RA Venner J.C., Tettelin H., Bryant D.A., Fraser C.M.;
RT "The complete genome sequence of Chlorobium tepidum TLS, a
RT photosynthetic, anaerobic, green-sulfur bacterium."
RT Proc. Natl. Acad. Sci. U.S.A. 99:9509-9514(2002).
RL EMBL: AE012874; NAM72363.1; -.
DR TIGR: CT1130; -.
DR InterPro: IPR002729; DUF48.
DR Pfam: PF01867; DUF48; 1.
DR PRODOM: PD008695; DUF48; 1.
DR TIGRPMAS: TIGR00287; TIGR00287; 1.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 343 AA; 38756 MW; 9D5FB16504974866 CRC64;

Query Match 55.5%; Score 40.5; DB 16; Length 343;
Best Local Similarity 66.7%; Pred. No. 31;
Matches 10; Conservative 2; Mismatches 2; Indels 1; Gaps 1;

OY 2 DRLVLSIRTRGOIHS 15
DB 257 DRLVLSLNRGOIHA 271
:|:::|::|

RESULT 13
O8UE41 PRELIMINARY; PRT; 141 AA.
ID O8UE41;
DT 01-JUN-2002 (TREMBLrel. 21, Created)
DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE 50S ribosomal protein L17.
GN RPL17 OR ATU01922 OR AGR_C3516.
OS Agrobacterium tumefaciens (strain C58 / ATCC 33970).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Rhizobiaceae; Rhizobium.
OC NCBI_Taxid-176299;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-21608550; PubMed-11743193;
Wood D.W., Setubal J.C., Kaul R., Monks D.E., Kitajima J.P., Woo L.,
RA Okura V.K., Zhou Y., Chen L., Wood G.E., Almeida N.F., Jr.,
RA Chapman P., Paulsen I.T., Eiden J.A., Karp P.D., Boyce D., Sr.,
RA Kutyavin T., Levy R., Li M.-T., McClelland E., Gillet W., Grant C.,
RA Raymond C., Rouse G., Saenphithachak C., Wu Z., Romero P., Gordon D.,
RA Zhang S., Xeo H., Tao Y., Riddle P., Jung M., Krespan P., Perry M.,
RA Gordon-Kamm B., Zhao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M.,
RA Chumley F., Tingey S.V., Tomb J.-F., Gordon M.P., Olson M.V.,
RA Nester E.W.;
RT "The genome of the natural genetic engineer Agrobacterium tumefaciens

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RT C58."
 RL Science 294:2317-2323(2001).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21608551; PubMed=11743194;
 RA Goodner B., Hinkle G., Gattung S., Miller N., Blanchard M.,
 RA Ourullo B., Goldman B.S., Cao Y., Askew M., Halling C., Mullin L.,
 RA Wollam C., Allinger M., Vaudin M., Iartchouk O., Bpp A., Liu F.,
 RA Planagan C., Crowell C., Gursen J., Lomo C., Sear C., Strub G.,
 RA Cielo C., Slater S.;
 RT "Genome sequence of the plant pathogen and biotechnology agent
 RT Agrobacterium tumefaciens C58."
 RL Science 294:2323-2328(2001).
 DR EMBL: AE009146; AAL42918.1;
 DR EMBL: AE008111; AAK87683.1;
 DR InterPro: IPR000456; Ribosomal_L17.
 DR Pfam: PF01196; Ribosomal_L17; 1.
 DR Prodom: PD004277; Ribosomal_L17; 1.
 DR TIGRFAMS: TIGR00059; L17; 1.
 DR PROSITE: PS01167; RIBOSOMAL_L17; 1.
 KW Ribosomal protein; Complete proteome.
 SQ SEQUENCE 141 AA; 15395 MW; CD37B5D4E2D79D35 CRC64;

Query Match 54.8%; Score 40; DB 16; Length 141;
 Best Local Similarity 40.0%; Pred. NO. 15;
 Matches 6; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

OY 1 IDRLVSIPTRGQIHS 15
 DB 48 VERLVTGKRGDLHA 62

RESULT 14
 O9RMC1 PRELIMINARY; PRT; 246 AA.
 ID O9RMC1:
 AC O9RMC1:
 DT 01-MAY-2000 (Tremblrel. 13, Created)
 DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
 DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
 DE RNA methyltransferase, TRMh family.
 GN DR0748.
 OS Deinococcus radiodurans.
 OC Bacteria; Deinococcus-thermus; Deinococci; Deinococcales;
 OC Delnoccaceae; Deinococcus.
 NC NCBI_TaxID=1299;
 RP SEQUENCE FROM N.A.
 RC STRAIN=RI:
 RX MEDLINE=20036896; PubMed=10567266;
 RA White O., Eisen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D.,
 RA Dodson R.J., Haft D.H., Gwinn M.L., Nelson W.C., Richardson D.L.,
 RA Moffat K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M.,
 RA Vanatavehan J.J., Lam P., McDonald L., Utterback T., Zaleski C.,
 RA Makarova K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.D.,
 RA Ketchum K.A., Nelson K.E., Salzberg S., Smith H.O., Venter J.C.,
 RA Fraser C.M.;
 RT "Genome sequence of the radioresistant bacterium Deinococcus
 RT radiodurans RI."
 RL Science 286:1571-1577(1999).
 DR EMBL: AE001930; AAF10325.1;
 DR TIGR: DR0748;
 DR InterPro: IPR004441; rRNA_methyl_3.
 DR InterPro: IPR001537; Spou_methylase.
 DR Pfam: PF00588; Spou_methylase; 1.
 DR Prodom: PD001243; Spou_methylase; 1.
 DR TIGRFAMS: TIGR00186; rRNA_methyl_3; 1.
 KW Transferase; Methyltransferase; Complete proteome.
 SQ SEQUENCE 246 AA; 26179 MW; 3E1827C743CE3A8 CRC64;

Query Match 54.8%; Score 40; DB 16; Length 246;
 Best Local Similarity 64.3%; Pred. NO. 27;
 Matches 9; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

OY 2 DRLVSIPTRGQIHS 15
 DB 208 DVLVSIPTRGQVOS 221

RESULT 15
 ID O8GUR0 PRELIMINARY; PRT; 416 AA.
 AC O8GUR0:
 DT 01-MAR-2003 (Tremblrel. 23, Created)
 DT 01-MAR-2003 (Tremblrel. 23, Last sequence update)
 DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
 DE Alpha-amylase precursor (EC 3.2.1.1).
 OS Musa acuminata (Banana).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Zingiberales; Musaceae;
 OC Musa.
 NC NCBI_TaxID=4641;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Nandica; TISSUE=leaf;
 RA Vieira A. Jr., Nascimento J.R.O., Lajolo F.M.;
 RT "Sequencing and molecular characterization of a banana alpha-amylase
 RT gene."
 RL Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AY171068; AAO11776.1;
 DR Signal; Hydrolase; Glycosidase.
 FT SIGNAL 1 15 POTENTIAL.
 FT CHAIN 16 416 ALPHA-AMYLASE.
 SQ SEQUENCE 416 AA; 46558 MW; 7D5EC630F221915 CRC64;

Query Match 54.8%; Score 40; DB 10; Length 416;
 Best Local Similarity 60.0%; Pred. NO. 47;
 Matches 9; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

OY 1 IDRLVSIPTRGQIHS 15
 DB 347 ITRLAKTRTRNGIHS 361

RESULT 16
 O8LQK4 PRELIMINARY; PRT; 906 AA.
 ID O8LQK4:
 AC O8LQK4:
 DT 01-OCT-2002 (Tremblrel. 22, Created)
 DT 01-OCT-2002 (Tremblrel. 22, Last sequence update)
 DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
 DE Putative alpha-amylase.
 GN B1131B07.22
 OS Oryza sativa (japonica cultivar-group).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Ehrhartoideae; Oryzaceae; Oryza.
 NC NCBI_TaxID=39947;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Nipondare;
 RA Sasaki T., Matsumoto T., Yamamoto K.;
 RT "Oryza sativa nipondare(GA3) genomic DNA, chromosome 1, BAC
 RT clone:B1131B07."
 RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF003408; BAB93360.1;
 DR Gramene; O8LQK4;
 DR InterPro: IPR006047; Alpha-amyl_cat.
 DR InterPro: IPR006589; Alp_amyl_cat_sub.
 DR InterPro: IPR006046; Glyco_hydro_13.
 DR Pfam: PF00128; alpha-amylase; 1.
 DR PRINTS: PR00110; ALPHAMYLASE.
 DR SMART: SM00642; Amyy; 1.
 SQ SEQUENCE 906 AA; 101641 MW; AEFD187910DD55C5 CRC64;

Query Match 54.8%; Score 40; DB 10; Length 906;

Best Local Similarity 57.1%; Pred. No. 1,le02;
Matches 8; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

OY 1 DRLVSIRTRG 14
Db 837 IAKLISIRTRG 850

RESULT 17

O9DA04 PRELIMINARY; PRT: 506 AA.

AC O9DA04; 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DE 170003E16R1K protein.
GN 170003E16R1K.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;

RN [1]
RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6J; TISSUE=Testis;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shidata K., Yoshino M., Itoh M., Ishii Y.,
RA Aikawa T., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda S.,
RA Aikawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Pleistman M., Gaasterland T., Gissi C., King B., Kochia H.,
RA Kuehl P., Lewis S., Matsuo Y., Nakai D., Pesole G., Quackenbush J.,
RA Schirral L.M., Stabili F., Suzuki R., Tomita M., Wagner L., Mashio T.,
RA Sakai K., Offito T., Furuno M., Aono H., Balderelli R., Barsh G.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamlya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez T., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seva T., Shihara Y., Storch K.-F.,
RA Suzuki H., Togo-Oka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
RA Wyszynski B., Yoshida K., Hasegawa Y., Kawai H., Kontsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection."
RT Nature 409:585-590(2001).
DR EMBL, AK005628, BAB24157.1;
DR MOP, MGI1919087, 170003E16R1K.
SQ SEQUENCE 506 AA; 35505 MW; 1AA360BCEDA709 CRC64;

Query Match 54.1%; Score 39.5; DB 11; Length 506;
Best Local Similarity 57.1%; Pred. No. 72;
Matches 8; Conservative 5; Mismatches 0; Indels 1; Gaps 1;

OY 2 DRLVSIRTRG 15
Db 189 DRL-SIKSGOLHS 201

RESULT 18

O94AT6 PRELIMINARY; PRT: 245 AA.

AC O94AT6; 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
DE 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Putative short-chain type dehydrogenase/reductase (Fragment).
GN AT3G04000.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;

RP SEQUENCE FROM N.A.

RA Yamada K., Liu S.X., Sakano H., Pham P.K., Banh J., Chung M.K.,
RA Goldsmith A.D., Lee J.M., Quach H.L., Toriumi M., Yu G., Bowser L.,
RA Carlinici P., Chen H., Cheuk R., Hayashizaki Y., Ishida J., Jones T.,
RA Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Lum B., Li J.,
RA Mirada M., Narusaka M., Nguyen M., Palm C.J., Sakurai T., Saccu M.,
RA Seki M., Shinn P., Southwick A., Shinzaki K., Davis R.W., Ecker J.R.,
RA Theologis A.;
RT "Arabidopsis full length cDNA clones."
RT Submitted (JUL-2001) to the EMBL/Genbank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
(SDR) FAMILY.
DR EMBL, AY045807; AAK76481.2;
DR InterPro: IPR002198; ADH_short.
DR Pfam: PF00106; adh_short; 1.
DR PRINTS: PR00080; SDRFAMILY.
KW Oxidoreductase.
FT NON_TER 1
SQ SEQUENCE 245 AA; 25906 MW; CE98FC78C53841P5 CRC64;

Query Match 53.4%; Score 39; DB 10; Length 245;
Best Local Similarity 60.0%; Pred. No. 42;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 2 DRLVSIRTRG 11
Db 105 DRLSVTRG 114

RESULT 19

O9SOR2 PRELIMINARY; PRT: 272 AA.

AC O9SOR2; 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DE 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Putative short-chain type dehydrogenase/reductase.
GN T11i18.11 OR AT3G04000
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;

RN [1]
RP SEQUENCE FROM N.A.

RC STRAIN=CV Columbia;
RA Lin X., Kaul S., Town C.D., Beilto M., Creasy T.H., Haas B.,
RA Ronning C.M., Koo H., Fujii C.Y., Utterback T.R., Barnstead M.E.,
RA Bowman C.L., White O., Nierman W.C., Fraser C.M.;
RT "Arabidopsis thaliana chromosome III BAC T11i18 genomic sequence."
RT Submitted (JAN-2001) to the EMBL/Genbank/DBJ databases.

RN [2]

RP SEQUENCE FROM N.A.
RA Yamada K., Chan M.M., Chang C.H., Dale J.M., Hsuan V.W., Lee J.M.,
RA Onodera C.S., Quach H.L., Tang C.C., Toriumi M., Wong C., Wu H.C.,
RA Yu G., Yuan S., Chen H., Cheuk R., Jones T., Kim C.J., Nguyen M.,
RA Palm C.J., Shinn P., Southwick A., Tripp M.G., Wu T., Davis R.W.,
RA Ecker J.R., Theologis A.;
RT "Arabidopsis Open Reading Frame (ORF) Clones."
RT Submitted (DEC-2002) to the EMBL/Genbank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
(SDR) FAMILY.
DR EMBL, AC011698; AAF05859.1;
DR EMBL, BT002321; AAN6154.1;
DR HSSP: Q12634; 1YBV.
DR InterPro: IPR002198; ADH_short.
DR Pfam: PF00106; adh_short; 1.
DR PRINTS: PR00080; SDRFAMILY.
KW Oxidoreductase.
SQ SEQUENCE 272 AA; 28434 MW; 1F0542BE7C599276 CRC64;

Query Match 53.4%; Score 39; DB 10; Length 272;
Best Local Similarity 60.0%; Pred. No. 47;

Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 2 DRLVSIRTRG 11
 |||:|: |||
 DB 132 DRLVSIRTRG 141

RESULT 20

OY 09C425 PRELIMINARY; PRT; 284 AA.

AC 09C425;
 DT 01-JUN-2001 (TREMBLrel. 17, last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, last sequence update)
 DT 01-MAR-2003 (TREMBLrel. 23, last annotation update)
 DE Reductase.
 OS Ophiostoma floccosum.
 CC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 CC Ophiostomatales; Ophiostomataceae; Ophiostoma.
 CC NCBI_TaxID=104300;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Wang H., Breuil C.;
 RT "A second reductase gene involved in melanin biosynthesis from the
 RT sapstaining fungus, Ophiostoma floccosum.";
 RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
 CC (SBR) FAMILY.
 DR EMBL; AF317668; AA07185.1; -.
 DR HSP; Q12634; 1YBY.
 DR InterPro: IPR002198; ADH_short.
 DR Pfam; PF00106; adh_short; 1.
 DR PRINTS; PR00080; SDRFAMILY.
 DR PROSITE; PS00061; ADH_SHORT; 1.
 DR Oxidoreductase.
 KW OXIDOREDUCTASE.
 SQ SEQUENCE 284 AA; 30141 MW; F35E0E0604DCE2 CRC64;

Query Match 53.4%; Score 39; DB 3; Length 284;
 Best Local Similarity 63.6%; Pred. No. 49;
 Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 2 DRLVSIRTRG 12
 ||:|: |||
 DB 134 DRLVSIRTRG 144

RESULT 21

OY 081W13 PRELIMINARY; PRT; 402 AA.

AC 081W13;
 DT 01-MAR-2003 (TREMBLrel. 23, last sequence update)
 DT 01-MAR-2003 (TREMBLrel. 23, last sequence update)
 DT 01-MAR-2003 (TREMBLrel. 23, last annotation update)
 DE Similar to nuclear receptor subfamily 1, group H, member 3.
 OS Homo sapiens (Human).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 CC NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Tissue=Brain;
 RA Strausberg R.;
 RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC041172; AA41172.1; -.
 KW Receptor.
 SQ SEQUENCE 402 AA; 45691 MW; 78EA53CFB2358E7 CRC64;

Query Match 53.4%; Score 39; DB 4; Length 402;
 Best Local Similarity 53.8%; Pred. No. 71;
 Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

OY 3 RLVSIIRTRGQHS 15
 :||:|:|: |||
 DB 365 KLVSIIRTRGQHS 377

RESULT 22

OY 08JHU1 PRELIMINARY; PRT; 409 AA.

AC 08JHU1;
 DT 01-OCT-2002 (TREMBLrel. 22, last sequence update)
 DT 01-OCT-2002 (TREMBLrel. 22, last sequence update)
 DT 01-MAR-2003 (TREMBLrel. 23, last annotation update)
 DE Liver x receptor.
 GN LXR.
 OS Gallus gallus (Chicken).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 CC Gallus.
 CC NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-22162479; PubMed-12045201;
 RA Handschin C., Podvinet M., Amherd R., Looser R., Ourlin J.C.,
 RA Meyer U.A.;
 RT "Cholesterol and Bile Acids Regulate Xenosensor Signaling in Drug-
 RT mediated Induction of Cytochromes P450.";
 RL J. Biol. Chem. 277:29561-29567(2002).
 CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTOR FAMILY.
 DR EMBL; AF492498; AA090897.1; -.
 DR InterPro: IPR000536; Hormone_rec_1lg.
 DR InterPro: IPR001723; Steroid_receptor.
 DR InterPro: IPR001628; Znf_C4steroid.
 DR Pfam; PF00104; hormone_rec; 1.
 DR Pfam; PF00105; Zf-C4; 1.
 DR PRINTS; PR00398; STROHOMNER.
 DR PRINTS; PR00047; STROIDFINGER.
 DR Prodom; PD000035; Znf_C4steroid; 1.
 DR SMART; SM00430; HOL1; 1.
 DR SMART; SM00399; ZOF_C4; 1.
 DR PROSITE; PS00031; NUCLEAR_RECEPTOR; 1.
 DR DNA-binding; Metal-binding; Nuclear protein; Receptor; Transcription;
 KW TRANSCRIPTION REGULATION; ZINC; ZINC-FINGER.
 SQ SEQUENCE 409 AA; 47056 MW; 156C9FAB92A46587 CRC64;

Query Match 53.4%; Score 39; DB 13; Length 409;
 Best Local Similarity 53.8%; Pred. No. 72;
 Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

OY 3 RLVSIIRTRGQHS 15
 :||:|:|: |||
 DB 372 KLVSIIRTRGQHS 384

RESULT 23

OY 006098 PRELIMINARY; PRT; 443 AA.

AC 006098;
 DT 01-NOV-1996 (TREMBLrel. 01, last sequence update)
 DT 01-NOV-1996 (TREMBLrel. 01, last sequence update)
 DT 01-MAR-2003 (TREMBLrel. 23, last annotation update)
 DE Similar to protein kinases GCN2.
 GN ISRL OR P8283.9 OR YPR106W.
 OS Saccharomyces cerevisiae (Baker's yeast).
 CC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 CC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
 CC NCBI_TaxID=4932;
 RN [1]
 RP SEQUENCE FROM N.A.
 RP STRAIN=S288C;
 RX MEDLINE-97313271; PubMed=9169875;
 RA Bussey H., Storms R.K., Ahmed A., Albermann K., Allen E., Anseorge W.,
 RA Araujo R., Aparicio A., Bartell B., Badcock K., Benes V., Bolstein D.,
 RA Bowman S., Bruckner M., Carpenter J., Cherry J.M., Chung E.,
 RA Churcher C., Coster F., Davis K., Davis R.W., Dietrich F.S.,
 RA Delius H., Dipolo T., Dubois E., Dusterhoft A., Duncan M., Floeth M.,

DT 01-OCT-2000 (TREMBlrel. 15, Created)
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
 DE Putative membrane protein.
 GN SCO2356 OR SCC8A.14.
 OS Streptomyces coelicolor.
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Streptomycinae; Streptomycetaceae; Streptomyces.
 NCBI_TaxID=1902;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-A3(2) / M145.
 RX MEDLINE=21996410; PubMed=12000953;
 RA Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
 RA Thomson N.R., James K.D., Harris D.E., Quail M.A., Kleser H.,
 RA Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
 RA Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
 RA Huang C.H., Kleser I., Larke L., Murphy L., Oliver K., O'Neill S.,
 RA Rabinowitsch E., Rajandream M.A., Rutherford K., Rutter S.,
 RA Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
 RA Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
 RA Hopwood D.A.;
 RT "Complete genome sequence of the model actinomycete Streptomyces
 coelicolor A3(2).";
 RL Nucleic Acids Res. 30:1-147(2002).
 DR EMBL; AL939112; CAB92832.1; -.
 KW Complete proteome.
 SQ SEQUENCE 467 AA; 51174 MW; CD8EB236C6A3C4E CRC64;

Query Match 53.4%; Score 39; DB 16; Length 467;
 Best Local Similarity 80.0%; Pred. No. 83;
 Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 3 RLVSIRTRGQ 12
 |||||
 DB 279 RLVSIRTRGQ 288

RESULT 27
 O9ADT8 PRELIMINARY; PRT; 847 AA.
 AC O9ADT8:
 DT 01-JUN-2001 (TREMBlrel. 17, Created)
 DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
 DE Putative subtilisin proteinase-like protein.
 GN S025.
 OS Salmonella enterica subsp. enterica serovar Typhimurium.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Salmonella.
 OX NCBI_TaxID=90371;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-96-5227;
 RX MEDLINE=21429247; PubMed=11544236;
 RA Boyd D., Peters G.A., Cloeckaert A., Boumediene K.S.,
 RA Chaslus-Dancla E., Imberechts H., Mulvey M.R.;
 RT "Complete Nucleotide Sequence of a 43-Kilobase Genomic Island
 Associated with the Multidrug Resistance Region of *Salmonella enterica*
 RT Serovar Typhimurium DT104 and Its Identification in Phage Type DT120
 RT and Serovar Agona";
 RT J. Bacteriol. 183:5725-5732(2001).
 DR EMBL; AF261825; AAK02042.1; -.
 DR InterPro; IPR000209; Peptidase-S8.
 DR PROSITE; PS00136; SUBTILASE ASP; 1.
 SQ SEQUENCE 847 AA; 95237 MW; 8EBD2843CE2E1B93 CRC64;

Query Match 53.4%; Score 39; DB 2; Length 847;
 Best Local Similarity 77.8%; Pred. No. 1.5e+02;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 OY 7 ITRGQIHS 15
 :|||||

DB 762 LTRGSIHS 770

RESULT 28
 O9A8S8 PRELIMINARY; PRT; 137 AA.
 AC O9A8S8:
 DT 01-JUN-2001 (TREMBlrel. 17, Created)
 DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
 DE Ribosomal protein L17.
 GN CCL273.
 OS Caulobacter crescentus.
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Caulobacterales;
 OC Caulobacteraceae; Caulobacter.
 OX NCBI_TaxID=155892;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-ATCC 19089 / CB15;
 RX MEDLINE=21173658; PubMed=11259647;
 RA Nierman W.C., Feldblyum T.V., Laub M.T., Paulsen I.T., Nelson K.E.,
 RA Eisen J., Heidelberg J.F., Alley M.R.K., Ohta N., Maddock J.R.,
 RA Potocka I., Nelson W.C., Newton A., Stephens C., Pladke N.D., Ely B.,
 RA Debay R.T., Dodson R.J., Durkin A.S., Gwinn M.L., Haft D.H.,
 RA Kolonay J.F., Smit J., Craven M.B., Khouri H., Ermolaeva M., White O.,
 RA Uiterberg S.L., Venter J.C., Shapiro L., Fraser C.M.;
 RA Salzberg S.L.;
 RT "Complete genome sequence of *Caulobacter crescentus*.";
 RL Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001).
 DR EMBL; AE005802; AAK23254.1; -.
 DR TIGR; CCL273; -.
 DR InterPro; IPR000456; Ribosomal_L17.
 DR Pfam; PF01196; Ribosomal_L17; 1.
 DR PRODOM; PD004277; Ribosomal_L17; 1.
 DR TIGRFAMS; TIGR00059; L17; 1.
 DR PROSITE; PS01167; RIBOSOMAL_L17; 1.
 KW Complete proteome.
 SQ SEQUENCE 137 AA; 15326 MW; F9F0EC66F33E6FE4 CRC64;

Query Match 52.1%; Score 38; DB 16; Length 137;
 Best Local Similarity 33.3%; Pred. No. 36;
 Matches 5; Conservative 7; Mismatches 3; Indels 0; Gaps 0;

OY 1 IDRVSIRTRGQIHS 15
 ::||::|
 DB 48 VERKLVTLAKRGDLHA 62

RESULT 29
 O91BD3 PRELIMINARY; PRT; 166 AA.
 AC O91BD3:
 DT 01-OCT-2000 (TREMBlrel. 15, Created)
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE Fructose-1,6-bisphosphatase (EC 3.1.3.11) (Fragment).
 GN FBP2.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Muscle;
 RA Tillmann H., Eschrich K.;
 RT "The gene duplication leading to present-day liver and muscle type
 RT genes of fructose-1,6-bisphosphatase occurred prior to the divergence
 RT of mammalia and amphibia";
 RT Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AJ276213; CAB99413.1; -.
 DR HSSP; P00636; IFRP.
 DR InterPro; IPR000146; In_FB_phphatase.

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 29, 2003, 18:35:10 ; Search time 30.5714 Seconds

(Without alignments)
51.920 Million cell updates/sec

Title: US-09-830-876-2

Perfect score: 61

Sequence: 1 CRDDPRPADG 10

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

A.Geneseq_19jun03.*
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23: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*
24: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA2003.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	61	100.0	10	21	AAV93372
2	61	100.0	425	21	AAV93374
3	44	72.1	189	21	AAAB16296
4	41.5	68.0	428	21	AAAB12798
5	41.5	68.0	428	22	AAAS0251
6	41.5	68.0	428	22	AAAB97245
7	41.5	68.0	429	16	AAAB76520
8	41.5	68.0	433	15	AAAS5130
9	41.5	68.0	434	14	AAAB32967

10	41.5	68.0	434	18	AAAB1871
11	41.5	68.0	434	20	AAV01375
12	41.5	68.0	434	20	AAAB4383
13	41.5	68.0	434	21	AAAB792
14	41	67.2	215	11	AAAB07659
15	39	63.9	594	22	AAAB59190
16	38	62.3	435	22	AAAB50253
17	38	62.3	435	22	AAAB97247
18	38	62.3	1036	20	AAAB81063
19	38	62.3	1036	22	AAAB59323
20	38	62.3	1036	22	AAAB28647
21	37	60.7	17	11	AAAB07159
22	37	60.7	17	11	AAAB07159
23	37	60.7	17	11	AAAB07159
24	37	60.7	118	14	AAAB41885
25	37	60.7	346	24	AAAB41533
26	37	60.7	413	23	AAAB96343
27	37	60.7	452	21	AAAB91957
28	37	60.7	593	14	AAAB48673
29	37	60.7	593	14	AAAB5475
30	37	60.7	593	23	AAAB20521
31	37	60.7	771	22	AAAB07869
32	37	60.7	845	22	AAAB07869
33	37	60.7	886	21	AAAB3370
34	37	60.7	926	22	AAAB3370
35	37	60.7	1281	22	AAAB10610
36	37	60.7	1281	22	AAAB10610
37	37	60.7	1617	22	AAAB07870
38	37	60.7	1691	22	AAAB10609
39	37	60.7	1691	22	AAAB07863
40	36	59.0	224	22	AAAB42728
41	36	59.0	246	22	AAAB35390
42	36	59.0	255	22	AAAB34688
43	36	59.0	255	22	AAAB34688
44	36	59.0	349	11	AAAB07668
45	36	59.0	2432	22	AAAB06023
46	36	59.0	4660	22	AAAB23830
47	36	59.0	4765	24	AAAB32730
48	35	58.2	4854	22	AAAB06027
49	35	58.2	280	23	AAAB93962
50	35	57.4	98	22	AAAB43583
51	35	57.4	98	22	AAAB43583
52	35	57.4	98	22	AAAB43583
53	35	57.4	114	22	AAAB94845
54	35	57.4	129	20	AAAB25030
55	35	57.4	165	22	AAAB70785
56	35	57.4	196	21	AAAB08436
57	35	57.4	196	21	AAAB08436
58	35	57.4	196	22	AAAB43325
59	35	57.4	196	22	AAAB43325
60	35	57.4	223	21	AAAB43324
61	35	57.4	223	21	AAAB43324
62	35	57.4	226	11	AAAB08435
63	35	57.4	226	13	AAAB25332
64	35	57.4	226	13	AAAB25332
65	35	57.4	226	15	AAAB46496
66	35	57.4	226	15	AAAB46496
67	35	57.4	227	11	AAAB05908
68	35	57.4	243	20	AAAB05908
69	35	57.4	306	21	AAAB68243
70	35	57.4	306	21	AAAB68243
71	35	57.4	306	22	AAAB52897
72	35	57.4	554	22	AAAB92535
73	35	57.4	554	22	AAAB92535
74	35	57.4	1264	18	AAAB62419
75	35	57.4	1864	18	AAAB62419
76	34	55.6	434	22	AAAB10469
77	34	55.6	63	22	AAAB10469
78	34	55.7	87	22	AAAB49827
79	34	55.7	94	22	AAAB17948
80	34	55.7	94	22	AAAB17948
81	34	55.7	117	24	AAAB71160
82	34	55.7	127	24	AAAB71160
			132	22	AAAB22550

Rice alpha-amylase
O. sativa alpha-am
Rice alpha-amylase
Rice alpha-amylase
Partial alpha-amyl
Drosophila melanog
Rice alpha-amylase
Alpha-amylase rela
Mammal acid sequenc
Drosophila melanog
Synthetic Nerve gr
NGF, chicken. Gal
Granulin E. Homo
Chicken mature NGF
Human mature NGF
Human DTRP protei
Human ovarian canc
Human cytoskeleton
Granulin sequence.
Human gp88 autocr
Human granulin/epi
Novel human protei
Novel human protei
Human ORF ORF264
NOV14 protein sequ
Human novel KIAI12
Human novel KIAI12
Novel human protei
Human novel KIAI12
Novel human protei
Hemophilus influe
E. coli cellular p
Salmonella typhi C
Partial alpha-amyl
Novel human diagn
Human BSR encoded
HRC3 protein Un
Novel human diagn
Arabidopsis thalian
Protonibacterium
Zea mays protein f
Protonibacterium
Human protein sequ
T. gondii immunoge
S. cerevisiae apopt
Arabidopsis thalian
Arabidopsis thalian
Protonibacterium
Arabidopsis thalian
Arabidopsis thalian
Rat neuronal growt
Sequence encoded b
Rat GAP-43. Rattu
Rat GAP-43. Rattu
Mouse neuronal gro
C. ensiformis chit
Mammal class I mol
Mammal class I mol
C glutamicum prote
Corynebacterium gl
Protonibacterium
Tylosine synthase
Rice alpha-synthase
Protonibacterium
Protonibacterium
Novel human diagn
Xenopus mature NGF
Drosophila melanog
Novel human diagn

83	34	55.7	144	24	ABU05287	Human diagnostics
84	34	55.7	329	23	ABG97429	S. ghanaensis UNBL
85	34	55.7	332	21	AA655461	Arabidopsis thalia
86	34	55.7	341	21	AA655460	Arabidopsis thalia
87	34	55.7	922	24	ABJ25866	Aspergillus fumiga
88	34	55.7	949	24	ABJ26466	Aspergillus fumiga
89	34	55.7	1021	19	AAW76192	Actinoplanes sp. a
90	34	55.7	1021	23	AAW49562	Actinoplanes sp. ac
91	34	55.7	1027	21	AAW79168	Pneumocystis carin
92	34	55.7	1029	21	AAW79167	Pneumocystis carin
93	34	55.7	1164	23	ABB92294	Herbicidally activ
94	34	55.7	1166	23	ABB91366	Herbicidally activ
95	34	55.7	1294	23	ABB78296	Amino acid sequenc
96	34	55.7	1349	19	AAW59359	Human retinal dege
97	34	54.1	30	22	ABG47757	Human liver Peptid
98	33	54.1	30	22	ABB27734	Human peptide #385
99	33	54.1	30	22	ABB32905	Peptide #411 encod
100	33	54.1	30	22	ABB18385	Protein #384 encod

ALIGNMENTS

RESULT 1

AAV93372
ID AAV93372 standard; peptide: 10 AA.

AC AAV93372:

DT 04-SEP-2000 (first entry)

DE Amino acid sequence of an epitope of the wheat alpha-amylase.

XX Epitope: wheat; alpha-amylase; two-site immunoassay; weather damage;

KW cereal grain.

XX Triticum aestivum.

OS WO200028319-A1.

PN 18-MAY-2000.

XX 11-NOV-1999; 99WO-AU00995.

XX 11-NOV-1998; 98AU-0007058.

PA (QUAL-) QUALITY WHEAT CRC LTD.

PI Skeritt JH;

XX WPI; 2000-376655/32.

XX Two site immunoassay for the qualitative or quantitative detection of
PT alpha-amylase in a test sample, used to detect weather damage in a
PT cereal grain, such as wheat, rye, triticale or barley -

XX Claim 1; Page 29; 52pp; English.

XX The present sequence represents an epitope from the wheat alpha-amylase.

XX Antibodies which recognise the epitope are used in a two-site

XX immunoassay for qualitative or quantitative detection of alpha-amylase

XX in a test sample. The assay is used for detecting weather damage in a

XX cereal grain. Weather damage is caused by the action of hydrolytic

XX enzymes, e.g. amylases, in the grain endosperm. These enzymes accelerate

XX the breakdown of starch granules and protein in the endosperm of

XX germinating grain. Individual growers can identify areas of sprouting
CC prior to harvest, preventing contamination of sound wheat by weather
CC damaged wheat. The damaged grain can be harvested separately from the
CC sound grain and financial losses resulting from down grading the whole
CC crop can be avoided. The two-site immunoassays can be applied at mill
CC or silo (elevator) receipt of grain or can be used on farms with minimal
CC equipment requirements.
XX

SO Sequence 10 AA;

Query Match

Best Local Similarity 100.0%; Score 61; DB 21; Length 10;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CRDDRPYADG 10

DB 1 CRDDRPYADG 10

RESULT 2

AAV93374
ID AAV93374 standard; protein: 425 AA.

AC AAV93374;

DT 04-SEP-2000 (first entry)

DE Amino acid sequence a wheat alpha-amylase.

XX Epitope: wheat; alpha-amylase; two-site immunoassay; weather damage;

KW cereal grain.

XX Triticum aestivum.

OS WO200028319-A1.

PN 18-MAY-2000.

XX 11-NOV-1999; 99WO-AU00995.

XX 11-NOV-1998; 98AU-0007058.

PA (QUAL-) QUALITY WHEAT CRC LTD.

PI Skeritt JH;

XX WPI; 2000-376655/32.

XX Two site immunoassay for the qualitative or quantitative detection of
PT alpha-amylase in a test sample, used to detect weather damage in a
PT cereal grain, such as wheat, rye, triticale or barley -

XX Disclosure; Fig 3; 52pp; English.

XX The present sequence represents a wheat alpha-amylase. Antibodies

XX which recognise epitopes from this protein are used in a two-site

XX immunoassay for qualitative or quantitative detection of alpha-amylase

XX in a test sample. The assay is used for detecting weather damage in a

XX cereal grain. Weather damage is caused by the action of hydrolytic

XX enzymes, e.g. amylases, in the grain endosperm. These enzymes accelerate

XX the breakdown of starch granules and protein in the endosperm of

XX germinating grain. Individual growers can identify areas of sprouting

XX prior to harvest, preventing contamination of sound wheat by weather

XX damaged wheat. The damaged grain can be harvested separately from the

XX sound grain and financial losses resulting from down grading the whole

XX crop can be avoided. The two-site immunoassays can be applied at mill
XX or silo (elevator) receipt of grain or can be used on farms with minimal
XX equipment requirements.
XX

RESULT 3

Query Match

Best Local Similarity 100.0%; Score 61; DB 21; Length 425;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CRDDRPYADG 10

DB 146 CRDDRPYADG 155

XX	AAAB16296	standard; Protein: 189 AA.
XX	AAAB16296	
XX	AAAB16296;	
DT	31-OCT-2000	(first entry)
DE	Eucalyptus grandis amylase protein sequence SEQ ID NO:82.	
XX	Eucalyptus grandis; pinus radiata; Monterey pine; modification;	
XX	plant cell wall; polysaccharide; polysaccharide biosynthetic pathway;	
XX	transgenic plant.	
OS	Eucalyptus grandis.	
XX	MO20002092-A2.	
PD	20-APR-2000.	
XX	08-OCT-1999;	99WO-N200169.
PF	13-OCT-1998;	98US-0170862.
PR	11-AUG-1999;	99US-0148426.
XX	(GENE-) GENESIS RES & DEV CORP LTD.	
PA	(FLET-) FLETCHER CHALLENGE FORESTS LTD.	
XX	Bloksberg LN.	
PI	WPI: 2000-339328/29.	
DR	N-PSDB; AAA67103.	
XX	New genes encoding proteins involved in a plant polysaccharide	
PT	biosynthetic pathway; useful for modulating or altering the	
PT	polysaccharide content, composition or structure of the plant -	
XX	Claim 17; Page 77; 301pp; English.	
XX	The present invention describes isolated polynucleotides (PN) comprising	
CC	a sequence selected from one of 835 nucleotide sequences given in	
CC	AA67073 to AA679307, their (reverse) complements, sequences producing	
CC	an expectation (E) value of 0.01 or less compared to the 835 sequences,	
CC	835 sequences at least 50% identical to them, 200, 100, 40 or 20-mers of the	
CC	835 sequences or sequences that are degenerately equivalent or allelic	
CC	to the 835 sequences. The polynucleotides are used to modify the	
CC	activity of a polypeptide involved in a polysaccharide biosynthetic	
CC	pathway in the plant. They are especially used to modulate or alter the	
CC	polysaccharide content, composition or structure of the plant. AA16268	
CC	to AA16340 are proteins encoded by some of the polynucleotide sequence	
CC	given in the present invention.	
XX	Sequence	189 AA;
XX	Query Match	72.1%; Score 44; DB 21; Length 189;
XX	Best Local Similarity	70.0%; Pred. No. 7.5;
XX	Matches	7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
OY	1 CRDDRPYADG 10	
DB	:-	
	142 CRDDTEYS DG 151	
RESULT 4		
AAAB12798		
ID	AAAB12798	standard; Protein: 428 AA.
XX	AAAB12798;	
XX	23-NOV-2000	(first entry)
XX	Rice alpha-Amy7-C protein SEQ ID NO:2.	
XX	Rice; alpha-Amy6-C; alpha-Amy7-C; alpha-Amy8-C; alpha-Amy10-C;	

KM	gene expression; promoter region; alpha-amylase; transgenic plant.
XX	
OS	Oryza sativa.
XX	
PN	JP2000157080-A.
XX	
PD	13-JUN-2000.
XX	
PE	04-NOV-1993; 99JP-0356560.
XX	
PR	05-NOV-1992; 92JP-0321274.
PR	04-NOV-1993; 93JP-0297607.
XX	
PA	(NASC-) NAT SCI COUNCIL.
XX	
DR	WPI; 2000-468171/41.
DR	N-PSDB; AAA72947.
PT	A gene expression system containing the promoter region of
PT	alpha-amylase gene, useful for mass production of a desired gene
XX	product in a plant host cell
XX	
PS	Example 1; Page 27-30; 39pp; Japanese.
XX	
CC	The present invention describes a gene expression system containing the
CC	promoter region of an alpha-amylase gene. Also described is a method for
CC	preparing a transgenic rice plant comprising: (1) infecting Agrobacterium
CC	into an unmutated embryo of a rice plant; (2) simultaneously culturing
CC	the embryo with a suspended culture of a dicotyledon during the
CC	transforming step; (3) growing the transformed embryo to a callus in a
CC	selective medium containing a plant growth hormone; and (4) regenerating
CC	the callus to roots and sprouts in a regeneration medium. The method can
CC	be used for mass production of a desired gene product in a plant host
CC	cell. The present sequence represents the rice alpha-Amv7-C protein,
CC	which is used in an example from the present invention.
XX	
SQ	Sequence 428 AA:
XX	
QY	I CRDPRPADG 10 11 11
Db	149 CRDD-PYGDG 157
XX	
RESULT 5	
ID	AAAM50251 standard; Protein: 428 AA.
XX	
AC	AAAM50251;
XX	
DT	21-JAN-2002 (first entry)
XX	
DE	Rice alpha-amylase (alpha-Amv7-C gene product).
KM	Alpha-amylase; promoter; rice; transgenic plant; angiosperm;
KW	monocot; cereal; brewing.
XX	
OS	Oryza sativa.
XX	
FN	key Location/Qualifiers
FT	peptide 1..251 signal_peptide
FT	Protein 26..428 /label= Mature_protein
FT	
PN	US6288302-B1.
XX	
PD	11-SEP-2001.
XX	
PF	04-MAY-1998; 98US-0072917.

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XX 04-NOV-1992; 92US-0973324.
PR 01-AUG-1995; 95US-0509962.
PR 08-OCT-1997; 97US-0947201.
PR 22-NOV-1994; 94US-0343380.
XX
PA (NASC-) NAT SCI COUNCIL ROC.
XX
PI Yu S, Liu L, Chan M;
DR WPI: 2001-647191/74.
DR N-PSDB; AAI70537.
XX
XX Producing a transgenic monocot plant comprising a transgene under
PT control of an alpha amylase promoter and signal peptide sequences,
PT provides transgenic plants particularly cereals for the brewing
PT industry.
XX
XX Example 1: Column 61-64; 44pp; English.
XX
XX The present sequence is that of rice (Oryza sativa) cv. M202
CC alpha-amylase, encoded by isolated genomic DNA clone alpha-Amy7-C
CC (see AAI70537). Expression of alpha-Amy7-C in cultured suspension
CC cells of rice was induced 6-fold at day 12 after sugar depletion,
CC and continued to increase up to day 14. The invention relates to
CC the use of an alpha-amylase gene promoter and signal sequence in
CC the production of recombinant proteins in transgenic plants and
CC transgenic plant seeds. In a claimed method, a transgenic monocot
CC is obtained by: transforming an immature embryo of the plant via
CC Agrobacterium-mediated transformation with DNA comprising a plant
CC alpha-amylase promoter (e.g. the rice alpha-Amy7-C promoter) that
CC is induced under sugar-depleted or sugar-free conditions, a signal
CC peptide sequence, and an exogenous sequence encoding a gene product;
CC regenerating the transformed plant; and growing the transgenic
CC plant, which expresses the gene product under sugar-depleted or
CC sugar-free conditions. The gene product may also be obtained by
CC cultivating an angiosperm host cell. The transgenic monocot plants
CC are especially useful in brewing and to produce glucose from starch.
XX
XX Sequence 428 AA:
SQ
Query Match 68.0%; Score 41.5; DB 22; Length 428;
Best Local Similarity 80.0%; Pred. No. 48;
Matches 8; Conservative 0; Mismatches 1; Indels 1; Gaps 1;
OY 1 CRDDRYADG 10
Db 149 CRDD-PYGDG 157

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XX Yu S, Liu L;
PI
XX WPI: 2001-167365/17.
DR N-PSDB; AAI20283.
XX
XX Gene expression system comprising the promoter region of alpha-amylase
PT gene, produces large quantities of alpha-amylase in culture medium of
PT sugar starved rice.
XX
XX Disclosure; Fig 8; 104pp; Chinese.
XX
XX This invention relates to a gene expression system comprising the
CC alpha-amylase gene promoter. DNA encoding the signal peptide of
CC alpha-amylase and the promoter along with the glucuronidase reporter gene
CC and hygromycin resistance gene are used in the construction of a GUS gene
CC expression vector, which when transformed into rice suspension-cultured
CC cells, can be used to investigate the expression of the vector under the
CC control of the promoter. The gene expression system can be used to
CC conduct gene regulation and protein expression and secretion using the
CC characteristics of the alpha-amylase gene promoter and the DNA sequence
CC encoding the signal peptide. The present sequence represents an
CC alpha-amylase related protein used in the course of the present
CC invention.
XX
XX Sequence 428 AA:
SQ
Query Match 68.0%; Score 41.5; DB 22; Length 428;
Best Local Similarity 80.0%; Pred. No. 48;
Matches 8; Conservative 0; Mismatches 1; Indels 1; Gaps 1;
OY 1 CRDDRYADG 10
Db 149 CRDD-PYGDG 157

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RESULT 6
AAB97245
ID AAB97245 standard; Protein; 428 AA.
XX
XX AAB97245;
XX
XX 31-JUL-2001 (first entry)
XX
XX Alpha-amylase related protein #1.
XX
XX Alpha-amylase; promoter; expression vector; rice.
XX
XX Unidentified.
XX
XX TW402638-A.
XX
XX 21-AUG-2000.
XX
XX 13-FEB-1992; 97TW-0101436.
XX
XX 13-FEB-1992; 97TW-0101436.
XX
XX (NASC-) NAT SCI COUNCIL.
PA

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RESULT 7
AAR76520
ID AAR76520 standard; Protein; 429 AA.
XX
XX AAR76520;
XX
XX 14-FEB-1996 (first entry)
XX
XX Alpha-amylase-7-C.
XX
XX Alpha-Amy-6-C; amylase; promoter; vector; heterologous;
XX gene expression system.
XX
XX Oryzae sativa.
XX
XX Key Location/Qualifiers
FH MISC-difference 35
FT /note= "corresp. to GAC codon"
FT MISC-difference 83
FT /note= "corresp. to CAG codon"
FT MISC-difference 158
FT /note= "corresp. to GAC codon"
FT MISC-difference 218
FT /note= "corresp. to TAC codon"
FT MISC-difference 224
FT /note= "corresp. to CGG codon"
FT MISC-difference 233
FT /note= "corresp. to CGT codon"
FT MISC-difference 294
FT /note= "corresp. to CAG codon"
XX
XX JP07143895-A.
XX
XX 06-JUN-1995.
XX
XX 04-NOV-1993; 93JP-0297607.
XX

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PR 05-NOV-1992; 92JP-0321274.
XX
XX (MASC-) NAT SCI COUNCIL.
XX
XX WPI; 1995-236472/31.
XX
XX N-PSDB; AA092806.
XX
XX Gene expression system contg. alpha-amylase gene promoter - for use
XX in plants for expression of heterologous genes
XX
XX Claim 3; Page 27-30; 42pp; Japanese.
XX
XX AA06519-R76521 represent the amylase gene products alpha-amylase-6-C,
XX alpha-amylase-7-C and alpha-amylase-8-C respectively. The promoter
XX regions of these amylase genes are used in a new gene expression system.
XX The system may be used for the expression of heterologous genes in plant
XX cells and for the large scale production of the encoded products of such
XX genes.
XX NB. Some amino acids in this sequence appear to have been wrongly
XX entered, see feature table and the corresp. DNA file AA092806.
XX
XX Sequence 429 AA:
SQ
Query Match 68.0%; Score 41.5; DB 16; Length 429;
Best Local Similarity 80.0%; Pred. No. 48;
Matches 8; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

OY 1 CRDDRPYADG 10
DB 150 CRDD-PYGDG 158

RESULT 8
AAR55130
ID AAR55130 standard; Protein; 433 AA.
XX
XX AAR55130;
XX
XX 25-MAR-2003 (updated)
XX 12-JAN-1995 (first entry)
XX
XX Rice alpha-amylase coding.
XX
XX Virus; recombination: plant virus; alpha trichosanthin; phenotype;
XX alpha amylase; alpha hemaglobin; bromo mosaic virus; gemini virus;
XX rice necrosis virus lodamovirus; gene expression; chinese cucumber.
XX
XX Oryza sativa.
XX
XX US5316931-A.
XX
XX 31-MAY-1994.
XX
XX 31-JUL-1992; 92US-0923692.
XX
XX 26-FEB-1988; 88US-0160766.
XX 26-FEB-1988; 88US-0160771.
XX 15-JUL-1988; 88US-0219279.
XX 17-FEB-1989; 89US-0310881.
XX 05-MAY-1989; 89US-0347637.
XX 08-JUN-1989; 89US-0363138.
XX 22-OCT-1990; 90US-0600244.
XX 16-JAN-1991; 91US-0641617.
XX 26-JUL-1991; 91US-0737899.
XX 01-AUG-1991; 91US-0739143.
XX
XX (BIOS-) BIOSOURCE GENETICS CORP.
XX
XX Dawson WO, Donson J, Garger SJ, Grantham GL, Gr111 LK;
XX Turpen AM, Turpen TH;
XX
XX WPI; 1994-176269/21.
XX
XX N-PSDB; AA065574.

```

```

XX
XX New recombinant plant viral nucleic acid - capable of systemic
XX infection and stable expression of non-native nucleic acid in
XX plant host
XX
XX Example 4; Columns 53-56; 44pp; English.
XX
XX The rice alpha-amylase gene may be inserted into a recombinant plant
XX virus which can then be used to infect plants for the production of
XX non-native products (in this case alpha-amylase). Other genes which
XX may be inserted into the virus are those which control a phenotypic
XX trait, such as male sterility, or sequences encoding anti-sense RNA
XX which can be useful to prevent the expression of undesired phenotypic
XX traits. The recombinant virus is derived from a plus sense, single
XX stranded virus selected from lodamovirus, bromo mosaic virus, rice
XX necrosis virus or a gemini virus.
XX (updated on 25-MAR-2003 to correct PF field.)
XX
XX Sequence 433 AA:
SQ
Query Match 68.0%; Score 41.5; DB 15; Length 433;
Best Local Similarity 80.0%; Pred. No. 49;
Matches 8; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

OY 1 CRDDRPYADG 10
DB 154 CRDD-PYGDG 162

RESULT 9
AAR32987
ID AAR32987 standard; Protein; 434 AA.
XX
XX AAR32987;
XX
XX 25-MAR-2003 (updated)
XX 17-JUN-1993 (first entry)
XX
XX Rice alpha-amylase.
XX
XX Recombinant products; commercial production; fermentation;
XX biosynthesis; natural products; recombinant proteins;
XX product expression; protein expression; expressed proteins.
XX
XX Oryza sativa.
XX
XX WO9303161-A1.
XX
XX 18-FEB-1993.
XX
XX 31-JUL-1992; 92WO-US06359.
XX 01-AUG-1991; 91US-0739143.
XX
XX (DAMS/) DAWSON W O.
XX (DONSON/) DONSON J.
XX (GARG/) GARGER S J.
XX (GRAN/) GRANTHAM G L.
XX (GRIL/) GRILLE L K.
XX (TURP/) TURPEN A M.
XX (TURP/) TURPEN T H.
XX
XX Donson J, Dawson WO, Grantham GL, Turpen TH, Turpen AM, Garger SJ;
XX Grille LK;
XX
XX WPI; 1993-076518/09.
XX N-PSDB; AA037680.
XX
XX Recombinant plant viral nucleic acids - used to express a prod.,
XX e.g. antibody or IL-1 in a plant
XX
XX Example 4; Page 96; 30pp; English.
XX

```

CC This sequence is rice alpha amylase. The coding sequence was inserted
CC into a recombinant plant viral nucleic acid which was then used to
CC express a recombinant product (in this case rice alpha-amylase) in a
CC plant. The plant viral sequence may be from tobacco mosaic, cucumber
CC green mottle, cowpea mosaic, bromo mosaic, broad bean mottle, rice
CC necrosis, geminiviruses, tomato golden mosaic, Cassava latent and
CC maize streak viruses.
CC (Updated on 25-MAR-2003 to correct PN field.)
CC (Updated on 25-MAR-2003 to correct PI field.)
CC
CC
SQ Sequence 434 AA;

Query Match 68.0%; Score 41.5; DB 14; Length 434;
Best Local Similarity 80.0%; Pred. No. 49;
Matches 8; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

OY 1 CRDDRPYADG 10
Db 155 CRDD-PYGDG 163
|||||

RESULT 10
AAW11871
ID AAW11871 standard; Protein: 434 AA.
AC AAW11871;
XX
DT 25-MAR-2003 (updated)
DT 21-APR-1997 (first entry)
XX
DE Rice alpha-amylase.
XX
KW Recombinant virus; alpha-haemoglobin; human; chinese cucumber;
KW alpha-ctrichosanthin; rice; alpha amylase; beta-haemoglobin;
KW subgenomic promoter; coat protein.
XX
OS Oryza sativa.
XX
PN US5589367-A.
PD 31-DEC-1996.
XX
PF 19-JAN-1994; 94US-0184237.
XX
PR 17-FEB-1989; 89US-0310881.
PR 05-MAY-1989; 89US-0347637.
PR 08-JUN-1989; 89US-0363138.
PR 31-JUL-1992; 92US-0923692.
PR 26-FEB-1988; 88US-0160771.
PR 26-FEB-1988; 88US-0219279.
PR 15-JUL-1988; 88US-0219279.
PR 22-OCT-1990; 90US-0600244.
PR 16-JAN-1991; 91US-0641617.
PR 26-JUL-1991; 91US-0737899.
PR 01-AUG-1991; 91US-0739143.
XX
PA (BIOS-) BIOSOURCE TECHNOLOGIES INC.
PI Dawson WO, Donson J, Garger SJ, Grantham GL, Grill LK;
PI Turpen AM, Turpen TH;
XX
DR WPI: 1997-076845/07.
DR N-PSDB: AAT61377.
XX
PT Recombinant viral DNA for altering plant phenotype or protein prodn
PT - contains non-native sub-genomic promoter for expression of
PT heterologous protein and native promoter for expression of coat
PT protein
XX
PS Example 4; Column 49-52; 42pp; English.
XX
CC The sequences given in AAW11868-71 represent proteins which were
CC produced by the recombinant viruses of the invention. The

CC viruses are recombinant plant viruses which comprise a native plant
CC virus subgenomic promoter, at least one non-native plant virus
CC subgenomic promoter, and a sequence encoding a plant virus coat
CC protein. These heterologous sequences are preferably under the
CC control of the native promoter sequence. By using a plant virus
CC existing cells can be altered with a new coding sequences without
CC involving germ cell. The recombinant viruses are stable and can
CC cause systemic infection, with stable expression/transcription in
CC plants that are hosts for the non-native part of the vector. The
CC nucleotide sequences encoding these protein preferably integrated
CC in plant viruses having either the O-coat protein or the UI-coat
CC protein gene.
CC (Updated on 25-MAR-2003 to correct PF field.)
CC (Updated on 25-MAR-2003 to correct PR field.)
CC
CC
SQ Sequence 434 AA;

Query Match 68.0%; Score 41.5; DB 18; Length 434;
Best Local Similarity 80.0%; Pred. No. 49;
Matches 8; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

OY 1 CRDDRPYADG 10
Db 155 CRDD-PYGDG 163
|||||

RESULT 11
AAV01375
ID AAV01375 standard; Protein: 434 AA.
AC AAV01375;
XX
DT 20-MAR-2003 (updated)
DT 04-JUN-1999 (first entry)
XX
DE O. sativa alpha-amylase.
XX
KW Recombinant; plant virus; coat protein; systemic infection;
KW transcription; therapeutic; rice; alpha-amylase.
XX
OS Oryza sativa.
XX
PN US5889190-A.
PD 30-MAR-1999.
XX
PF 07-JUN-1995; 95US-0480432.
XX
PR 17-FEB-1989; 89US-0310881.
PR 05-MAY-1989; 89US-0347637.
PR 08-JUN-1989; 89US-0363138.
PR 31-JUL-1992; 92US-0923692.
PR 19-JAN-1994; 94US-0184237.
PR 26-FEB-1988; 88US-0160771.
PR 26-FEB-1988; 88US-0160771.
PR 15-JUL-1988; 88US-0219279.
PR 22-OCT-1990; 90US-0600244.
PR 16-JAN-1991; 91US-0641617.
PR 26-JUL-1991; 91US-0737899.
PR 01-AUG-1991; 91US-0739143.
XX
PA (BIOS-) BIOSOURCE TECHNOLOGIES INC.
PI Dawson WO, Donson J, Garger SJ, Grantham GL, Grill LK;
PI Turpen AM, Turpen TH;
XX
DR WPI: 1999-243290/20.
DR N-PSDB: AAX23144.
XX
PT Recombinant plant viral nucleic acid derived from a plus sense,
PT single stranded RNA plant virus - useful for the transcription of
PT products in a host
XX

PS Example 4; Columns 47-51; 46pp; English.

CC The invention relates to a recombinant plant viral nucleic acid derived
 CC from a plus sense, single stranded RNA plant virus. The recombinant plant
 CC viral nucleic acid comprises: (a) a first plant viral subgenomic promoter
 CC that is native to the plus sense, single stranded RNA plant virus and
 CC operably joined to a first nucleic acid expression sequence; and (b) a
 CC second plant viral subgenomic promoter that is non-native and is operably
 CC joined to a second nucleic acid expression sequence; where, (i) (a) and
 CC (b) are incapable of recombination with one another, (ii) either the
 CC first or the second nucleic acid expression sequence is a plant viral
 CC coat protein coding sequence. The recombinant plant viral nucleic acid
 CC allows the transcription of products in a host, such as therapeutic and
 CC other useful polypeptides or proteins e.g. enzymes, complex biomolecules
 CC and ribozymes. It also gives the option of applying the coding sequence
 CC to the desired organism, tissue, organ or cell, is stable for the foreign
 CC coding sequences and is capable of systemic infection in the plant host.
 CC The transformation and regeneration of target organisms become
 CC unnecessary.
 CC (Updated on 20-MAR-2003 to correct PR field.)

CC Sequence 434 AA;

Query Match 68.0%; Score 41.5; DB 20; Length 434;

Best Local Similarity 80.0%; Pred. No. 49;

Matches 8; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

OY 1 CRDPRPYADG 10
 |||||
 DB 155 CRDD-PYGDG 163

RESULT 12

ID AAM84383 standard; Protein; 434 AA.

AC AAM84383;

DT 01-APR-1999 (first entry)

DE Rice alpha-amylase sequence.

XX Rice; alpha-amylase; plant virus; RNA plant virus promoter;

KW systemic infection; foreign gene expression; AIDS therapeutic drug.

XX Oryza sativa.

XX US5866785-A.

XX 02-FEB-1999.

PD 07-JUN-1995; 95US-0482920.

PF 31-JUL-1992; 92US-0923692.

PR 26-FEB-1988; 88US-0160766.

PR 15-JUL-1988; 88US-0160771.

PR 17-FEB-1989; 89US-0219279.

PR 05-MAY-1989; 89US-0347637.

PR 08-JUN-1989; 89US-0363138.

PR 22-OCT-1990; 90US-0600244.

PR 16-JAN-1991; 91US-0641617.

PR 26-JUL-1991; 91US-0737899.

PR 01-AUG-1991; 91US-0739143.

PR 19-JAN-1994; 94US-0184237.

PR 07-JUN-1995; 95US-0482920.

PA (BIOS-) BIOSOURCE TECHNOLOGIES INC.

PI Dawson WO, Donson J, Garger SJ, Grantham GL, Grill LK;

PT Turpen AM, Turpen TH;

XX WPI; 1999-142035/12.

DR N-PSDB; AAX03386.

PT Recombinant plant viral vector - that is capable of systemic
 PT infection in host plant and stable production of heterologous DNA
 PT useful for producing therapeutic proteins for treating e.g. AIDS

PS Example 4; Columns 51-54; 45pp; English.

CC The present sequence represents rice alpha-amylase. The nucleic
 CC acid sequence can be expressed in the plant viral constructs of the
 CC invention. The specification describes a recombinant plant viral
 CC nucleic acid derived from a positive (+)-sense RNA plant virus comprising
 CC a native (+)-sense RNA plant virus promoter that is linked to an
 CC expression sequence and a heterologous (+)-sense RNA plant virus
 CC promoter that is linked to an expression sequence. The promoters are
 CC incapable of recombination with each other, and one of the expression
 CC sequences encodes a plant viral coat protein while the other is
 CC optionally a heterologous coding sequence. The plant viral nucleic acid
 CC is capable of systemic infection in a host plant. The viral construct is
 CC useful for the introduction and expression of non-viral foreign genes
 CC in plants and the production of e.g. potential AIDS therapeutic drugs.

CC Sequence 434 AA;

Query Match 68.0%; Score 41.5; DB 20; Length 434;

Best Local Similarity 80.0%; Pred. No. 49;

Matches 8; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

OY 1 CRDPRPYADG 10
 |||||
 DB 155 CRDD-PYGDG 163

RESULT 13

ID AAY87792 standard; Protein; 434 AA.

AC AAY87792;

DT 24-AUG-2000 (first entry)

DE Rice alpha-amylase protein.

XX Animal RNA virus; viral coat protein; plant; male sterility;

KW Interleukin; EPO; erythropoietin; CSF; colony stimulating factor;

KW Factor VIII; hGH; human growth hormone; melanin; insulin; vaccine;

XX stereo specific catalysts; alpha-amylase; rice.

XX Oryza sativa.

XX US6054566-A.

XX 25-APR-2000.

PD 07-JUN-1995; 95US-0484341.

PF 17-FEB-1989; 89US-0310881.

PR 08-JUN-1989; 89US-0363138.

PR 26-FEB-1988; 88US-0160766.

PR 15-JUL-1988; 88US-0160771.

PR 05-MAY-1989; 89US-0219279.

PR 22-OCT-1990; 90US-0600244.

PR 16-JAN-1991; 91US-0641617.

PR 26-JUL-1991; 91US-0737899.

PR 01-AUG-1991; 91US-0739143.

PR 31-JUL-1992; 92US-0923692.

PA (BIOS-) BIOSOURCE TECHNOLOGIES INC.

PI Garger SJ, Grill LK, Turpen TH, Grantham GL, Dawson WO, Turpen AM;

PT Donson J;

XX

DR WPI: 2000-338510/29.
 DR N-PSDB; AAA12394.
 XX
 PT Recombinant non-retroviral nucleic acid for producing proteins such as
 PT Interleukin, melanin and vaccines, comprises subgenomic promoters
 PT linked to sequences coding for viral coat protein and heterologous
 PT proteins -
 XX
 PS Example 4; Column 65-68; 51pp; English.
 CC This invention describes a novel recombinant viral nucleic acid (1)
 CC from a non-retroviral (+) sense, single stranded animal RNA virus
 CC comprising a nucleic acid sequence coding for a viral coat protein
 CC regulated by a native subgenomic promoter and other two heterologous
 CC nucleic acid sequences regulated by two other subgenomic promoters.
 CC (1) is useful for expressing foreign genes e.g. genes inducing male
 CC sterility in plants. (1) is also useful for producing proteins such as
 CC Interleukin, EPO (erythropoietin), CSF (colony stimulating factor),
 CC Factor VIII, hGH (human growth hormone), melanin, insulin, vaccines
 CC etc., and enzymes that are useful for stereo specific catalysis of
 CC organic compounds. (1) is stable and transcribed systemically. The dual
 CC subgenomic promoter system reduces the frequency of recombination thus
 CC reducing regeneration of the wild type virus. This sequence represents
 CC a rice alpha-amylase protein which is described in the method of the
 CC invention.
 CC
 XX
 SQ Sequence 434 AA;
 Query Match 68.0%; Score 41.5; DB 21; Length 434;
 Best Local Similarity 80.0%; Pred. No. 49;
 Matches 8; Conservative 0; Mismatches 1; Indels 1; Gaps 1;
 OY 1 CRDDRPYADG 10
 11111111
 Db 155 CRDD-PYGDG 163
 RESULT 14
 AAR07669
 ID AAR07669 standard; protein; 215 AA.
 AC AAR07669;
 XX
 XX 25-MAR-2003 (updated)
 DT 15-FEB-1991 (first entry)
 DE Partial alpha-amylase precursor coded by clone Amyz6 from potato.
 DE
 XX potato; alpha-amylase; starch degradation.
 KW
 XX Solanum tuberosum.
 OS
 XX WO9012876-A.
 PN
 XX 01-NOV-1990.
 PD
 XX 24-APR-1990; 90WO-DK00108.
 PF
 XX 24-APR-1989; 89DK-0001980.
 PR
 XX (DASP-) DANKE SPRITFARIKKER DANISCO AS.
 PA (DANI-) DANISCO A/S.
 PA
 PI Gausing K, Kreiberg JD;
 PI
 XX WPI: 1990-348479/46.
 DR N-PSDB; AA006479.
 DR
 XX DNA fragments encoding alpha-amylase in dicotyledonous plants -
 PT are used for detecting gene organisation etc.
 XX
 PS Claim 26; Fig 4; 1pp; English.
 XX

CC Amyz6 was isolated from a cDNA library prepared from RNA
 CC extracted from sprouts of a potato. The library was screened with a
 CC barley alpha amylase probe. The nucleic acid sequence encodes a
 CC partial alpha-amylase precursor commencing at amino acid residue
 CC 133 of the full-length protein.
 CC See also AA006476-8 and AA006553.
 CC (Updated on 25-MAR-2003 to correct PA field.)
 CC
 XX
 SQ Sequence 215 AA;
 Query Match 67.2%; Score 41; DB 11; Length 215;
 Best Local Similarity 60.0%; Pred. No. 29;
 Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 OY 1 CRDDRPYADG 10
 11111111
 Db 5 CRDDPYSDG 14
 RESULT 15
 ABB59190
 ID ABB59190 standard; Protein; 594 AA.
 XX
 XX ABB59190;
 AC
 XX 26-MAR-2002 (first entry)
 DT
 XX Drosophila melanogaster polypeptide SEQ ID NO 4362.
 DE
 XX Drosophila; developmental biology; cell signalling; insecticide;
 KW pharmaceutical.
 KM
 XX Drosophila melanogaster.
 OS
 XX WO200171042-A2.
 PN
 XX 27-SEP-2001.
 PD
 XX 23-MAR-2001; 2001WO-US09231.
 PF
 XX 23-MAR-2000; 2000US-191637P.
 PR 11-JUL-2000; 2000US-0614150.
 PR
 XX (PEKE) PE CORP NY.
 PA
 XX Venter JC, Adams M, Li PWD, Myers EW;
 PI
 XX WPI: 2001-656860/75.
 DR N-PSDB; ABL03293.
 DR
 XX New isolated nucleic acid detection reagent for detecting 1000 or more
 PT genes from Drosophila and for elucidating cell signalling and cell-cell
 PT interactions -
 PT
 XX Disclosure; SEQ ID NO 4362; 21pp + Sequence Listing; English.
 PS
 XX The invention relates to an isolated nucleic acid detection reagent
 CC capable of detecting 1000 or more genes from Drosophila. The invention is
 CC useful in developmental biology and in elucidating cell signalling and
 CC cell-cell interactions in higher eukaryotes for the development of
 CC insecticides, therapeutics and pharmaceutical drugs. The invention
 CC discloses genomic DNA sequences (AB16176-AB130511), expressed DNA
 CC sequences (AB101840-AB16175) and the encoded proteins
 CC (ABBS7737-ABBS7072).
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.
 CC
 XX
 SQ Sequence 594 AA;
 Query Match 63.9%; Score 39; DB 22; Length 594;
 Best Local Similarity 66.7%; Pred. No. 1.9e+02;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 CRDDRYPAD 9
 1:|||||
 DB 463 CRDRAYED 471

RESULT 16

AAW50253
 ID AAW50253 standard; Protein: 435 AA.

AC AAW50253;

DT 21-JAN-2002 (first entry)

DE Rice alpha-amylase (alpha-Amy3-C gene product).

KM Alpha-amylase; promoter; rice; transgenic plant; angiosperm;

XX monoco; cereal; brewing.

OS Oryza sativa.

XX Key Location/Qualifiers

FT Peptide 1..25

FT Protein /label= Signal_peptide

FT Protein /label= Mature_protein

XX US6288302-B1.

PD 11-SEP-2001.

PF 04-MAY-1998; 98US-0072917.

XX 04-NOV-1992; 92US-0973324.

PR 01-AUG-1995; 95US-0509662.

PR 08-OCT-1997; 97US-0947201.

PR 22-NOV-1994; 94US-0343380.

XX (NASC-) NAT SCI COUNCIL ROC.

PI Yu S, Liu L, Chan M.

DR WPI: 2001-647191/74.

DR N-PSDB; AAI70540.

PT Producing a transgenic monocot plant comprising a transgene under

PT control of an alpha amylase promoter and signal peptide sequences,

PT provides transgenic plants particularly cereals for the brewing

XX Industry -

PS Disclosure: Column 79-82; 44pp; English.

XX The present sequence is that of alpha-amylase encoded by DNA clone

CC alpha-Amy3-C (see AAI70540). Expression of alpha-Amy3-C increases

CC 5-fold following sugar starvation. The invention relates to

CC the use of an alpha-amylase gene promoter and signal sequence in

CC the production of recombinant proteins in transgenic plants and

CC transgenic plant seeds. In a claimed method, a transgenic monocot

CC is obtained by: transforming an immature embryo of the plant via

CC Agrobacterium-mediated transformation with DNA comprising a plant

CC alpha-amylase promoter (e.g. the rice alpha-Amy3-C promoter) that

CC is induced under sugar-depleted or sugar-free conditions, a signal

CC peptide sequence, and an exogenous sequence encoding a gene product;

CC regenerating the transformed plant; and growing the transgenic

CC plant, which expresses the gene product under sugar-depleted or

CC sugar-free conditions. The gene product may also be obtained by

CC culturing an angiosperm host cell. The transgenic monocot plants

CC are especially useful in brewing and to produce glucose from starch.

XX Sequence 435 AA;

Query Match 62.3%; Score 38; DB 22; Length 435;
 Best Local Similarity 60.0%; Pred. No. 2e+02;

Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 OY 1 CRDDRYPADG 10
 1:|||||
 DB 148 CSDDTYSDG 157

RESULT 17

AAW97247
 ID AAW97247 standard; Protein: 435 AA.

AC AAW97247;

DT 31-JUL-2001 (first entry)

DE Alpha-amylase related protein #3.

KM Alpha-amylase; promoter; expression vector; rice.

XX unidentified.

OS unidentified.

XX TWA02638-A.

PN 21-AUG-2000.

PD 13-FEB-1992; 97TW-0101436.

PF 13-FEB-1992; 97TW-0101436.

PR 13-FEB-1992; 97TW-0101436.

XX (NASC-) NAT SCI COUNCIL.

PI Yu S, Liu L;

DR WPI: 2001-167365/17.

DR N-PSDB; AAW20285.

PT Gene expression system comprising the promoter region of alpha-amylase

PT gene, produces large quantities of alpha-amylase in culture medium of

PT sugar starved rice.

XX Disclosure; Fig 12; 104pp; Chinese.

XX This invention relates to a gene expression system comprising the

CC alpha-amylase gene promoter, DNA encoding the signal peptide of

CC alpha-amylase and the promoter along with the glucuronidase reporter gene

CC and hygromycin resistance gene are used in the construction of a GUS gene

CC expression vector, which when transformed into rice suspension-cultured

CC cells, can be used to investigate the expression of the vector under the

CC control of the promoter. The gene expression system can be used to

CC conduct gene regulation and protein expression and secretion using the

CC characteristics of the alpha-amylase gene promoter and the DNA sequence

CC encoding the signal peptide. The present sequence represents an

CC alpha-amylase related protein used in the course of the present

CC invention.

XX Sequence 435 AA;

Query Match 62.3%; Score 38; DB 22; Length 435;
 Best Local Similarity 60.0%; Pred. No. 2e+02;
 Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 1 CRDDRYPADG 10
 1:|||||
 DB 148 CSDDTYSDG 157

RESULT 18

AAW81063
 ID AAW81063 standard; Protein: 1036 AA.

AC AAW81063;

DT 02-JUN-1999 (first entry)

XX Amino acid sequence of the Drosophila smoothened polypeptide.
 DE Drosophila: smoothened gene; smoothened peptide; SP;
 XX cell proliferation; cell differentiation; spermatogenesis;
 KW osteogenesis; chondrogenesis; apoptosis; degenerative disorder;
 KW neoplastic disorder; hyperplastic disorder; varicella-zoster;
 KW tumour; liver repair.
 XX Drosophila sp.
 OS WO9901468-A2.
 XX PN 14-JAN-1999.
 XX PD 01-JUL-1998; 98WO-US13793.
 XX PF 21-JUL-1997; 97US-0897798.
 XX PR 01-JUL-1997; 97US-0051407.
 XX PA (INGH/) INGHAM P W.
 XX PA (ONTO-) ONTOGENY INC.
 XX PA (VHEU/) VAN DEN HEUVEL M.
 XX WI: 1999-105996/09.
 DR N-PSDB; AAV99968.
 XX PT New isolated smoothened genes - used to develop products for
 PT treating e.g. cancers, neurodegenerative disorders, nervous system
 PT injury, immunological diseases or infections
 XX Claim 1; Pages 94-97; 107pp; English.
 PS This is the amino acid sequence of the novel Drosophila smoothened
 XX polypeptide (SP) used in the method of the invention. The SPs can
 CC modulate at least one of proliferation, differentiation or survival
 CC of a cell which expresses the SP. The products can be used to
 CC modulate spermatogenesis, osteogenesis, chondrogenesis or neuronal
 CC cell differentiation or to enhance survival of neuronal cells, e.g.
 CC to prevent apoptosis. They can be used for treating e.g.
 CC degenerative disorders marked by loss of particular cell-types,
 CC apoptosis, neoplastic and/or hyperplastic disorders. In particular
 CC they can be used to treat neurological conditions derived from
 CC acute, subacute, or chronic injury to the nervous system, aging of
 CC the nervous system, chronic neurodegenerative diseases of the
 CC nervous system, chronic immunological diseases of the nervous
 CC system or affecting the nervous system. They can also treat be used
 CC to CNS trauma infarction, infection (such as viral infection with
 CC varicella-zoster), metabolic disease, nutritional deficiency,
 CC toxic agents (such as cisplatin treatment), chronic pain syndromes
 CC or in nerve prostheses for the repair of central and peripheral
 CC nerve damage, malignant gliomas, medulloblastomas, neuroectodermal
 CC tumours, ependymomas and for liver repair and regeneration of lung
 CC tissue in the treatment of emphysema, or for enhancing bond
 CC formation, tissue formation or fertility. The products can also be
 CC used for detection, diagnosis and drug screening.
 CC SQ Sequence 1036 AA;
 SQ
 Query Match 62.3%; Score 38; DB 20; Length 1036;
 Best Local Similarity 66.7%; Pred. NO. 4.9e+02;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 OY 2 RDDRPYADG 10
 Db 68 RDDKPFWDG 76
 |||:|:|
 RESULT 19
 ABB59323
 ID ABB59323 standard; Protein: 1036 AA.
 XX ABB59323;
 AC

XX 26-MAR-2002 (first entry)
 DT Drosophila melanogaster polypeptide SEQ ID NO 4761.
 XX DE Drosophila: developmental biology; cell signalling; insecticide;
 XX KW pharmaceutical.
 XX KW Drosophila melanogaster.
 OS WO200171042-A2.
 XX PN 27-SEP-2001.
 XX PD 23-MAR-2001; 2001WO-US09231.
 XX PF 23-MAR-2000; 2000US-191637P.
 XX PR 11-JUL-2000; 2000US-0614150.
 XX PA (PEKE) PE CORP NY.
 XX PA Venter JC, Adams M, Li PWD, Myers EW;
 XX WI: 2001-655660/75.
 DR N-PSDB; ABL03426.
 XX PT New isolated nucleic acid detection reagent for detecting 1000 or more
 PT genes from Drosophila and for elucidating cell signalling and cell-cell
 PT interactions -
 XX Disclosure; SEQ ID NO 4761; 21pp + Sequence Listing; English.
 PS The invention relates to an isolated nucleic acid detection reagent
 XX capable of detecting 1000 or more genes from Drosophila. The invention is
 CC useful in developmental biology and in elucidating cell signalling and
 CC cell-cell interactions in higher eukaryotes for the development of
 CC insecticides, therapeutics and pharmaceutical drugs. The invention
 CC discloses genomic DNA sequences (AB101840-AB116175), expressed DNA
 CC sequences (AB101840-AB116175) and the encoded proteins
 CC (ABB57737-ABB72072).
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.
 CC SQ Sequence 1036 AA;
 SQ
 Query Match 62.3%; Score 38; DB 22; Length 1036;
 Best Local Similarity 66.7%; Pred. NO. 4.9e+02;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 OY 2 RDDRPYADG 10
 Db 68 RDDKPFWDG 76
 |||:|:|
 RESULT 20
 AAB28647
 ID AAB28647 standard; Protein: 1036 AA.
 XX AAB28647;
 AC 13-FEB-2001 (first entry)
 DT Drosophila smoothened.
 XX DE Drosophila: smoothened; cell proliferation; cell differentiation;
 XX KW cell signalling.
 XX KW Drosophila melanogaster.
 OS US6136958-A.
 XX PN 24-OCT-2000.
 XX PD

```

XX 30-SEP-1997; 97US-0953823.
PF
XX 30-SEP-1996; 96US-0027070.
PR
XX (GETH ) GENENTECH INC.
PA
XX Stone DM, De Sauvage FJ, Rosenthal A;
PI
XX WPI: 2001-006229/01.
DR
XX Antibodies to vertebrate smoothened proteins which relate to Hedgehog
PT and patched signaling molecules involved in cell proliferation and
PS differentiation
XX
XX Example 3; Fig 5; 38pp; English.
PS
XX The present sequence was used for comparison studies with vertebrate
CC smoothened polypeptides. Smoothened interacts with Hedgehog and Patched
CC signalling molecules involved in cell proliferation and differentiation.
CC Rat smoothened cDNA was isolated from an embryonic day 9-10 rat cDNA
CC library. The rat smoothened cDNA was then used as a probe to isolate the
CC human homologue from a human embryonic lung cDNA library. Antibodies
CC which specifically bind to the vertebrate smoothened polypeptides were
CC identified.
XX
SQ Sequence 1036 AA;
Query Match 62.3%; Score 38; DB 22; Length 1036;
Best Local Similarity 66.7%; Pred. No. 4,9e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
OY 2 CRDPRPYADG 10
DB 68 RDKRPFWDG 76
RESULT 21
AA07159
ID AA07159 standard; protein; 17 AA.
XX
AC AA07159;
XX
XX 24-JAN-1991 (first entry)
DT
XX
XX Synthetic Nerve growth factor (NGF) peptide fragment.
DE
XX Nervous disorders; Alzheimer's disease; Parkinson's disease; stroke.
KM
XX Synthetic.
OS
XX WO9010644-A.
PN
XX 20-SEP-1990.
PD
XX 08-MAR-1990; 90MO-0000149.
PF
XX 14-MAR-1989; 89SE-0000899.
PR
XX (LOPE-) LOPE MED AB.
PA
XX Olsson L, Persson H, Ebendal T;
PI
XX WPI: 1990-304983/40.
DR
XX
XX New peptide fragments of nerve growth factor or its precursor -
PT used to raise specific antibodies for immunoassay, esp. for brain
PT tissue
XX
XX Disclosure: Page 11; 24pp; English.
XX
XX Peptides are Abs raised to them are useful in detecting the presence
CC of NGF and precursors, allowing early diagnosis and treatment of

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CC nervous disorders eg. Alzheimer's and Parkinson's disease, spinal
CC cord injury, stroke etc.
CC Peptide corresponds to AAs 54 to 69 of chicken NGF.
XX
XX
SQ Sequence 17 AA;
Query Match 60.7%; Score 37; DB 11; Length 17;
Best Local Similarity 60.0%; Pred. No. 10;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
OY 1 CRDPRPYADG 10
DB 5 CRDPRVSSG 14
RESULT 22
AA029474
ID AA029474 standard; Protein; 42 AA.
XX
AC AA029474;
XX
XX 25-MAR-2003 (updated)
DT
XX 22-APR-1993 (first entry)
DT
XX NGF, chicken.
DE
XX
XX Neurotrophin; NT: nerve growth factor; NGF;
KM brain-derived neurotrophic factor; BDNF; probe; primer.
XX
XX Gallus sp.
OS
XX WO9220365-A1.
PN
XX 26-NOV-1992.
PD
XX 20-MAY-1992; 92MO-US04266.
DE
XX
XX 21-MAY-1991; 91US-0703450.
PR
XX 12-JUL-1991; 91US-0729253.
PR
XX 23-JUL-1991; 91US-0734422.
PR
XX 28-AUG-1991; 91US-0751356.
PR
XX 20-SEP-1991; 91US-0762674.
PR
XX 14-NOV-1991; 91US-0791924.
XX
XX (REG-) REGENERON PHARM INC.
PA
XX Hallbook F, Ibanez Moliner CF, Persson HB, Yancopoulos GD;
PI
XX WPI: 1992-415468/50.
DR
XX N-PSDB: AAQ32200.
DE
XX
XX Use of neurotrophin-4 for promoting growth and survival of nerve
PT cells - useful in treating neurological, fertility and
PT immunological disorders and in diagnosis
XX
XX Disclosure: Page 96-97; 180pp; English.
PS
XX
XX Oligonucleotide probes and primers were synthesised based on the NT
CC family including NGF, BDNF and NT-3. These were used to isolate DNA
CC encoding NT-4 from nucleic acid from Xenopus ovaries. This DNA was
CC then used to isolate other mammalian DNA encoding NT-4, including
CC human NT-4 DNA.
CC (updated on 25-MAR-2003 to correct PN field.)
XX
XX
SQ Sequence 42 AA;
Query Match 60.7%; Score 37; DB 13; Length 42;
Best Local Similarity 60.0%; Pred. No. 26;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
OY 1 CRDPRPYADG 10
DB 2 CRDPRVSSG 11

```

RESULT 23
AAR41885
ID AAR41885 standard; peptide; 56 AA.
XX
XX
AC AAR41885;
XX
XX
DT 25-MAR-2003 (updated)
DT 22-APR-1994 (first entry)
XX
DE Granulin E.
XX
XX Granulin; keratinocytes; wound healing; inhibition; peptide;
KM granulocytes; leucocytes.
OS
XX Homo sapiens.
XX
XX W09315195-A1.
XX
XX PD 05-AUG-1993.
XX
XX PF 28-FEB-1992; 92MO-CA00089.
XX
XX PR 03-FEB-1992; 92US-0829233.
XX
XX PA (SOLO/) SOLOMON S.
XX
XX PI Solomon S;
XX
XX DR WPI; 1993-320328/40.
XX
XX PT New cysteine rich granulin peptide(s) from leucocyte(s) - are
PT keratinocyte inhibitors useful topically for wound healing
PS Claim 8; Page 33; 53pp; English.
XX
XX CC The granulin inhibits keratinocytes and is useful in formulations
CC for promoting the healing of wounds. This peptide was designated
CC granulin E.
CC (Updated on 25-MAR-2003 to correct PN field.)
XX
XX SQ Sequence 56 AA;
QY
Db 1 CRDR-----PYADG 10
17 CRDREGWACCPYAG 32

Query Match 60.7%; Score 37; DB 14; Length 56;
Best Local Similarity 50.0%; Pred. No. 36;
Matches 8; Conservative 1; Mismatches 1; Indels 6; Gaps 1;

RESULT 24
ABP71159
ID ABP71159 standard; protein; 118 AA.
XX
XX
AC ABP71159;
XX
XX
DT 14-APR-2003 (first entry)
XX
XX
DE Chicken mature NGF domain fragment.
XX
XX Proneurotrophin; nerve growth factor; NGF; neurotrophin; NT-3; NT4; NT5;
KM brain derived neurotrophic factor; BDNF; vasotrophic; cerebroprotective;
KM antimicrobial; cardiant; virucide; antibacterial; neuroprotective; MMP;
KM neurotrophic; antiinflammatory; anticonvulsant; plasminogen; plasmin; p75;
KM apoptosis; chicken.
XX
XX OS Gallus sp.
XX
XX PN W0200296356-A2.
XX

PD 05-DEC-2002.
XX
XX
XX PF 24-MAY-2002; 2002MO-US16540.
XX
XX PR 25-MAY-2001; 2001US-293823P.
XX
XX PR 13-JUL-2001; 2001US-305510P.
XX
XX PA (CORR) CORNELL RES FOUND INC.
XX
XX PI Hempstead BL, Lee R, Teng KK, Kermani P;
XX
XX DR WPI; 2003-140406/13.
XX
XX PT Novel protein for inducing apoptosis, has proneurotrophin pro-domain
PT with conserved regions, mature neurotrophin domain, and connector that
PT joins conserved region to mature domain and resistant to protease
PT cleavage -
XX
XX PS Disclosure; Page 23; 124pp; English.
XX
XX CC The invention relates to an isolated protein comprising a pro-domain (PD)
CC of a proneurotrophin, where PD comprises a pro-domain conserved region,
CC or a modified proneurotrophin protein (Ib) with a PD, a mature
CC neurotrophin domain (MD), and a connector that joins the pro-domain
CC conserved region to MD and resistant to protease cleavage. The PD is
CC selected from specific peptide fragments of human nerve growth factor
CC (NGF), human brain derived neurotrophic factor (BDNF), human neurotrophin
CC 3 (NT-3) or human neurotrophin 4/5 (NT4/5). (Ib) is useful for inducing
CC apoptosis in a cell comprising p75 receptors (normal number or higher
CC than the normal number of p75 receptors) on its surface, by causing the
CC p75 receptor to bind (Ib), in vitro, in mammals or humans. The method is
CC useful for treating vascular smooth muscle plaque e.g. atherosclerotic
CC plaque. The cell is a malignant cell e.g. cells of tumour, melanoma,
CC prostate, pancreas, nervous system (e.g. medulloblastoma or astrocytoma),
CC leukemia, lymphoma, testicular, lung, brain, malignant oligodendrocyte,
CC heart, vascular smooth muscle or neural cell. A molecule that inhibits
CC the binding of proneurotrophin to a p75 receptor is useful in a method
CC for inhibiting apoptosis of a cell in a mammal e.g. human suffering from
CC a condition associated with undesired apoptosis due to binding of a
CC proneurotrophin to p75 receptor. The condition is the result of an injury
CC or an environmental insult, e.g. nervous system injury, caused by a
CC chemical or radiation or occurring during cancer treatment, hypoxic
CC ischaemia caused by stroke or heart attack, viral or microbial infection,
CC meningitis, encephalitis or abscesses, neurodegenerative disorders e.g.
CC Alzheimer's disease, familial dysautonomia, ataxia telangiectasia,
CC Charcot-Marie-Tooth disease, Adreno leuko dystrophy, spinal muscular
CC atrophy or Friedreich's ataxia, or multiple sclerosis, convulsions,
CC epilepsy and spinal cord injury. Sequences ABP71151-60 represent pro and
CC mature domains of NGF from various species.
XX
XX SQ Sequence 118 AA;
QY
Db 1 CRDPRPYADG 10
57 CRDPRPVSSG 66

Query Match 60.7%; Score 37; DB 24; Length 118;
Best Local Similarity 60.0%; Pred. No. 77;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

RESULT 25
ABR41533
ID ABR41533 standard; protein; 346 AA.
XX
XX
AC ABR41533;
XX
XX
DT 02-JUN-2003 (first entry)
XX
XX
DE Human DTRHP protein modification/maintenance protein.
XX
XX
XX Human; dtrhp; diagnostic and therapeutic polynucleotide; diagnosis;
KM cancer; cell proliferative disorder; autoimmune disorder;
KM

inflammatory disorder; infection; hormonal disorder; metabolic disorder;
 inflammatory disorder; gastrointestinal disorder; transpore disorder;
 connective tissue disorder; drug screening; proteome analysis;
 gene therapy; antisense therapy; genotyping; transgenic animal; knock in;
 disease model; toxicological testing; transcript imaging;
 protein modification; protein maintenance.
 Homo sapiens.
 WO200297031-A2.
 05-DEC-2002.
 27-MAR-2002; 2002WO-US10056.
 28-MAR-2001; 2001US-278619P.
 29-MAR-2001; 2001US-280067P.
 29-MAR-2001; 2001US-280068P.
 15-MAR-2001; 2001US-281280P.
 17-MAR-2001; 2001US-281829P.
 17-MAR-2001; 2001US-281849P.
 19-JUN-2001; 2001US-289428P.
 20-JUN-2001; 2001US-289776P.
 20-JUN-2001; 2001US-300001P.
 (INCYTE GENOMICS INC.
 Daffo A, Jones AL, Tran AB, Dahl CR, Gietzen D, Chinn J;
 Dufour GE, Hillman JL, Yu JY, Tuason O, Yap PE, Amshay SR;
 Daughtery SC, Dam TC, Liu RF, Nguyen DA, Kleeferld Y, Gerstin EH;
 Perralta CH, David MH, Lewis SA, Chen AJ, Panzer SR, Harris B;
 Flores V, Marwaha R, Lo A, Lan RX, Urashka ME;
 WPI: 2003-129518/12.
 N-PSDB: ACC46471.
 Novel human diagnostic and therapeutic polypeptide useful for
 identifying test compound which specifically binds to a polypeptide
 encoded by human diagnostic and therapeutic polynucleotide, and to
 induce antibodies
 Claim 27; SEQ ID NO 1068; 591pp; English.
 The invention relates to novel human diagnostic and therapeutic
 polynucleotides designated dithp (ACC46080-ACC46749) and to their
 encoded proteins (DITHP; ABR41136-ABR41812). The invention also relates
 to polynucleotide sequences at least 90% identical to the dithp cDNA
 sequences of the invention; recombinant vectors, host cells and
 transgenic organisms comprising a dithp nucleic acid sequence; the
 recombinant production of DITHP proteins; antibodies specific for DITHP
 proteins; microarrays comprising dithp nucleic acid sequences; methods
 of detecting dithp nucleotide and protein sequences; methods of screening
 for compounds which specifically bind a DITHP protein; and methods of
 assessing the toxicity of test compounds using a dithp hybridisation
 probe. Dithp nucleic acid sequences and DITHP proteins may be used in the
 diagnosis of a wide variety of conditions including cancer and other cell
 proliferative disorders; autoimmune or inflammatory disorders; bacterial,
 viral, fungal or parasitic infections; hormonal disorders; metabolic
 disorders; neurological disorders; gastrointestinal disorders; transport
 disorders; and connective tissue disorders. They may also be used to
 screen for modulators of protein activity or gene expression. DITHP
 proteins can additionally be used in analysis of the proteome of a tissue
 or cell type and to induce antibodies. The dithp nucleic acids are
 additionally useful in somatic or germline gene therapy of the disorders
 mentioned above, as a source of antisense sequences, as a source of
 probes and primers, in genotyping and identification of individuals, in
 the generation of transgenic animal models of human disease or knock in
 humanised animals, in toxicological testing, and in transcript imaging.
 The present sequence represents a DITHP protein which is involved in
 protein modification and/or maintenance.
 Note: The sequence data for this patent did not form part of the printed
 specification, but was obtained in electronic format directly from WIPO
 at http://wipo.int/pub/published_pcc/sequences.

XX Sequence 346 AA.
 SQ Query Match 60.7%; Score 37; DB 24; Length 346;
 Best Local Similarity 62.5%; Pred. No. 2,4e+02;
 Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
 OY 1 CRDPRYA 8
 |||::|:
 Db 244 CRDPRYA 251
 RESULT 26
 ABR69343
 ID ABR69343 standard; Protein; 413 AA.
 AC ABR69343;
 DT 11-DEC-2002 (first entry)
 XX Human ovarian cancer marker OV27.
 DE Human ovarian cancer marker OV27.
 XX Human; ovarian cancer; marker; cancer; familial history; brain disorder;
 KW central nervous system disorder; bacterial meningitis; viral meningitis;
 KW Alzheimer's disease; Parkinson's disease; cerebral oedema; hydrocephalus;
 KW brain herniation; inflammation; encephalitis; testicular disorder;
 KW nonbenign granulomatous orchitis; connective tissue disorder;
 KW heart disorder; ischemic heart disease; atherosclerosis; neoplasm;
 KW histological type; carcinogenic; ovarian cancer marker.
 OS Homo sapiens.
 XX
 PN WO200271928-A2.
 XX 19-SEP-2002.
 PD 14-MAR-2002; 2002WO-US07826.
 PF 14-MAR-2001; 2001US-276025P.
 XX 14-MAR-2001; 2001US-276026P.
 PR 10-AUG-2001; 2001US-311732P.
 PR 19-SEP-2001; 2001US-323580P.
 PR 26-SEP-2001; 2001US-324967P.
 PR 26-SEP-2001; 2001US-325102P.
 PR 26-SEP-2001; 2001US-325149P.
 XX (MILL-) MILLENNIUM PHARM INC.
 XX Monahan JE, Gannavarapu M, Hoersch S, Kamatkar S, Kovatis SG;
 PI Meyers RE, Morrissey MP, Olandt PJ, Sen A, Vleby PO, Mills GB;
 PI Bast RC, Lu K, Schmandt RE, Zhao X, Glatz K;
 XX WPI: 2002-723277/78.
 DR N-PSDB: ABR69439.
 XX Assessing whether a patient is afflicted with ovarian cancer, useful in
 PT assessing the stage or progression of the disease, comprises comparing
 PT the expression level of a cancer marker in a sample from a patient and
 PT from a non cancer patient -
 XX
 XX Disclosure: Page 258-259; 481pp; English.
 PS The present invention relates to a new method for assessing whether a
 CC patient is afflicted with ovarian cancer. The method involves comparing
 CC the expression level of a marker in a patient sample and the normal level
 CC of expression of the marker in a control non-ovarian cancer sample, where
 CC the marker is selected from 363 cancer markers described in the
 CC specification. The method of the invention is useful in diagnosing or
 CC characterising cancer, in detecting the presence of cancer as early as
 CC possible, and the recurrence of ovarian cancer. The method may also be of
 CC particular use with patients having an enhanced risk of developing
 CC ovarian cancer (e.g. patients having a familial history of ovarian
 CC cancer). The cancer markers may be used in the management and treatment

DT 22-APR-1994 (first entry)
XX Granulin sequence.
DE
XX Granulin; keratinocytes; wound healing; inhibition; peptide;
KM granulocytes; leucocytes.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Misc-difference 452
FT /note= "Valine encoded by ATG."
FT MISC-difference 539
FT /note= "Glycine encoded by CAG."
XX
XX MO9315195-A1.
XX
XX 05-AUG-1993.
XX
XX 28-FEB-1992; 92MO-CA00089.
XX
XX 03-FEB-1992; 92US-0829233.
XX
XX (SOLO/) SOLOMON S.
XX
XX Solomon S;
XX
XX WPI: 1993-320328/40.
DR N-PSDB; AAQ49052.
XX
XX New cystine rich granulin peptide(s) from leucocyte(s) - are
PT keratinocyte inhibitors useful topically for wound healing
XX
XX PS Disclosure; Figure 4c; 53pp; English.
XX
XX The granulin inhibits keratinocytes and is useful in formulations
CC for promoting the healing of wounds.
CC (Updated on 25-MAR-2003 to correct PN field.)
XX
XX Sequence 593 AA;
SQ
Query Match 60.7%; Score 37; DB 14; Length 593;
Best Local Similarity 50.0%; Pred. No. 4.1e+02;
Matches 8; Conservative 1; Mismatches 1; Indels 6; Gaps 1;
QY 1 CPDDR-----PYADG 10
DB 534 CRDNRGMACCPYAG 549
RESULT 29
AAW85475
ID AAW85475 standard; Protein: 593 AA.
XX
XX AAW85475;
AC
XX
XX 15-MAR-1999 (first entry)
DT
XX
XX Human GP88 autocrine growth factor.
DE
XX
XX GP88; granulin; epithelin; human; growth factor; autocrine; tumour;
KM cancer; viral infection; antagonist; therapy; diagnosis.
XX
XX Homo sapiens.
OS
XX
XX Key Location/Qualifiers
FH 340..364
FT /note= "E19Y peptide used to raise antibody"
FT 566..579
FT /note= "A14R peptide used to raise antibody"
XX
XX MO9852607-A1.

PD 26-NOV-1998.
XX
XX 22-MAY-1998; 98MO-US10555.
XX
XX 16-DEC-1997; 97US-0991862.
PR 23-MAY-1997; 97US-0863079.
XX
XX (SERR/) SERRERO G.
XX
XX Serrero G;
PI
XX WPI: 1999-045276/04.
DR N-PSDB; AAW82825.
XX
XX Composition containing antagonist of growth factor GP88 - useful for
PT treating cancer and viral diseases and also for diagnosing disease
PT from altered GP88 expression
XX
XX Example 5; Fig 9A; 86pp; English.
XX
XX PS This is the amino acid sequence of human GP88, an 88 kDa
CC glycoprotein autocrine growth factor and epithelin/granulin
CC precursor that is expressed in a tightly regulated manner in normal
CC cells, is overexpressed and upregulated in highly tumorigenic cells
CC derived from normal cells, and which acts as a stringently required
CC growth stimulator for the tumorigenic cells. Inhibition of GP88
CC expression or action in the tumorigenic cells results in an
CC inhibition of the tumorigenic properties of the overproducing
CC cells. Antagonists to GP88 are used to treat diseases associated
CC with increased expression of GP88, particularly cancer but also
CC viral infections. Fragments of GP88 are used to raise specific
CC antibodies (used as antagonists, as diagnostic reagents and for
CC delivering toxins or other compounds to GP88-expressing cells) and
CC to screen for antibodies. Methods are provided for diagnosing
CC disease, or determining susceptibility to disease, resulting from
CC altered GP88 activity.
XX
XX Sequence 593 AA;
SQ
Query Match 60.7%; Score 37; DB 20; Length 593;
Best Local Similarity 50.0%; Pred. No. 4.1e+02;
Matches 8; Conservative 1; Mismatches 1; Indels 6; Gaps 1;
QY 1 CPDDR-----PYADG 10
DB 534 CRDNRGMACCPYAG 549
RESULT 30
AAE20521
ID AAE20521 standard; Protein: 593 AA.
XX
XX AAE20521;
AC
XX
XX 01-JUL-2002 (first entry)
DT
XX
XX Human granulin/epithelin precursor (GP88) protein.
DE
XX
XX Human; granulin precursor; GP88; cytostatic; tumorigenicity; tamoxifen;
KM antineoplastic; antioestrogen therapy; skin cancer.
XX
XX Homo sapiens.
OS
XX
XX Key Location/Qualifiers
FH Misc-difference 273
FT /note= "Encoded by AAG"
FT 346..364
FT Region
FT /note= "Region used as antigen to develop anti-human
XX GP88 neutralising antibody"
XX
XX US2002025543-A1.
XX
XX 28-FEB-2002.
PD

XX 15-JUN-2001; 2001US-0880842.

PF

XX 23-MAY-1997; 97US-0863079.

PR

PR 08-DEC-1999; 99US-0456886.

XX

PA (SERR/) SERRERO G.

XX

PI Serrero G;

XX

DR WPI: 2002-267529/31.

XX

DR N-PSDB; AAO32850.

XX

PT Diagnosing tumorigenicity in a human, comprising obtaining a cell sample, detecting GP88 in the cells, and determining the number of GP88 positive cells in the sample -

PT

XX

PS Disclosure; Fig 9B; 50pp; English.

XX

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Search completed: August 29, 2003, 18:43:59
Job time : 33.5714 secs

SQ Sequence 593 AA;

Query Match

Best Local Similarity

Matches

8; Conservative

1; Mismatches

Indels

Gaps

1;

Score 37; DB 23; Length 593;

Pred. No. 4.1e+02;

Indels 6; Gaps 1;

Score 37; DB 23; Length 593;

Pred. No. 4.1e+02;

Indels 6; Gaps 1;

Score 37; DB 23; Length 593;

Pred. No. 4.1e+02;

Indels 6; Gaps 1;

Score 37; DB 23; Length 593;

Pred. No. 4.1e+02;

Indels 6; Gaps 1;

Score 37; DB 23; Length 593;

Pred. No. 4.1e+02;

Indels 6; Gaps 1;

Score 37; DB 23; Length 593;

Pred. No. 4.1e+02;

Indels 6; Gaps 1;

Score 37; DB 23; Length 593;

Pred. No. 4.1e+02;

Indels 6; Gaps 1;

Score 37; DB 23; Length 593;

Pred. No. 4.1e+02;

Indels 6; Gaps 1;

Score 37; DB 23; Length 593;

Pred. No. 4.1e+02;

Indels 6; Gaps 1;

Score 37; DB 23; Length 593;

Pred. No. 4.1e+02;

Indels 6; Gaps 1;

Score 37; DB 23; Length 593;

Pred. No. 4.1e+02;

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OM protein - protein search, using sw model

Run on: August 29, 2003, 18:38:06 ; Search time 10.5714 Seconds
(without alignments)
40.024 Million cell updates/sec

Title: US-09-830-876-2
Perfect score: 61
Sequence: 1 CRDPRYADG 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database :

Issued Patents, AA: *
1: /cgn2_6/prodata/1/1aa/5A.COMB.pep: *
2: /cgn2_6/prodata/1/1aa/5B.COMB.pep: *
3: /cgn2_6/prodata/1/1aa/6A.COMB.pep: *
4: /cgn2_6/prodata/1/1aa/6B.COMB.pep: *
5: /cgn2_6/prodata/1/1aa/PCPMUS.COMB.pep: *
6: /cgn2_6/prodata/1/1aa/backfilltest.pep: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	41.5	68.0	428	1	US-07-973-324A-4
2	41.5	68.0	428	1	US-08-343-380-4
3	41.5	68.0	428	3	US-09-072-435-4
4	41.5	68.0	428	3	US-09-072-917A-4
5	41.5	68.0	434	1	US-07-923-692C-6
6	41.5	68.0	434	1	US-08-184-237-6
7	41.5	68.0	434	2	US-08-482-920-6
8	41.5	68.0	434	3	US-08-482-920-6
9	41.5	68.0	434	3	US-08-482-920-6
10	41.5	68.0	434	4	US-08-482-920-6
11	38	62.3	151	4	US-09-726-651A-6
12	38	62.3	151	4	US-09-252-991A-31890
13	38	62.3	384	4	US-09-252-991A-24086
14	38	62.3	500	4	US-09-072-917A-9
15	38	62.3	1036	2	US-09-252-991A-1739
16	38	62.3	1036	2	US-08-720-484A-5
17	38	62.3	1036	4	US-09-398-239-5
18	38	62.3	1036	4	US-09-560-876A-5
19	38	62.3	1065	4	US-09-560-876A-5
20	37	60.7	217	4	US-09-328-352-7068
21	37	60.7	593	4	US-08-981-862-17
22	36	50.7	568	4	US-09-252-991A-22461
23	35	57.4	129	4	US-09-216-693B-62
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25	35	57.4	165	3	US-08-352-967-6
26	35	57.4	306	2	US-08-481-903-75
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34	34	55.7	277	4	US-09-252-991A-29257	Sequence 29257, A
35	34	55.7	318	4	US-09-252-991A-31545	Sequence 31545, A
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37	34	55.7	475	4	US-09-252-991A-32806	Sequence 32806, A
38	34	55.7	691	4	US-09-252-991A-16809	Sequence 16809, A
39	34	55.7	1349	4	US-08-938-291A-6	Sequence 6, Appl
40	34	55.7	1349	4	US-09-589-619-6	Sequence 6, Appl
41	33	54.1	259	4	US-09-522-714-18	Sequence 18, Appl
42	33	54.1	437	1	US-07-973-324A-6	Sequence 6, Appl
43	33	54.1	437	1	US-08-343-380-6	Sequence 6, Appl
44	33	54.1	437	1	US-09-072-435-6	Sequence 6, Appl
45	33	54.1	437	3	US-09-072-917A-6	Sequence 6, Appl
46	33	54.1	438	1	US-07-973-324A-2	Sequence 2, Appl
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51	33	54.1	546	4	US-08-311-731A-248	Sequence 248, App
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53	32.5	53.3	92	2	US-08-378-548-19	Sequence 19, Appl
54	32	52.5	139	4	US-08-857-076-20	Sequence 20, Appl
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57	32	52.5	202	2	US-08-469-658-56	Sequence 56, Appl
58	32	52.5	211	4	US-09-252-991A-26873	Sequence 26873, A
59	32	52.5	254	4	US-09-252-991A-18950	Sequence 18950, A
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62	32	52.5	327	4	US-09-252-991A-32140	Sequence 32140, A
63	32	52.5	327	4	US-09-252-991A-31442	Sequence 31442, A
64	32	52.5	370	4	US-09-252-991A-20088	Sequence 20088, A
65	32	52.5	389	4	US-09-134-001C-4306	Sequence 4306, A
66	32	52.5	405	4	US-09-252-991A-24057	Sequence 24057, A
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68	32	52.5	411	1	US-07-602-828A-3	Sequence 3, Appl
69	32	52.5	411	1	US-07-983-451-3	Sequence 3, Appl
70	32	52.5	411	1	US-08-261-578-2	Sequence 2, Appl
71	32	52.5	411	1	US-08-261-578-2	Sequence 2, Appl
72	32	52.5	411	1	US-09-070-356-3	Sequence 3, Appl
73	32	52.5	411	3	US-09-252-991A-27367	Sequence 27367, A
74	32	52.5	464	4	US-08-489-733-1	Sequence 1, Appl
75	32	52.5	510	1	US-08-993-581B-1	Sequence 1, Appl
76	32	52.5	510	2	US-09-134-078-22	Sequence 22, Appl
77	32	52.5	593	1	US-07-668-648-4	Sequence 4, Appl
78	32	52.5	593	2	US-08-429-998-4	Sequence 4, Appl
79	32	52.5	593	2	US-08-431-333-4	Sequence 4, Appl
80	32	52.5	593	2	PCT-US91-02331-4	Sequence 4, Appl
81	32	52.5	593	4	US-09-608-790-1	Sequence 1, Appl
82	32	52.5	616	4	US-09-188-930-303	Sequence 303, Appl
83	32	52.5	617	3	US-09-312-283C-303	Sequence 303, App
84	32	52.5	655	4	US-09-252-991A-31645	Sequence 31645, A
85	32	52.5	833	4	US-09-328-352-4401	Sequence 4401, Ap
86	32	52.5	944	4	US-09-252-991A-18729	Sequence 18729, A
87	32	52.5	1125	4	US-09-589-619-5	Sequence 5, Appl
88	32	52.5	1244	4	US-09-252-991A-23150	Sequence 23150, A
89	32	52.5	1269	4	US-08-093-453B-2	Sequence 2, Appl
90	32	52.5	2205	1	US-09-252-991A-32788	Sequence 32788, A
91	32	52.5	376	4	US-09-134-001C-4314	Sequence 4314, Ap
92	31	51.6	806	4	US-09-252-991A-23661	Sequence 23661, A
93	31	50.8	119	4	US-09-598-747-2	Sequence 2, Appl
94	31	50.8	131	4	US-09-252-991A-28746	Sequence 28746, A
95	31	50.8	187	4	US-09-252-991A-28746	Sequence 28746, A
96	31	50.8	219	4	US-09-252-991A-28381	Sequence 28381, A
97	31	50.8	228	4		

ALIGNMENTS

RESULT 1
US-07-973-324A-4
Sequence 4, Application US/07973324A
Patent No. 5460952
GENERAL INFORMATION:
APPLICANT: Yu, Su-May
APPLICANT: Liu, Li-Fei
TITLE OF INVENTION: Gene Expression System Comprising the
TITLE OF INVENTION: Promoter Region of the Alpha-Amylase Genes
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESS: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/973,324A
FILING DATE: 04-NOV-1992
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Borun, Michael F.
REGISTRATION NUMBER: 25447
REFERENCE/DOCKET NUMBER: 31149
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 428 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-973-324A-4
Query Match 68.0%; Score 41.5; DB 1; Length 428;
Best Local Similarity 80.0%; Pred. No. 9.8;
Matches 8; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 1 CRDPRPYADG 10
|||||
DB 149 CRDD-PYGDG 157

RESULT 2
US-08-343-380-4
Sequence 4, Application US/08343380
Patent No. 5712112
GENERAL INFORMATION:
APPLICANT: Yu, Su-May
APPLICANT: Liu, Li-Fei
TITLE OF INVENTION: Gene Expression System Comprising the
TITLE OF INVENTION: Promoter Region of the Alpha-Amylase Genes
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESS: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/343,380
FILING DATE: 22-NOV-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/973,324
FILING DATE: 04-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: Borun, Michael F.
REGISTRATION NUMBER: 25447
REFERENCE/DOCKET NUMBER: 31149
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 428 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-343-380-4
Query Match 68.0%; Score 41.5; DB 1; Length 428;
Best Local Similarity 80.0%; Pred. No. 9.8;
Matches 8; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 1 CRDPRPYADG 10
|||||
DB 149 CRDD-PYGDG 157

RESULT 3
US-09-072-435-4
Sequence 4, Application US/09072435
Patent No. 6215051
GENERAL INFORMATION:
APPLICANT: Yu, Su-May
APPLICANT: Liu, Li-Fei
TITLE OF INVENTION: Gene Expression System Comprising the
TITLE OF INVENTION: Promoter Region of the Alpha-Amylase Genes
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESS: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive/6300 Sears Tower
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/072,435
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/639,792
FILING DATE: 29-APR-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/973,324
FILING DATE: 04-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: Gass, David A.
REGISTRATION NUMBER: 38,153

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: REFERENCE/DOCKET NUMBER: 28123/34274
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (312) 474-6300
: TELEFAX: (312) 474-0448
: INFORMATION FOR SEQ ID NO: 4:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 428 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: US-09-072-435-4
:
: Query Match      68.0%; Score 41.5; DB 3; Length 428;
: Best Local Similarity 80.0%; Pred. No. 9.8;
: Matches      8; Conservative 0; Mismatches 1; Indels 1; Gaps 1;
:
: Oy      1 CRDDPYAGD 10
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:         149 CRDD-PYGDG 157
:
: RESULT 4
: US-09-072-917A-4
: Sequence 4, Application US/09072917A
: Patent No. 6288302
: GENERAL INFORMATION:
: APPLICANT: Yu, Su-May
: APPLICANT: Liu, Li-Fei
: APPLICANT: Chan, Ming-Tsair
: TITLE OF INVENTION: Application of Alpha-Amylase Gene
: TITLE OF INVENTION: Promoter and Signal Sequence in the Production of
: Patent No. 6288302
: TITLE OF INVENTION: Recombinant Proteins in Transgenic Plants and Transgenic
: TITLE OF INVENTION: Plant Seeds
: NUMBER OF SEQUENCES: 15
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Marshall, O'Toole, Garstein, Murray & Borun
: STREET: 233 South Wacker Drive/6300 Sears Tower
: CITY: Chicago
: STATE: Illinois
: COUNTRY: United States of America
: ZIP: 60606
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent in Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/072,917A
: FILING DATE:
: CLASSIFICATION: 800
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/509,962
: FILING DATE: 01-AUG-1995
: ATTORNEY/AGENT INFORMATION:
: NAME: Gass, David A.
: REGISTRATION NUMBER: 38,153
: REFERENCE/DOCKET NUMBER: 28123/34257
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (312) 474-6300
: TELEFAX: (312) 474-0448
: INFORMATION FOR SEQ ID NO: 4:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 428 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: US-09-072-917A-4
:
: Query Match      68.0%; Score 41.5; DB 3; Length 428;
: Best Local Similarity 80.0%; Pred. No. 9.8;
: Matches      8; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

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: Oy      1 CRDDPYAGD 10
:         1111 11 11
:         149 CRDD-PYGDG 157
:
: RESULT 5
: US-07-923-692C-6
: Sequence 6, Application US/07923692C
: Patent No. 5316931
: GENERAL INFORMATION:
: APPLICANT: Donson, Jon
: APPLICANT: Dawson, William O.
: APPLICANT: Grantham, George L.
: APPLICANT: Turpen, Thomas H.
: APPLICANT: Turpen, Ann Myers
: APPLICANT: Garger, Stephen J.
: APPLICANT: Grill, Laurence K.
: TITLE OF INVENTION: RECOMBINANT PLANT VIRAL NUCLEIC ACIDS
: NUMBER OF SEQUENCES: 11
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Limbach & Limbach
: STREET: 2001 Ferry Building
: CITY: San Francisco
: STATE: CAL
: ZIP: 94111
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent in Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/07/923,692C
: FILING DATE: 31-JUL-1992
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 600,244
: FILING DATE: 22-OCT-1990
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 641,617
: FILING DATE: 16-JAN-1991
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 310,881
: FILING DATE: 17-FEB-1989
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 160,766
: FILING DATE: 26-FEB-1988
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 160,771
: FILING DATE: 26-FEB-1988
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 347,637
: FILING DATE: 05-MAY-1989
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 363,138
: FILING DATE: 08-JUN-1989
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 219,279
: FILING DATE: 15-JUL-1988
: ATTORNEY/AGENT INFORMATION:
: NAME: Halluin, Albert P.
: REGISTRATION NUMBER: 28,957
: REFERENCE/DOCKET NUMBER: BIOG-20121
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 415-433-4150
: TELEFAX: 415-433-8716
: INFORMATION FOR SEQ ID NO: 6:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 434 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: US-07-923-692C-6

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Query Match 68.0%; Score 41.5; DB 1; Length 434;
Best Local Similarity 80.0%; Pred. No. 9.9;
Matches 8; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

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11111111
Db 155 CRDD-PYGDG 163

RESULT 6
US-08-184-237-6

Sequence 6, Application US/08184237
Patent No. 5589367
GENERAL INFORMATION:
APPLICANT: Donson, Jon
APPLICANT: Dawson, William O.
APPLICANT: Grantham, George L.
APPLICANT: Turpen, Thomas H.
APPLICANT: Turpen, Ann Myers
APPLICANT: Garger, Stephen J.
APPLICANT: Grill, Laurence K.
TITLE OF INVENTION: RECOMBINANT PLANT VIRAL NUCLEIC ACIDS
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Limbach & Limbach
STREET: 2001 Ferry Building
CITY: San Francisco
STATE: CAL
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/184,237
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 923,692
FILING DATE: 31-JUL-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 600,244
FILING DATE: 22-OCT-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 641,617
FILING DATE: 16-JAN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 310,881
FILING DATE: 17-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 160,766
FILING DATE: 26-FEB-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 160,771
FILING DATE: 26-FEB-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 347,637
FILING DATE: 05-MAY-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 363,138
FILING DATE: 08-JUN-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 219,279
FILING DATE: 15-JUL-1988
ATTORNEY/AGENT INFORMATION:
NAME: Halluin, Albert P.
REGISTRATION NUMBER: 28,957
REFERENCE/DOCKET NUMBER: BIOG-20121 USA
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-433-4150
TELEFAX: 415-433-8716

INFORMATION FOR SEQ. ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 434 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-184-237-6

Query Match 68.0%; Score 41.5; DB 1; Length 434;
Best Local Similarity 80.0%; Pred. No. 9.9;
Matches 8; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

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Db 155 CRDD-PYGDG 163

RESULT 7

US-08-482-920-6
Sequence 6, Application US/08482920
Patent No. 5866785
GENERAL INFORMATION:
APPLICANT: Donson, Jon
APPLICANT: Dawson, William O.
APPLICANT: Grantham, George L.
APPLICANT: Turpen, Thomas H.
APPLICANT: Turpen, Ann Myers
APPLICANT: Garger, Stephen J.
APPLICANT: Grill, Laurence K.
TITLE OF INVENTION: RECOMBINANT PLANT VIRAL NUCLEIC ACIDS
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennile & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,920
FILING DATE: 07-JUNE-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 184,237
FILING DATE: 19-JAN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 600,244
FILING DATE: 22-OCT-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 641,617
FILING DATE: 16-JAN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 310,881
FILING DATE: 17-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 160,766
FILING DATE: 26-FEB-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 160,771
FILING DATE: 26-FEB-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 347,637
FILING DATE: 05-MAY-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 363,138
FILING DATE: 08-JUN-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 219,279
FILING DATE: 15-JUL-1988
ATTORNEY/AGENT INFORMATION:

NAME: Halluin, Albert P.
REGISTRATION NUMBER: 28,957
REFERENCE/DOCKET NUMBER: 8129-112
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-854-3660
TELEFAX: 415-854-3660
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 434 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-482-920-6

Query Match 68.0%; Score 41.5; DB 2; Length 434;
Best Local Similarity 80.0%; Pred. No. 9.9;
Matches 8; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 1 CRDRPYADG 10
1111 11 11
DB 155 CRDD-PYGDG 163

RESULT 8
US-08-484-341-6
Sequence 6, Application US/08484341
GENERAL INFORMATION:
APPLICANT: Dawson, Jon
Dawson, William O.
Grantham, George L.
Turpen, Thomas H.
Turpen, Ann Myers
Garger, Stephen J.
Grill, Laurence K.
TITLE OF INVENTION: RECOMBINANT PLANT VIRAL NUCLEIC ACIDS
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSER: Limbach & Limbach
STREET: 2001 Ferry Building
CITY: San Francisco
STATE: CA
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,341
FILING DATE: 07-Jun-1995
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/184,237
FILING DATE: <Unknown>
APPLICATION NUMBER: US 600,244
FILING DATE: 22-OCT-1990
APPLICATION NUMBER: US 641,617
FILING DATE: 16-JAN-1991
APPLICATION NUMBER: US 310,881
FILING DATE: 17-FEB-1989
APPLICATION NUMBER: US 160,766
FILING DATE: 26-FEB-1988
APPLICATION NUMBER: US 160,771
FILING DATE: 26-FEB-1988
APPLICATION NUMBER: US 347,637
FILING DATE: 05-MAY-1989
APPLICATION NUMBER: US 363,138
FILING DATE: 08-JUN-1989
APPLICATION NUMBER: US 219,279
FILING DATE: 15-JUL-1988
ATTORNEY/AGENT INFORMATION:
NAME: Halluin, Albert P.
REGISTRATION NUMBER: 28,957

REFERENCE/DOCKET NUMBER: BIOG-20121 USA
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-433-4150
TELEFAX: 415-433-8716
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 434 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-08-484-341-6

Query Match 68.0%; Score 41.5; DB 3; Length 434;
Best Local Similarity 80.0%; Pred. No. 9.9;
Matches 8; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 1 CRDRPYADG 10
1111 11 11
DB 155 CRDD-PYGDG 163

RESULT 9
US-08-483-502-6
Sequence 6, Application US/08483502
Patent No. 6284492
GENERAL INFORMATION:
APPLICANT: Dawson, Jon
Dawson, William O.
Grantham, George L.
Turpen, Thomas H.
Turpen, Ann Myers
Garger, Stephen J.
Grill, Laurence K.
TITLE OF INVENTION: RECOMBINANT PLANT VIRAL NUCLEIC ACIDS
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSER: Venable, Baetjer, Howard & Civiletti
STREET: 1201 New York Avenue N.W., Suite 1000
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/483,502
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/739,143
FILING DATE:
APPLICATION NUMBER: US 600,244
FILING DATE: 22-OCT-1990
APPLICATION NUMBER: US 641,617
FILING DATE: 16-JAN-1991
APPLICATION NUMBER: US 310,881
FILING DATE: 17-FEB-1989
APPLICATION NUMBER: US 160,766
FILING DATE: 26-FEB-1988
APPLICATION NUMBER: US 160,771
FILING DATE: 26-FEB-1988
APPLICATION NUMBER: US 347,637
FILING DATE: 05-MAY-1989
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 363,138
FILING DATE: 08-JUN-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 219,279
FILING DATE: 15-JUL-1988
ATTORNEY/AGENT INFORMATION:
NAME: Ihnen, Jeffrey L.
REGISTRATION NUMBER: 28,957
REFERENCE/DOCKET NUMBER: 18604-090574
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-962-4810
TELEFAX: 202-962-8300
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 434 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-483-502-6

Query Match 68.0%; Score 41.5; DB 3; Length 434;
Best Local Similarity 80.0%; Pred. No. 9.9;
Matches 8; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

OY 1 CRDDRPYADG 10
1111111111
Db 155 CRDD-PYGDG 163

RESULT 10
US-09-726-651A-6
Sequence 6, Application US/09726651A
Patent No. 6448046
GENERAL INFORMATION:
APPLICANT: Dawson, Jon
APPLICANT: GRANTHAM, GEORGE L.
APPLICANT: TURPEN, Thomas H.
APPLICANT: TURPEN, Ann M.
APPLICANT: GARGER, Stephen J.
APPLICANT: GRILL, Laurence K.
TITLE OF INVENTION: RECOMBINANT ANIMAL VIRUS NUCLEIC ACIDS
FILE REFERENCE: 008010023CINUS01
CURRENT APPLICATION NUMBER: US/09/726,651A
PRIOR FILING DATE: 2002-05-02
PRIOR APPLICATION NUMBER: 08/483,502
PRIOR FILING DATE: 1995-06-07
PRIOR APPLICATION NUMBER: 08/184,237
PRIOR FILING DATE: 1994-01-19
PRIOR APPLICATION NUMBER: 07/923,652
PRIOR FILING DATE: 1992-07-31
PRIOR APPLICATION NUMBER: 07/600,244
PRIOR FILING DATE: 1990-10-22
PRIOR APPLICATION NUMBER: 07/641,617
PRIOR FILING DATE: 1991-01-16
PRIOR APPLICATION NUMBER: 07/737,899
PRIOR FILING DATE: 1991-07-26
NUMBER OF SEQ ID NOS: 19
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 6
LENGTH: 434
TYPE: PRT
ORGANISM: Oryza sativa
FEATURE:
OTHER INFORMATION: CLONE: alpha-amylase
OTHER INFORMATION: protein
US-09-726-651A-6

Query Match 68.0%; Score 41.5; DB 4; Length 434;
Best Local Similarity 80.0%; Pred. No. 9.9;
Matches 8; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

OY 1 CRDDRPYADG 10

Db 155 CRDD-PYGDG 163
1111111111

RESULT 11
US-09-252-991A-31890
Sequence 31890, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
PRIOR FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 31890
LENGTH: 151
TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-31890

Query Match 62.3%; Score 38; DB 4; Length 151;
Best Local Similarity 70.0%; Pred. No. 14;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 CRDDRPYADG 10
1111111111
Db 112 CRRSREPTAG 121

RESULT 12
US-09-252-991A-24086
Sequence 24086, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
PRIOR FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 24086
LENGTH: 384
TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-24086

Query Match 62.3%; Score 38; DB 4; Length 384;
Best Local Similarity 70.0%; Pred. No. 36;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 CRDDRPYADG 10
1111111111
Db 37 CRADRPVAVG 46

RESULT 13
US-09-072-917A-9
Sequence 9, Application US/09072917A
Patent No. 6288302
GENERAL INFORMATION:
APPLICANT: Yu, Su-May
APPLICANT: Liu, Li-Fei


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APPLICANT: Chan, Ming-Tsair
TITLE OF INVENTION: Application of Alpha-Amylase Gene
TITLE OF INVENTION: Promoter and signal Sequence in the Production of
Patent No. 6288302
TITLE OF INVENTION: Recombinant Proteins in Transgenic Plants and Transgenic
TITLE OF INVENTION: Plant Seeds
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESS: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive/6300 Sears tower
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/072.917A
FILING DATE:
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/509,962
FILING DATE: 01-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: Gass, David A.
REGISTRATION NUMBER: 38,153
REFERENCE/DOCKET NUMBER: 28123/34257
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-0448
TELEFAX: (312) 474-6300
INFORMATION FOR SEQ. ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 435 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-072-917A-9

Query Match 62.3%; Score 38; DB 3; Length 435;
Best local Similarity 60.0%; Pred. No. 41;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 CRDPRYADG 10
Db 148 CSDDTYSDG 157

RESULT 14
US-09-252-991A-19739
: Sequence 19739, Application US/09252991A
: Patent No. 6531795
: GENERAL INFORMATION:
: APPLICANT: Marc J. Rubenfield et al.
: TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
: TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
: FILE REFERENCE: 107196,136
: CURRENT APPLICATION NUMBER: US/09/252.991A
: CURRENT FILING DATE: 1999-02-18
: PRIOR APPLICATION NUMBER: US 60/074,788
: PRIOR FILING DATE: 1998-02-18
: PRIOR APPLICATION NUMBER: US 60/094,190
: PRIOR FILING DATE: 1998-07-27
: NUMBER OF SEQ. ID NOS: 35142
: SEQ. ID NO 19739
: LENGTH: 500
: TYPE: PRT
: ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-19739
Query Match 62.3%; Score 38; DB 4; Length 500;

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Query Match      62.3%; Score 38; DB 2; Length 1036;
Best Local Similarity 66.7%; Pred. No. 1e+02;
Matches      6; Conservative      2; Mismatches      1; Indels      0; Gaps      0;

OY      2 RDDRPYADG 10
      |||:|:|
Db      68 RDDKPPWFDG 76

US-08-720-484A-5
GENERAL INFORMATION:
APPLICANT: Desauvage, Frederic
APPLICANT: Rosenthal, Arnon
TITLE OF INVENTION: Vertebrate Smoothened Proteins
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESS: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US-08/720,484A
FILING DATE: 30-Sep-1996
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Syvoda, Craig G.
REGISTRATION NUMBER: 39,044
REFERENCE/DOCKET NUMBER: P1050
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1489
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 1036 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear

US-08-720-484A-5
GENERAL INFORMATION:
APPLICANT: Desauvage, Frederic
APPLICANT: Rosenthal, Arnon
TITLE OF INVENTION: Vertebrate Smoothened Proteins
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESS: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US-08/720,484A
FILING DATE: 30-Sep-1996
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Syvoda, Craig G.
REGISTRATION NUMBER: 39,044
REFERENCE/DOCKET NUMBER: P1050
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1489
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 1036 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear

US-08-720-484A-5
GENERAL INFORMATION:
APPLICANT: Desauvage, Frederic
APPLICANT: Rosenthal, Arnon
TITLE OF INVENTION: Vertebrate Smoothened Proteins
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESS: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US-08/720,484A
FILING DATE: 30-Sep-1996
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Syvoda, Craig G.
REGISTRATION NUMBER: 39,044
REFERENCE/DOCKET NUMBER: P1050
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1489
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 1036 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear

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ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION NUMBER: US/08/953,823A
APPLICATION NUMBER: US/08/953,823A
FILING DATE: 30-Sep-1997
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/027070
FILING DATE: 30-Sep-1996
ATTORNEY/AGENT INFORMATION:
NAME: Svoboda, Craig G.
REGISTRATION NUMBER: 39,044
REFERENCE/DOCKET NUMBER: P1050R1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1489
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 1036 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-08-953-823A-5

Query Match 62.3%; Score 38; DB 3; Length 1036;
Best Local Similarity 66.7%; Pred. No. 1e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 RDDRPRYADG 10
|||:|:|
Db 68 RDDKPWFDDG 76

RESULT 17
US-09-398-239-5
Sequence 5, Application US/09398239
Patent No. 6407216
GENERAL INFORMATION:
APPLICANT: Desauvage, Frederic
APPLICANT: Rosenthal, Arnon
APPLICANT: Stone, Donna
TITLE OF INVENTION: Vertebrate Smoothed Proteins
FILE REFERENCE: P1050D1
CURRENT APPLICATION NUMBER: US/09/398,239
CURRENT FILING DATE: 1999-09-20
EARLIER APPLICATION NUMBER: US 08/720,484
EARLIER FILING DATE: 1996-09-30
NUMBER OF SEQ ID NOS: 5
SEQ ID NO 5
LENGTH: 1036
TYPE: PRT
ORGANISM: Drosophila melanogaster
US-09-398-239-5

Query Match 62.3%; Score 38; DB 4; Length 1036;
Best Local Similarity 66.7%; Pred. No. 1e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 RDDRPRYADG 10
|||:|:|
Db 68 RDDKPWFDDG 76

RESULT 18
US-09-560-876A-5
Sequence 5, Application US/09560876A
Patent No. 6492139
GENERAL INFORMATION:
APPLICANT: de Sauvage, Frederic
APPLICANT: Rosenthal, Arnon

APPLICANT: Stone, Donna
TITLE OF INVENTION: Vertebrate Smoothed Proteins
FILE REFERENCE: P1050R1D1
CURRENT APPLICATION NUMBER: US/09/560,876A
CURRENT FILING DATE: 2002-05-22
PRIOR APPLICATION NUMBER: US 60/027,070
PRIOR FILING DATE: 1996-09-30
PRIOR APPLICATION NUMBER: US 08/953,823
PRIOR FILING DATE: 1997-09-30
NUMBER OF SEQ ID NOS: 6
SEQ ID NO 5
LENGTH: 1036
TYPE: PRT
ORGANISM: Drosophila melanogaster
US-09-560-876A-5

Query Match 62.3%; Score 38; DB 4; Length 1036;
Best Local Similarity 66.7%; Pred. No. 1e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 RDDRPRYADG 10
|||:|:|
Db 68 RDDKPWFDDG 76

RESULT 19
US-09-560-876A-6
Sequence 6, Application US/09560876A
Patent No. 6492139
GENERAL INFORMATION:
APPLICANT: de Sauvage, Frederic
APPLICANT: Rosenthal, Arnon
APPLICANT: Stone, Donna
TITLE OF INVENTION: Vertebrate Smoothed Proteins
FILE REFERENCE: P1050R1D1
CURRENT APPLICATION NUMBER: US/09/560,876A
CURRENT FILING DATE: 2002-05-22
PRIOR APPLICATION NUMBER: US 60/027,070
PRIOR FILING DATE: 1996-09-30
PRIOR APPLICATION NUMBER: US 08/953,823
PRIOR FILING DATE: 1997-09-30
NUMBER OF SEQ ID NOS: 6
SEQ ID NO 6
LENGTH: 1065
TYPE: PRT
ORGANISM: Drosophila melanogaster
FEATURE:
NAME/KEY: unsure
LOCATION: 3
OTHER INFORMATION: unknown amino acid
US-09-560-876A-6

Query Match 62.3%; Score 38; DB 4; Length 1065;
Best Local Similarity 66.7%; Pred. No. 1e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 RDDRPRYADG 10
|||:|:|
Db 97 RDDKPWFDDG 105

RESULT 20
US-09-328-352-7068
Sequence 7068, Application US/09328352
Patent No. 6562958
GENERAL INFORMATION:
APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTE
FILE REFERENCE: GTC99-03PA
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252

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; SEQ ID NO 7068
; LENGTH: 217
; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-328-352-7068

Query Match
Best Local Similarity 77.8%; Score 37; DB 4; Length 217;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 RDDRPRYADG 10
Db 185 RDDRPRYIDG 193

RESULT 21
US-08-991-862-17
; Sequence 17, Application US/08991862
; Patent No. 6309826
; GENERAL INFORMATION:
; APPLICANT: Serreio, GINETTE
; TITLE OF INVENTION: 88 KDA TUMORIGENIC GROWTH FACTOR AND ANTAGONISTS
; FILE REFERENCE: 29996.488/P001-A
; CURRENT FILING DATE: US/08/991.862
; PRIOR FILING DATE: 1998-08-17
; EARLIER FILING DATE: 1997-05-23
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 17
; LENGTH: 593
; TYPE: PRT
; ORGANISM: Human GP88 CDNA
US-08-991-862-17

Query Match
Best Local Similarity 60.7%; Score 37; DB 4; Length 593;
Matches 8; Conservative 1; Mismatches 1; Indels 6; Gaps 1;

OY 1 CRDR-----PYADG 10
Db 534 CRDRNQCACCPYAG 549

RESULT 22
US-09-252-991A-22461
; Sequence 22461, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT FILING DATE: US/09/252.991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 22461
; LENGTH: 568
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-22461

Query Match
Best Local Similarity 59.8%; Score 36; DB 4; Length 568;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 CRDRPRYADG 10
Db 211 CRDRPRPRAAG 220

; SEQ ID NO 7069
; LENGTH: 217
; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-328-352-7069

Query Match
Best Local Similarity 77.8%; Score 37; DB 4; Length 217;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 RDDRPRYADG 10
Db 185 RDDRPRYIDG 193

RESULT 23
US-09-216-393B-62
; Sequence 62, Application US/09216393B
; Patent No. 6511694
; GENERAL INFORMATION:
; APPLICANT: Milhaussen, Michael James
; TITLE OF INVENTION: TOXOPLASMA GONDII PROTEINS, NUCLEIC ACID MOLECULES, AND USES T
; FILE REFERENCE: TX-1-C2
; CURRENT FILING DATE: US/09/216.393B
; PRIOR FILING DATE: 1998-12-18
; PRIOR APPLICATION NUMBER: 08/994,825
; PRIOR FILING DATE: 1997-12-19
; NUMBER OF SEQ ID NOS: 366
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 62
; LENGTH: 129
; TYPE: PRT
; ORGANISM: Toxoplasma gondii
US-09-216-393B-62

Query Match
Best Local Similarity 57.4%; Score 35; DB 4; Length 129;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 1 CRDRPRYADG 10
Db 112 CRDRRLASG 121

RESULT 24
US-08-965-689A-6
; Sequence 6, Application US/08965689A
; Patent No. 6015702
; GENERAL INFORMATION:
; APPLICANT: Lal, Preeti
; APPLICANT: Hillman, Jennifer L.
; TITLE OF INVENTION: HUMAN UBIQUITIN CONJUGATING ENZYMES
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/965.689A
; FILING DATE: Herewith
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/933,750
; FILING DATE: September 23, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0356-1 CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 165 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
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TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: Genbank
CLONE: 4257
US-08-965-689A-6

Query Match 57.4%; Score 35; DB 3; Length 165;
Best Local Similarity 85.7%; Pred. No. 52;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 4 DRPYADG 10
111111
DB 46 DTPYADG 52

RESULT 25

US-09-359-967-6
Sequence 6, Application US/09359967
Patent No. 6146624
GENERAL INFORMATION:
APPLICANT: Lal, Preeti
APPLICANT: Hillman, Jennifer L.
APPLICANT: Corley, Neil C.
TITLE OF INVENTION: HUMAN UBIQUITIN CONJUGATING ENZYMES
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/359,967
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/965,689
FILING DATE:
APPLICATION NUMBER: 08/933,750
FILING DATE: September 23, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PP-0356-1 CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
TELEFAX: 650-845-4166
TELEX:
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 165 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: Genbank
CLONE: 4257
US-09-359-967-6

Query Match 57.4%; Score 35; DB 3; Length 165;
Best Local Similarity 85.7%; Pred. No. 52;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 4 DRPYADG 10
111111
DB 46 DTPYADG 52

RESULT 26
US-08-484-905-75
Sequence 75, Application US/08484905
Patent No. 5976551
GENERAL INFORMATION:
APPLICANT: Mottez, Estelle
APPLICANT: Abastado, Jean-Pierre
APPLICANT: Kourilsky, Philippe
TITLE OF INVENTION: An Altered Major Histocompatibility
TITLE OF INVENTION: Complex(MHC) Determinant and Methods for Using the
NUMBER OF SEQUENCES: 127
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
ADDRESSEE: Dunner
STREET: 1300 I Street, N.W., Suite 700
CITY: Washington
STATE: D.C.
ZIP: 20005-3315

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS-/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,905
FILING DATE: 07-JUNE-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/801,818
FILING DATE: 05-DEC-1991
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/792,473
FILING DATE: 15-NOV-1991
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Potler, Jane E. R.
REGISTRATION NUMBER: 33,332
REFERENCE/DOCKET NUMBER: 03495.0106-03000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 75:
SEQUENCE CHARACTERISTICS:
LENGTH: 306 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-484-905-75

Query Match 57.4%; Score 35; DB 2; Length 306;
Best Local Similarity 66.7%; Pred. No. 98;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 2 RDDRYADG 10
111111
DB 155 RDDRYADG 163

RESULT 27
US-08-481-985B-75
Sequence 75, Application US/08481985B
Patent No. 6011146
GENERAL INFORMATION:
APPLICANT: Mottez, Estelle
APPLICANT: Abastado, Jean-Pierre
APPLICANT: Kourilsky, Philippe
TITLE OF INVENTION: Altered Major Histocompatibility Complex
TITLE OF INVENTION:
NUMBER OF SEQUENCES: 148
CORRESPONDENCE ADDRESS:

Query Match 57.4%; Score 35; DB 3; Length 165;
Best Local Similarity 85.7%; Pred. No. 52;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

ADDRESSEE: Finnegan, Henderson, Farbow, Garrett &
ADDRESSEE: Dunnet
STREET: 1300 I Street, N.W., Suite 700
CITY: Washington
STATE: D.C.
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/481,985B
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/801,818
FILING DATE: 05-DEC-1991
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/792,473
FILING DATE: 15-NOV-1991
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Meyers, Kenneth J.
REGISTRATION NUMBER: 25,146
REFERENCE/DOCKET NUMBER: 03495.0106-04000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 75:
SEQUENCE CHARACTERISTICS:
LENGTH: 306 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-481-985B-75

Query Match 57.4%; Score 35; DB 3; Length 306;
Best Local Similarity 66.7%; Pred. No. 98;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 RDRLPYADG 10
DB 155 RDRAYLEG 163

RESULT 28
US-08-370-476-75
Sequence 75, Application US/08370476
Patent No. 6153408
GENERAL INFORMATION:
APPLICANT: Motiez, Estelle
APPLICANT: Abastado, Jean-Pierre
APPLICANT: Koutilsky, Philippe
APPLICANT: Leme, Yu-Chun
APPLICANT: Ojcius, David
APPLICANT: Garstouge, Amanda
TITLE OF INVENTION: Altered Major Histocompatibility Complex
NUMBER OF SEQUENCES: 127
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farbow, Garrett &
ADDRESS: Dunnet
STREET: 1300 I Street, N.W., Suite 700
CITY: Washington
STATE: D.C.
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/370,476
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/117,575
FILING DATE: 07-SEP-1993
APPLICATION NUMBER: US 08/072,787
FILING DATE: 06-JUN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/801,818
FILING DATE: 05-DEC-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/792,473
FILING DATE: 15-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: Meyers, Kenneth J.
REGISTRATION NUMBER: 25,146
REFERENCE/DOCKET NUMBER: 05243.0001-01000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 75:
SEQUENCE CHARACTERISTICS:
LENGTH: 306 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-370-476-75

Query Match 57.4%; Score 35; DB 3; Length 306;
Best Local Similarity 66.7%; Pred. No. 98;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 RDRLPYADG 10
DB 155 RDRAYLEG 163

RESULT 29
US-08-846-762-84
Sequence 84, Application US/08846762A
Patent No. 5994072
GENERAL INFORMATION:
APPLICANT: Lam, Joseph S.
APPLICANT: Burrows, Lori
APPLICANT: Charter, Deborah
APPLICANT: de Kievit, Teresa
TITLE OF INVENTION: of O-antigen in Pseudomonas Aeruginosa
FILE REFERENCE: 6580-089
CURRENT APPLICATION NUMBER: US/08/846,762A
NUMBER OF SEQ ID NOS: 100
SOFTWARE: Patentln Ver. 2.0
SEQ ID NO 84
LENGTH: 362
TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
US-08-846-762-84

Query Match 57.4%; Score 35; DB 2; Length 362;
Best Local Similarity 66.7%; Pred. No. 1.2e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 RDRLPYADG 10
DB 341 RDVOPYGDS 349

RESULT 30
US-09-252-991A-18424
Sequence 18424, Application US/09252991A

; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196, 136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ. ID NOS: 33142
; SEQ ID NO 18424
; LENGTH: 444
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-18424

Query Match 57.4%; Score 35; DB 4; Length 444;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Caps 0;

QY 3 DDRPYA 8
| | | | |
Db 198 DDRPYA 203

Search completed: August 29, 2003, 18:44:40
Job time: 11.5714 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 29, 2003, 18:42:11 : Search time 15.7143 Seconds

(without alignments)
87.043 Million cell updates/sec

Title: us-09-830-876-2

Perfect score: 61

Sequence: 1 CRDDRYADG 10

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

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Total number of hits satisfying chosen parameters: 510680

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

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- 18: /cgn2_6/ptodata/2/pubppa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	38	62.3	740	15	US-10-156-761-6392
3	37	60.7	118	15	US-10-155-886-40
4	37	60.7	293	15	US-10-155-886-11
5	37	60.7	413	15	US-10-097-340-141
6	37	60.7	593	9	US-09-813-156-17
7	37	60.7	593	9	US-09-824-807-17
8	37	60.7	593	10	US-09-824-647-17
9	37	60.7	593	15	US-10-218-509-17
10	37	60.7	593	15	US-10-281-160-17
11	37	60.7	771	9	US-09-784-358-14
12	37	60.7	845	9	US-09-784-358-12
13	37	60.7	1023	11	US-09-789-390-25
14	37	60.7	1023	11	US-09-789-390-27
15	37	60.7	1023	11	US-09-789-390-28

15	37	60.7	1023	11	US-09-789-390-59	Sequence 59, Appl
16	37	60.7	1023	11	US-09-789-390-61	Sequence 61, Appl
17	37	60.7	1281	11	US-09-789-390-2	Sequence 2, Appl
18	37	60.7	1281	11	US-09-789-390-5	Sequence 5, Appl
19	37	60.7	1617	9	US-09-784-358-16	Sequence 16, Appl
20	37	60.7	1691	9	US-09-784-358-2	Sequence 2, Appl
21	37	60.7	1691	11	US-09-789-390-4	Sequence 4, Appl
22	37	60.7	1691	11	US-09-815-242-10983	Sequence 10983, A
23	36	59.0	246	9	US-09-815-242-10261	Sequence 10261, A
24	36	59.0	255	9	US-09-815-242-14085	Sequence 14085, A
25	36	59.0	255	9	US-10-156-761-7849	Sequence 7849, Ap
26	36	59.0	4834	15	US-10-156-761-7849	Sequence 207, App
27	36	59.0	4834	15	US-09-934-455-200	Sequence 14, Appl
28	36	58.2	1288	16	US-10-233-526-14	Sequence 62, Appl
29	35.5	58.2	1298	9	US-09-216-393-62	Sequence 33, Appl
30	35	57.4	165	15	US-10-157-669-33	Sequence 84, Appl
31	35	57.4	165	15	US-10-216-209-84	Sequence 6289, Ap
32	35	57.4	554	10	US-09-738-626-6289	Sequence 12824, A
33	35	57.4	775	15	US-10-156-761-12824	Sequence 42, Appl
34	35	55.7	117	15	US-10-155-886-42	Sequence 12819, A
35	34	55.7	235	15	US-10-155-886-12	Sequence 3524, Ap
36	34	55.7	931	15	US-10-156-761-14719	Sequence 8524, Ap
37	34	55.7	922	15	US-10-128-714-3524	Sequence 33683, A
38	34	55.7	949	15	US-10-128-714-8524	Sequence 12737, A
39	34	55.7	949	15	US-09-864-761-33683	Sequence 18, Appl
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41	33	54.1	177	15	US-10-304-928-18	Sequence 51, Appl
42	33	54.1	259	15	US-10-156-761-9961	Sequence 8346, Ap
43	33	54.1	361	15	US-10-228-063-51	Sequence 10868, A
44	33	54.1	439	12	US-10-156-761-8346	Sequence 1147, A
45	33	54.1	439	15	US-09-312-762A-15	Sequence 201, App
46	33	54.1	496	10	US-10-156-761-10868	Sequence 1863, Ap
47	33	54.1	532	15	US-10-156-761-11347	Sequence 20, Appl
48	33	54.1	733	15	US-10-156-761-11347	Sequence 451, Appl
49	33	53.3	203	15	US-10-156-761-11347	Sequence 14866, A
50	32.5	52.5	66	15	US-10-000-256A-201	Sequence 7930, Ap
51	32	52.5	71	15	US-10-156-761-10479	Sequence 62, Appl
52	32	52.5	105	9	US-09-764-877-1863	Sequence 62, Appl
53	32	52.5	139	9	US-09-605-658-20	Sequence 11946, A
54	32	52.5	139	9	US-09-844-353A-20	Sequence 4, Appl
55	32	52.5	147	9	US-09-925-302-451	Sequence 12842, A
56	32	52.5	148	15	US-10-156-761-14866	Sequence 3579, Ap
57	32	52.5	153	15	US-10-156-761-14866	Sequence 358, App
58	32	52.5	153	15	US-10-156-761-79581	Sequence 8523, Ap
59	32	52.5	202	11	US-09-924-600A-62	Sequence 8579, Ap
60	32	52.5	202	11	US-09-924-600A-62	Sequence 7, Appl
61	32	52.5	202	12	US-09-924-600A-62	Sequence 22, Appl
62	32	52.5	202	15	US-10-000-489-62	Sequence 22, Appl
63	32	52.5	202	15	US-10-000-489-62	Sequence 6665, Ap
64	32	52.5	252	9	US-09-815-242-11820	Sequence 4492, A
65	32	52.5	252	9	US-09-815-242-11820	Sequence 4492, A
66	32	52.5	324	10	US-09-816-095-4	Sequence 6525, A
67	32	52.5	328	15	US-10-156-761-12842	Sequence 44719, A
68	32	52.5	416	15	US-10-128-714-3579	Sequence 3191, Ap
69	32	52.5	423	14	US-10-062-254-358	Sequence 676, App
70	32	52.5	423	15	US-10-128-714-8223	Sequence 676, App
71	32	52.5	428	15	US-10-128-714-8223	Sequence 676, App
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73	32	52.5	510	14	US-09-369-735B-7	Sequence 676, App
74	32	52.5	510	14	US-10-121-032-22	Sequence 676, App
75	32	52.5	510	14	US-10-093-037-22	Sequence 676, App
76	32	52.5	516	10	US-09-738-626-6665	Sequence 676, App
77	32	52.5	516	10	US-09-738-626-6665	Sequence 676, App
78	32	52.5	617	11	US-09-866-050A-303	Sequence 676, App
79	32	52.5	621	9	US-09-925-301-1416	Sequence 676, App
80	32	52.5	751	10	US-09-738-626-6525	Sequence 676, App
81	31	50.8	905	9	US-09-864-761-44719	Sequence 676, App
82	31	50.8	905	9	US-09-925-297-676	Sequence 676, App
83	31	50.8	105	11	US-09-764-891-3191	Sequence 676, App
84	31	50.8	119	12	US-10-306-292-2	Sequence 676, App
85	31	50.8	130	12	US-09-893-737-144	Sequence 676, App
86	31	50.8	158	10	US-09-764-868-948	Sequence 676, App
87	31	50.8	179	15	US-10-156-761-11443	Sequence 676, App
88	31	50.8	182	12	US-10-181-590-7	Sequence 676, App

89 31 50.8 200 9 US-09-734-569-138 Sequence 138, App
90 31 50.8 222 9 US-09-815-242-13842 Sequence 13842, A
91 31 50.8 238 15 US-10-153-668-264 Sequence 264, App
92 31 50.8 239 9 US-09-815-242-13417 Sequence 13417, A
93 31 50.8 239 9 US-09-815-242-13569 Sequence 13569, A
94 31 50.8 239 11 US-09-929-769-6 Sequence 6, Appl
95 31 50.8 239 11 US-09-846-374-324 Sequence 324, App
96 31 50.8 239 12 US-10-015-3874-324 Sequence 324, App
97 31 50.8 239 12 US-10-006-1304-324 Sequence 324, App
98 31 50.8 239 12 US-10-199-672-354 Sequence 354, App
99 31 50.8 239 12 US-10-006-172A-324 Sequence 324, App
100 31 50.8 239 12 US-10-187-749-354 Sequence 354, App

ALIGNMENTS

RESULT 1
US-10-280-679B-6
; Sequence 6, Application US/10280679B
; Publication No. US20030150019A1
; GENERAL INFORMATION:
; APPLICANT: Large Scale Biology Corporation
; TITLE OF INVENTION: Monoparticle RNA Virus Transformation Vectors
; FILE REFERENCE: LSBC-0109-US03
; CURRENT APPLICATION NUMBER: US/10/280,679B
; CURRENT FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: 09/557,941
; PRIOR FILING DATE: 2000-04-24
; PRIOR APPLICATION NUMBER: 08/484,341
; PRIOR FILING DATE: 1995-06-07
; PRIOR APPLICATION NUMBER: 07/923,692
; PRIOR FILING DATE: 1992-07-31
; PRIOR APPLICATION NUMBER: 07/600,244
; PRIOR FILING DATE: 1990-10-22
; PRIOR APPLICATION NUMBER: 07/641,617
; PRIOR FILING DATE: 1991-01-16
; PRIOR APPLICATION NUMBER: 07/737,899
; PRIOR FILING DATE: 1991-07-26
; PRIOR APPLICATION NUMBER: 07/739,143
; PRIOR FILING DATE: 1991-08-01
; PRIOR APPLICATION NUMBER: 07/310,881
; PRIOR FILING DATE: 1989-02-17
; PRIOR APPLICATION NUMBER: 07/160,766
; PRIOR FILING DATE: 1988-02-26
; PRIOR APPLICATION NUMBER: 07/160,771
; PRIOR FILING DATE: 1988-02-26
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 434
; TYPE: PRT
; ORGANISM: Rice alpha-amylase
US-10-280-679B-6

Query Match 68.0%; Score 41.5; DB 12; Length 434;
Best Local Similarity 80.0%; Pred. No. 16;
Matches 8; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

Oy 1 CRDDPYADG 10
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RESULT 2
US-10-156-761-8392
; Sequence 8392, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN

; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 8392
; LENGTH: 740
; TYPE: PRT
; ORGANISM: Streptomyces avermitilis
US-10-156-761-8392

Query Match 62.3%; Score 38; DB 15; Length 740;
Best Local Similarity 66.7%; Pred. No. 1,2e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

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Db 717 REDTPYGDG 725

RESULT 3
US-10-155-886-40
; Sequence 40, Application US/10155886
; Publication No. US20030087804A1
; GENERAL INFORMATION:
; APPLICANT: Hempstead, Barbara L.
; APPLICANT: Lee, Ramee
; APPLICANT: Teng, Kenneth K.
; APPLICANT: Kernani, Pouneh
; TITLE OF INVENTION: High Affinity Ligand For p75 Neurotrophin Receptor
; FILE REFERENCE: 955-21 Sequence No. US20030087804A1. 1-68
; CURRENT APPLICATION NUMBER: US/10/155,886
; CURRENT FILING DATE: 2002-08-05
; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 40
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; TYPE: PRT
; ORGANISM: Gallus gallus
US-10-155-886-40

Query Match 60.7%; Score 37; DB 15; Length 118;
Best Local Similarity 60.0%; Pred. No. 26;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Oy 1 CRDDPYADG 10
Db 57 CRDDPYVSSG 66

RESULT 4
US-10-155-886-11
; Sequence 11, Application US/10155886
; Publication No. US20030087804A1
; GENERAL INFORMATION:
; APPLICANT: Hempstead, Barbara L.
; APPLICANT: Lee, Ramee
; APPLICANT: Teng, Kenneth K.
; APPLICANT: Kernani, Pouneh
; TITLE OF INVENTION: High Affinity Ligand For p75 Neurotrophin Receptor
; FILE REFERENCE: 955-21 Sequence No. US20030087804A1. 1-68
; CURRENT APPLICATION NUMBER: US/10/155,886
; CURRENT FILING DATE: 2002-08-05
; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: PatentIn version 3.1


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; SEQ ID NO 11
; LENGTH: 243
; TYPE: PRT
; ORGANISM: Gallus gallus
US-10-155-886-11

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Query Match	60.7%;	Score 37;	DB 15;	Length 243;
Best Local Similarity	60.0%;	Pred. No. 55;		
Matches	6;	Conservative	1;	Mismatches 3; Indels 0; Gaps 0;

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Db      182 CRDPRVSSG 191
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RESULT 5
US-10-097-340-141
; Sequence 141, Application US/10097340
; Publication No. US20030087250A1
GENERAL INFORMATION:

```

APPLICANT: John MONAHAN
APPLICANT: Manjula GANNANVARAPU
APPLICANT: Sebastian HOERSCH
APPLICANT: Shubhangi KAMATKAR
APPLICANT: Steve G. KOVATS
APPLICANT: Rachel E. MEYERS
APPLICANT: Michael MORRISEY
APPLICANT: Peter OLANDT
APPLICANT: Ami SEN
APPLICANT: Peter VEIRY
APPLICANT: Gordon B. MILLS
APPLICANT: Robert C. BAST, Jr.
APPLICANT: Karen LU
APPLICANT: Rosemarie SCHMANDT
APPLICANT: Xumel ZHAO
APPLICANT: Karen GIANTT
TITLE OF INVENTION: Nucleic Acid Molecules and Proteins For The Identification
TITLE OF INVENTION: Assessment, Prevention, and Therapy of Ovarian Cancer
FILE REFERENCE: MRI-030
CURRENT FILING DATE: 2002-03-14
CURRENT FILING DATE: 2002-03-14
PRIOR APPLICATION NUMBER: 60/276,025
PRIOR FILING DATE: 2001-03-14
PRIOR APPLICATION NUMBER: 60/325,149
PRIOR FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: 60/276,026
PRIOR FILING DATE: 2001-03-14
PRIOR APPLICATION NUMBER: 60/324,967
PRIOR FILING DATE: 2001/09/26
PRIOR APPLICATION NUMBER: 60/311,732
PRIOR FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: 60/325,102
PRIOR FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: 60/323,580
PRIOR FILING DATE: 2001-09-15
NUMBER OF SEQ. ID NOS: 363
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 141
LENGTH: 413
TYPE: PRT
ORGANISM: Homo sapiens
US-10-097-340-141

```

Query Match	60.78;	Score 37;	DB 15;	Length 413;
Best Local Similarity	87.58;	Pred. No. 95;		
Matches	7;	Conservative	0;	Mismatches 1; Indels 0; Gaps 0;

QY	2	RDDRPYAD	9
Db	147	RDYRPYAD	154

RESULT 6

US-09-813-156-17
; Sequence 17, Application US/09813156
; Patent No. US20020061859A1
GENERAL INFORMATION

APPLICANT: Seriero, Ginette
TITLE OF INVENTION: 88 KDA TUMORIGENIC GROWTH FACTOR AND ANTAGONISTS
FILE REFERENCE: 29996.488/P001-A
CURRENT ADDITION NUMBER: US 09/913 156

; CURRENT FILING DATE: 2001-03-21
 ; PRIOR APPLICATION NUMBER: 08/991,862
 ; PRIOR FILING DATE: 1997-12-16
 ; PRIOR ADDITION NUMBER: 08/053,853

```

; PRIOR FILING DATE: 1997-05-23
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 17

```

```

; LENGTH: 593
; TYPE: PRT
; ORGANISM: Human GP88 CDNA
US-09-813-156-17

```

Query Match	60.7%;	Score 37;	DB 9;	Length 593;
Best Local Similarity	50.0%;	Pred. NO. 1.4e+02;		
Matches	8;	Conservative	1;	Mismatches 1;
				Indels 6;
				Gaps 1;

```
QY      1 CRDDR-----PYADG 10
          |||:|      |||
Db      534 CRDNRQGWACCPYAQG 545
```

RESULT 7
US-09-824-807-17

Patent No. US20020094966A1
GENERAL INFORMATION:
APPLICANT: Serrero, Ginette
TITLE OF INVENTION: 88 KDa PROPOGICENTO PROTEIN ENCODED AND AMINOACIDS

```

: FILE REFERENCE: 29996.488/P001-A
: CURRENT APPLICATION NUMBER: US/09/824,807.
: CURRENT FILING DATE: 2001-04-04
: PRIOR APPLICATION NUMBER: 08/0901,963

```

; PRIOR FILING DATE: 1997-12-16
 ; PRIOR APPLICATION NUMBER: 08/863,862
 ; PRIOR FILING DATE: 1997-05-23
 ; NUMBER OF SEQ IDNOS: 17

```

; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 17
; LENGTH: 593
; TYPE: PRT

```

```

; ORGANISM: Human GP88 CDNA
US-09-824-807-17
Query Match 60

```

```

00      1 CRDDR-----PYARG 10
      Best Local Similarity  50.0%;  Pred. No. 1.4e+02;
      Matches      8;  Conservative      1;  Mismatches      1;
      Indels      6;  Gaps      1.

```

Db 534 CRDNRQGWACCPYAQG 549

RESULT 8
US-09-824-647-17
; Sequence 17, Application US/09824647
; Publication No. US20020183270A1

```

GENERAL INFORMATION:
APPLICANT: Serrero, GINETTE
TITLE OF INVENTION: 88 KDA TUMORIGENIC GROWTH FACTOR AND ANTAGONISTS
FILE REFERENCE: 29996.488/P001-A

```

CURRENT APPLICATION NUMBER: 08/991,862
 CURRENT FILING DATE: 2001-04-04
 PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 08/991,862
 PRIOR FILING DATE: EARLIER FILING DATE: 1998-08-17

PRIOR ;

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 08/863,862
PRIOR FILING DATE: EARLIER FILING DATE: 1997-05-23
NUMBER OF SEQ ID NOS: 17
SOFTWARE: Patentln Ver. 2.0
SEQ ID NO 17
LENGTH: 593
TYPE: PRT
ORGANISM: Human GP88 cDNA
US-09-824-647-17

Query Match 60.7%; Score 37; DB 10; Length 593;
Best Local Similarity 50.0%; Pred. No. 1.4e+02;
Matches 8; Conservative 1; Mismatches 1; Indels 6; Gaps 1;

QY 1 CRDR-----PYADG 10
DB 534 CRDRGACCPYAOG 549

RESULT 9
US-10-218-509-17
Sequence 17, Application US/10218509
Publication No. US20030092661A1
GENERAL INFORMATION:
APPLICANT: Sertero, GINETTE
TITLE OF INVENTION: 88 KDA TUMORIGENIC GROWTH FACTOR AND ANTAGONISTS
FILE REFERENCE: 29996,488/P001-A
CURRENT APPLICATION NUMBER: US/10/218,509
CURRENT FILING DATE: 2002-08-15
PRIOR APPLICATION NUMBER: 08/991,862
PRIOR FILING DATE: 1998-08-17
PRIOR APPLICATION NUMBER: 08/863,862
PRIOR FILING DATE: 1997-05-23
NUMBER OF SEQ ID NOS: 17
SOFTWARE: Patentln Ver. 2.0
SEQ ID NO 17
LENGTH: 593
TYPE: PRT
ORGANISM: Human GP88 cDNA
US-10-218-509-17

Query Match 60.7%; Score 37; DB 15; Length 593;
Best Local Similarity 50.0%; Pred. No. 1.4e+02;
Matches 8; Conservative 1; Mismatches 1; Indels 6; Gaps 1;

QY 1 CRDR-----PYADG 10
DB 534 CRDRGACCPYAOG 549

RESULT 10
US-10-281-160-17
Sequence 17, Application US/10281160
Publication No. US20030108950A1
GENERAL INFORMATION:
APPLICANT: Sertero, GINETTE
TITLE OF INVENTION: 88 KDA TUMORIGENIC GROWTH FACTOR AND ANTAGONISTS
FILE REFERENCE: 29996,488/P001-A
CURRENT APPLICATION NUMBER: US/10/281,160
CURRENT FILING DATE: 2002-10-28
PRIOR APPLICATION NUMBER: US/08/991,862
PRIOR FILING DATE: 1998-08-17
PRIOR APPLICATION NUMBER: 08/863,862
PRIOR FILING DATE: 1997-05-23
NUMBER OF SEQ ID NOS: 17
SOFTWARE: Patentln Ver. 2.0
SEQ ID NO 17
LENGTH: 593
TYPE: PRT
ORGANISM: Human GP88 cDNA
US-10-281-160-17

Query Match 60.7%; Score 37; DB 15; Length 593;

Best Local Similarity 50.0%; Pred. No. 1.4e+02;
Matches 8; Conservative 1; Mismatches 1; Indels 6; Gaps 1;

QY 1 CRDR-----PYADG 10
DB 534 CRDRGACCPYAOG 549

RESULT 11
US-09-784-358-14
Sequence 14, Application US/09784358
Patent No. US20020099027A1
GENERAL INFORMATION:
APPLICANT: Donoho, Gregory
APPLICANT: Scoville, John
APPLICANT: Turner, C. Alexander Jr.
APPLICANT: Friedrich, Glenn
APPLICANT: Zambrowicz, Brian
APPLICANT: Sands, Arthur T.
TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING THE SAME
FILE REFERENCE: LEX-0134-USA
CURRENT APPLICATION NUMBER: US/09/784,358
CURRENT FILING DATE: 2001-02-15
PRIOR APPLICATION NUMBER: US 60/183,282
PRIOR FILING DATE: 2000-02-17
NUMBER OF SEQ ID NOS: 17
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 14
LENGTH: 771
TYPE: PRT
ORGANISM: homo sapiens
US-09-784-358-14

Query Match 60.7%; Score 37; DB 9; Length 771;
Best Local Similarity 62.5%; Pred. No. 1.8e+02;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRDRPYA 8
DB 669 CRDEKPHA 676

RESULT 12
US-09-784-358-12
Sequence 12, Application US/09784358
Patent No. US20020099027A1
GENERAL INFORMATION:
APPLICANT: Donoho, Gregory
APPLICANT: Scoville, John
APPLICANT: Turner, C. Alexander Jr.
APPLICANT: Friedrich, Glenn
APPLICANT: Zambrowicz, Brian
APPLICANT: Sands, Arthur T.
TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING THE SAME
FILE REFERENCE: LEX-0134-USA
CURRENT APPLICATION NUMBER: US/09/784,358
CURRENT FILING DATE: 2001-02-15
PRIOR APPLICATION NUMBER: US 60/183,282
PRIOR FILING DATE: 2000-02-17
NUMBER OF SEQ ID NOS: 17
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 12
LENGTH: 845
TYPE: PRT
ORGANISM: homo sapiens
US-09-784-358-12

Query Match 60.7%; Score 37; DB 9; Length 845;
Best Local Similarity 62.5%; Pred. No. 2e+02;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

```
OY      1 CRDDRPA 8
      11111111
Db      743 CRDEKPA 750

RESULT 13
US-09-789-390-25
; Sequence 25, Application US/09789390
; Publication No. US20030059768A1
; GENERAL INFORMATION:
; APPLICANT: Vernet, Corine
; APPLICANT: Fernandes, Elma
; APPLICANT: MacDougall, John
; APPLICANT: Shinkets, Richard A
; TITLE OF INVENTION: NOVEL POLYPEPTIDES AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 15966-692
; CURRENT APPLICATION NUMBER: US/09/789,390
; PRIOR FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: 60/185,548
; PRIOR FILING DATE: 2000-02-28
; PRIOR APPLICATION NUMBER: 60/199,957
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: 60/184,951
; PRIOR FILING DATE: 2000-02-25
; PRIOR APPLICATION NUMBER: 60/185,967
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: 60/197,723
; PRIOR FILING DATE: 2000-04-18
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 25
; LENGTH: 1023
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-789-390-25

Query Match      60.7%; Score 37; DB 11; Length 1023;
Best Local Similarity 62.5%; Pred. No. 2.4e+02;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

OY      1 CRDDRPA 8
      11111111
Db      75 CRDEKPA 82

RESULT 14
US-09-789-390-27
; Sequence 27, Application US/09789390
; Publication No. US20030059768A1
; GENERAL INFORMATION:
; APPLICANT: Vernet, Corine
; APPLICANT: Fernandes, Elma
; APPLICANT: MacDougall, John
; APPLICANT: Shinkets, Richard A
; APPLICANT: Spaderna, Steven K
; TITLE OF INVENTION: NOVEL POLYPEPTIDES AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 15966-692
; CURRENT APPLICATION NUMBER: US/09/789,390
; PRIOR FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: 60/185,548
; PRIOR FILING DATE: 2000-02-28
; PRIOR APPLICATION NUMBER: 60/199,957
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: 60/184,951
; PRIOR FILING DATE: 2000-02-25
; PRIOR APPLICATION NUMBER: 60/185,967
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: 60/197,723
; PRIOR FILING DATE: 2000-04-18
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 27

Query Match      60.7%; Score 37; DB 11; Length 1023;
Best Local Similarity 62.5%; Pred. No. 2.4e+02;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

OY      1 CRDDRPA 8
      11111111
Db      75 CRDEKPA 82

RESULT 15
US-09-789-390-28
; Sequence 28, Application US/09789390
; Publication No. US20030059768A1
; GENERAL INFORMATION:
; APPLICANT: Vernet, Corine
; APPLICANT: Fernandes, Elma
; APPLICANT: MacDougall, John
; APPLICANT: Shinkets, Richard A
; APPLICANT: Spaderna, Steven K
; TITLE OF INVENTION: NOVEL POLYPEPTIDES AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 15966-692
; CURRENT APPLICATION NUMBER: US/09/789,390
; PRIOR FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: 60/185,548
; PRIOR FILING DATE: 2000-02-28
; PRIOR APPLICATION NUMBER: 60/199,957
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: 60/184,951
; PRIOR FILING DATE: 2000-02-25
; PRIOR APPLICATION NUMBER: 60/185,967
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: 60/197,723
; PRIOR FILING DATE: 2000-04-18
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 28
; LENGTH: 1023
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-789-390-28

Query Match      60.7%; Score 37; DB 11; Length 1023;
Best Local Similarity 62.5%; Pred. No. 2.4e+02;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

OY      1 CRDDRPA 8
      11111111
Db      75 CRDEKPA 82

RESULT 16
US-09-789-390-59
; Sequence 59, Application US/09789390
; Publication No. US20030059768A1
; GENERAL INFORMATION:
; APPLICANT: Vernet, Corine
; APPLICANT: Fernandes, Elma
; APPLICANT: MacDougall, John
; APPLICANT: Shinkets, Richard A
; APPLICANT: Spaderna, Steven K
; TITLE OF INVENTION: NOVEL POLYPEPTIDES AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 15966-692
; CURRENT APPLICATION NUMBER: US/09/789,390
; PRIOR FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: 60/185,548
; PRIOR FILING DATE: 2000-02-28
; PRIOR APPLICATION NUMBER: 60/199,957
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: 60/184,951
; PRIOR FILING DATE: 2000-02-25
; PRIOR APPLICATION NUMBER: 60/185,967
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: 60/197,723
; PRIOR FILING DATE: 2000-04-18
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 59
```

;; PRIOR APPLICATION NUMBER: 60/184,951
;; PRIOR FILING DATE: 2000-02-25
;; PRIOR APPLICATION NUMBER: 60/185,967
;; PRIOR FILING DATE: 2000-03-01
;; PRIOR APPLICATION NUMBER: 60/197,723
;; PRIOR FILING DATE: 2000-04-18
;; NUMBER OF SEQ ID NOS: 77
;; SOFTWARE: PatentIn Ver. 2.1
;; SEQ ID NO 59
;; LENGTH: 1023
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-09-789-390-59

Query Match 60.7%; Score 37; DB 11; Length 1023;
Best Local Similarity 62.5%; Pred. No. 2.4e+02;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRDRPYA 8
|||:|:|
Db 75 CRDEKPHA 82

RESULT 17
US-09-789-390-61
;; Sequence 61, Application US/09789390
;; Publication No. US20030059768A1
;; GENERAL INFORMATION:
;; APPLICANT: Vernet, Corine
;; APPLICANT: Fernandes, Elma
;; APPLICANT: MacDougall, John
;; APPLICANT: Shinkels, Richard A
;; APPLICANT: Spaderna, Steven K
;; TITLE OF INVENTION: NOVEL POLYPEPTIDES AND NUCLEIC ACIDS ENCODING SAME
;; FILE REFERENCE: 15966-692
;; CURRENT APPLICATION NUMBER: US/09/789,390
;; CURRENT FILING DATE: 2001-02-23
;; PRIOR APPLICATION NUMBER: 60/185,548
;; PRIOR FILING DATE: 2000-02-28
;; PRIOR APPLICATION NUMBER: 60/199,957
;; PRIOR FILING DATE: 2000-04-27
;; PRIOR APPLICATION NUMBER: 60/184,951
;; PRIOR FILING DATE: 2000-02-25
;; PRIOR APPLICATION NUMBER: 60/185,967
;; PRIOR FILING DATE: 2000-03-01
;; PRIOR APPLICATION NUMBER: 60/197,723
;; PRIOR FILING DATE: 2000-04-18
;; NUMBER OF SEQ ID NOS: 77
;; SOFTWARE: PatentIn Ver. 2.1
;; SEQ ID NO 61
;; LENGTH: 1023
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-09-789-390-61

Query Match 60.7%; Score 37; DB 11; Length 1023;
Best Local Similarity 62.5%; Pred. No. 2.4e+02;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRDRPYA 8
|||:|:|
Db 75 CRDEKPHA 82

RESULT 18
US-09-789-390-2
;; Sequence 2, Application US/09789390
;; Publication No. US20030059768A1
;; GENERAL INFORMATION:
;; APPLICANT: Vernet, Corine
;; APPLICANT: Fernandes, Elma
;; APPLICANT: MacDougall, John
;; APPLICANT: Shinkels, Richard A

;; APPLICANT: Spaderna, Steven K
;; TITLE OF INVENTION: NOVEL POLYPEPTIDES AND NUCLEIC ACIDS ENCODING SAME
;; FILE REFERENCE: 15966-692
;; CURRENT APPLICATION NUMBER: US/09/789,390
;; CURRENT FILING DATE: 2001-02-23
;; PRIOR APPLICATION NUMBER: 60/185,548
;; PRIOR FILING DATE: 2000-02-28
;; PRIOR APPLICATION NUMBER: 60/199,957
;; PRIOR FILING DATE: 2000-04-27
;; PRIOR APPLICATION NUMBER: 60/184,951
;; PRIOR FILING DATE: 2000-02-25
;; PRIOR APPLICATION NUMBER: 60/185,967
;; PRIOR FILING DATE: 2000-03-01
;; PRIOR APPLICATION NUMBER: 60/197,723
;; PRIOR FILING DATE: 2000-04-18
;; NUMBER OF SEQ ID NOS: 77
;; SOFTWARE: PatentIn Ver. 2.1
;; SEQ ID NO 2
;; LENGTH: 1281
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-09-789-390-2

Query Match 60.7%; Score 37; DB 11; Length 1281;
Best Local Similarity 62.5%; Pred. No. 3.1e+02;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRDRPYA 8
|||:|:|
Db 333 CRDEKPHA 340

RESULT 19
US-09-789-390-5
;; Sequence 5, Application US/09789390
;; Publication No. US20030059768A1
;; GENERAL INFORMATION:
;; APPLICANT: Vernet, Corine
;; APPLICANT: Fernandes, Elma
;; APPLICANT: MacDougall, John
;; APPLICANT: Shinkels, Richard A
;; APPLICANT: Spaderna, Steven K
;; TITLE OF INVENTION: NOVEL POLYPEPTIDES AND NUCLEIC ACIDS ENCODING SAME
;; FILE REFERENCE: 15966-692
;; CURRENT APPLICATION NUMBER: US/09/789,390
;; CURRENT FILING DATE: 2001-02-23
;; PRIOR APPLICATION NUMBER: 60/185,548
;; PRIOR FILING DATE: 2000-02-28
;; PRIOR APPLICATION NUMBER: 60/199,957
;; PRIOR FILING DATE: 2000-04-27
;; PRIOR APPLICATION NUMBER: 60/184,951
;; PRIOR FILING DATE: 2000-02-25
;; PRIOR APPLICATION NUMBER: 60/185,967
;; PRIOR FILING DATE: 2000-03-01
;; PRIOR APPLICATION NUMBER: 60/197,723
;; PRIOR FILING DATE: 2000-04-18
;; NUMBER OF SEQ ID NOS: 77
;; SOFTWARE: PatentIn Ver. 2.1
;; SEQ ID NO 5
;; LENGTH: 1281
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-09-789-390-5

Query Match 60.7%; Score 37; DB 11; Length 1281;
Best Local Similarity 62.5%; Pred. No. 3.1e+02;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRDRPYA 8
|||:|:|
Db 333 CRDEKPHA 340

```
RESULT 20
US-09-784-358-16
; Sequence 16, Application US/09784358
; Patent No. US20020099027A1
; GENERAL INFORMATION:
; APPLICANT: Donoho, Gregory
; APPLICANT: Scoville, John
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Friedlich, Glenn
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: NOVEL HUMAN THROMBOSPONDIN REPEAT PROTEINS AND
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING THE SAME
; FILE REFERENCE: LEX-0134-USA
; CURRENT APPLICATION NUMBER: US/09/784,358
; PRIOR FILING DATE: 2001-02-15
; PRIOR APPLICATION NUMBER: US 60/183,282
; PRIOR FILING DATE: 2000-02-17
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 1617
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-784-358-16

Query Match      60.7%; Score 37; DB 9; Length 1617;
Best Local Similarity 62.5%; Pred. No. 3.9e+02;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

OY      1 CRDPRYA 8
DB      669 CRDPRYA 676

RESULT 21
US-09-784-358-2
; Sequence 2, Application US/09784358
; Patent No. US20020099027A1
; GENERAL INFORMATION:
; APPLICANT: Donoho, Gregory
; APPLICANT: Scoville, John
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Friedlich, Glenn
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: NOVEL HUMAN THROMBOSPONDIN REPEAT PROTEINS AND
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING THE SAME
; FILE REFERENCE: LEX-0134-USA
; CURRENT APPLICATION NUMBER: US/09/784,358
; PRIOR FILING DATE: 2001-02-15
; PRIOR APPLICATION NUMBER: US 60/183,282
; PRIOR FILING DATE: 2000-02-17
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 1691
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-784-358-2

Query Match      60.7%; Score 37; DB 9; Length 1691;
Best Local Similarity 62.5%; Pred. No. 4.1e+02;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

OY      1 CRDPRYA 8
DB      743 CRDPRYA 750

RESULT 22
US-09-789-390-4
; Sequence 4, Application US/09789390
; Publication No. US20030059768A1
; GENERAL INFORMATION:
; APPLICANT: Vernet, Corine
; APPLICANT: Fernandes, Elma
; APPLICANT: MacDougall, John
; APPLICANT: Shinkels, Richard A
; APPLICANT: Spaderna, Steven K
; TITLE OF INVENTION: NOVEL POLYPEPTIDES AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 15966-692
; CURRENT APPLICATION NUMBER: US/09/789,390
; CURRENT FILING DATE: 2001-02-23
; PRIOR FILING DATE: 2000-02-28
; PRIOR APPLICATION NUMBER: 60/185,548
; PRIOR FILING DATE: 2000-02-28
; PRIOR APPLICATION NUMBER: 60/199,957
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: 60/184,951
; PRIOR FILING DATE: 2000-02-25
; PRIOR APPLICATION NUMBER: 60/185,967
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: 60/197,723
; PRIOR FILING DATE: 2000-04-18
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 4
; LENGTH: 1691
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-789-390-4

Query Match      60.7%; Score 37; DB 11; Length 1691;
Best Local Similarity 62.5%; Pred. No. 4.1e+02;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

OY      1 CRDPRYA 8
DB      743 CRDPRYA 750

RESULT 23
US-09-813-242-10983
; Sequence 10983, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Karl L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; TITLE OF INVENTION: Prokaryotes
; FILE REFERENCE: ELITRA 011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10983
```

LENGTH: 246
TYPE: PRT
ORGANISM: Haemophilus influenzae
US-09-815-242-10983

Query Match
Best Local Similarity 59.0%; Score 36; DB 9; Length 246;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 DDRPYADG 10
|||||
Db 50 DDRPYGGG 57

RESULT 24
US-09-815-242-10261
Sequence 10261, Application US/09815242
Patent No. US20020061569A1

GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Karl L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant J.
APPLICANT: Yamamoto, Robert T.
TITLE OF INVENTION: Identification of Essential Genes in
FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 10261
LENGTH: 255
TYPE: PRT
ORGANISM: Escherichia coli

US-09-815-242-10261

Query Match
Best Local Similarity 59.0%; Score 36; DB 9; Length 255;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 DDRPYADG 10
|||||
Db 50 DDRPYGGG 57

RESULT 25
US-09-815-242-14085
Sequence 14085, Application US/09815242
Patent No. US20020061569A1

GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Karl L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.

APPLICANT: Carr, Grant J.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 14085
LENGTH: 255
TYPE: PRT
ORGANISM: Salmonella typhi

US-09-815-242-14085

Query Match
Best Local Similarity 59.0%; Score 36; DB 9; Length 255;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 DDRPYADG 10
|||||
Db 50 DDRPYGGG 57

RESULT 26
US-10-156-761-7849
Sequence 7849, Application US/10156761
Publication No. US20030119018A1

GENERAL INFORMATION:
APPLICANT: OMURA, SATOSHI
APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAWA, JUN
APPLICANT: HORIKAWA, HIROSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR FILING DATE: 2001-05-30
PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR FILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 7849
LENGTH: 353
TYPE: PRT
ORGANISM: Streptomyces avermitilis
US-10-156-761-7849

Query Match
Best Local Similarity 59.0%; Score 36; DB 15; Length 353;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 RDDRPY 7
|||||
Db 264 RDDRPY 269

```

RESULT 27
US-10-097-534-27
; Sequence 27, Application US/10097534
; Publication No. US20030049607A1
GENERAL INFORMATION:
APPLICANT: GREENER, TSVITA
APPLICANT: REISS, HAIM
APPLICANT: MOSKOWITZ, HAIM
APPLICANT: AROV, IRIS
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE MODULATION OF VIRAL
FILE REFERENCE: PLY-001.01
CURRENT FILING DATE: 2002-03-12
PRIOR APPLICATION NUMBER: 60/275,224
PRIOR FILING DATE: 2001-03-12
PRIOR APPLICATION NUMBER: 60/308,958
PRIOR FILING DATE: 2001-07-31
PRIOR APPLICATION NUMBER: 60/340,170
PRIOR FILING DATE: 2001-12-07
NUMBER OF SEQ ID NOS: 71
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 27
LENGTH: 4834
TYPE: PRT
ORGANISM: Homo sapiens
US-10-097-534-27

Query Match          59.0%; Score 36; DB 15; Length 4834;
Best local similarity 50.0%; Pctd. No. 1.8e+03;
Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY      1 CRDREYKADG 10
Db      349 CRKDAPHSEG 358

RESULT 28
US-09-934-455-200
; Sequence 200, Application US/09934455
; Publication No. US20030121070A1
GENERAL INFORMATION:
APPLICANT: Adam, Luc
APPLICANT: Creelman, Robert
APPLICANT: Dubell, Arnold
APPLICANT: Heard, Jacqueline
APPLICANT: Jiang, Cai-Zhong
APPLICANT: Keddie, James
APPLICANT: Pilgrim, Marsha
APPLICANT: Ratcliffe, Oliver
APPLICANT: Reuber, Lynne
APPLICANT: Riechmann, Jose Luis
APPLICANT: Yu, Guo-Iiang
APPLICANT: Pineda, Omaira
TITLE OF INVENTION: Genes for Modifying Plant Traits IV
FILE REFERENCE: MBI-0025
CURRENT FILING DATE: 2001-08-22
CURRENT APPLICATION NUMBER: US/09/934,455
PRIOR FILING DATE: 2001-08-22
PRIOR APPLICATION NUMBER: 60/227439
PRIOR FILING DATE: 2000-08-22
PRIOR APPLICATION NUMBER: MBI-0022
PRIOR FILING DATE: 2001-11-16
PRIOR APPLICATION NUMBER: MBI-0023
PRIOR FILING DATE: 2001-04-17
NUMBER OF SEQ ID NOS: 516
SOFTWARE: PatentIn version 3.1
SEQ ID NO 200
LENGTH: 280
TYPE: PRT
ORGANISM: Arabidopsis thaliana
US-09-934-455-200

```

```

Query Match      58.2%; Score 35.5; DB 11; Length 280;
Best Local Similarity 63.6%; Pred. No. 1.2e+02;
Matches 7; Conservative 0; Mismatches 3; Indels 1; Gaps 1.

OY      1 CRDP-PPVADG 10
      |||||
Db      194 CRDTPPYVADG 204

RESULT 29
US-10-233-926-14
: Sequence 14, Application US/10233926
: Publication No. US20030131382A1
: GENERAL INFORMATION:
: APPLICANT: Allen, Stephen M.
: APPLICANT: Kinney, Anthony J.
: APPLICANT: Falco, S. Carl
: TITLE OF INVENTION: PLANT CHOLINE PHOSPHATE CYTIDYLTRANSFERASE
: FILE REFERENCE: BB1419 US NA
: CURRENT FILING DATE: 2002-09-03
: PRIOR APPLICATION NUMBER: US/09/735,846
: PRIOR FILING DATE: 2000-12-13
: NUMBER OF SEQ ID NOS: 25
: SOFTWARE: Microsoft Office 97
: SEQ ID NO 14
: LENGTH: 328
: TYPE: PRT
: ORGANISM: Zea mays
US-10-233-926-14

Query Match      58.2%; Score 35.5; DB 16; Length 328;
Best Local Similarity 72.7%; Pred. No. 1.4e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 3; Gaps 1;

OY      3 DRP--YADG 10
      |||||
Db      72 DRPVRVYVADG 82

RESULT 30
US-09-216-393-62
: Sequence 62, Application US/09216393
: Patent No. US2001001447A1
: GENERAL INFORMATION:
: APPLICANT: Milhausen, Michael James
: TITLE OF INVENTION: TOXOPLASMA GONDII PROTEINS, NUCLEIC ACID MOLECULES, AND
: FILE REFERENCE: TX-1-C2
: CURRENT FILING DATE: US/09/216,393
: EARLIER APPLICATION NUMBER: 1998-12-18
: EARLIER FILING DATE: 1997-12-19
: NUMBER OF SEQ ID NOS: 364
: SOFTWARE: Patentin Ver. 2.0
: SEQ ID NO 62
: LENGTH: 129
: TYPE: PRT
: ORGANISM: Toxoplasma gondii
US-09-216-393-62

Query Match      57.4%; Score 35; DB 9; Length 129;
Best Local Similarity 60.0%; Pred. No. 66;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY      1 CRDP-PPVADG 10
      |||||
Db      112 CRDRELASG 121

Search completed: August 29, 2003, 18:47:47
Job time : 17.7143 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 29, 2003, 18:44:06 ; Search time 10.2857 Seconds

(without alignments)
93.457 Million cell updates/sec

Title: US-09-830-876-2

Perfect score: 61

Sequence: 1 CRDDPRYADG 10

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

1: PIR_76:*

2: PIR2:*

3: PIR3:*

4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Query Length	DB ID	Description
1	61	100	0	ALBHR	alpha-amylose (BC
2	56	91	8	JR0406	alpha-amylose (BC
3	44	72	1	S10514	alpha-amylose (BC
4	44	72	1	S07040	alpha-amylose (BC
5	44	72	1	ALBHR	alpha-amylose (BC
6	41.5	68	0	S10013	alpha-amylose (BC
7	41.5	68	0	S12775	alpha-amylose (BC
8	41	67	2	S04123	hypothetical prote
9	41	67	2	B93345	hypothetical prote
10	41	67	2	T09942	probable chitinase
11	41	67	2	T09942	alpha-amylose (BC
12	41	67	2	T24216	chromosome condens
13	40	65	6	AE0281	two-component regu
14	40	65	6	J01527	alpha-amylose (BC
15	40	65	6	S19990	hypothetical prote
16	39	63	9	H70971	hypothetical prote
17	39	63	9	AB7358	hypothetical prote
18	38	62	3	J01648	30S ribosomal prot
19	38	62	3	AB7358	SHL2 protein - hum
20	38	62	3	T43962	hypothetical prote
21	38	62	3	T44151	hypothetical prote
22	38	62	3	S12625	alpha-amylose (BC
23	38	62	3	S71804	receptor-like facto
24	37	60	7	A26311	nerve growth facto
25	37	60	7	253 1	orfi 3' of bah - St
26	37	60	7	T11610	probable cinnamyl-
27	37	60	7	T29442	hypothetical prote
28	37	60	7	F87317	hypothetical prote
29	37	60	7	S71008	propionyl-CoA carb

30	36	59.0	237	2	C84976	tRNA (guanine-N1-)
31	36	59.0	246	2	C64054	tRNA (guanine-N1-)
32	36	59.0	256	2	A10399	tRNA (guanine-N1-)
33	36	59.0	255	1	XYECG1	tRNA (guanine-N1-)
34	36	59.0	255	2	S37175	tRNA (guanine-N1-)
35	36	59.0	255	2	B85907	tRNA (guanine-N1-)
36	36	59.0	255	2	F91062	tRNA (guanine-N1-)
37	36	59.0	255	2	AF0833	tRNA (guanine-N1-)
38	36	59.0	282	2	T35294	probable endo alpha
39	36	59.0	423	2	T15350	hypothetical protei
40	36	59.0	440	2	S14958	alpha-amyrase (EC
41	36	59.0	440	2	H87233	probable secreted
42	36	59.0	1123	2	T19713	hypothetical protei
43	35.5	58.2	206	2	T19501	probable transcrip
44	35.5	58.2	280	2	T49901	probable transcrip
45	35.5	58.2	764	2	A72394	alpha-xylosidase -
46	35	57.4	85	2	F69933	hypothetical protei
47	35	57.4	153	2	T31701	ubiquitin-conjugat
48	35	57.4	165	2	S28951	neutroal growth-re
49	35	57.4	196	2	E84638	neutroal RS2p22 sp
50	35	57.4	226	2	A26964	neutroal growth-re
51	35	57.4	227	2	A29800	neutroal growth-re
52	35	57.4	295	2	S44973	lmbd protein - Str
53	35	57.4	362	2	S70675	bpld protein - Bor
54	35	57.4	443	2	T08905	hypothetical protei
55	35	57.4	469	2	T36441	hypothetical protei
56	35	57.4	553	2	T36441	probable alkaline
57	35	57.4	579	2	A84227	hypothetical protei
58	35	57.4	659	2	S36551	el protein - human
59	34.5	56.6	191	2	T35949	hypothetical protei
60	34	55.7	164	2	T35949	methyiated-DNA-lp
61	34	55.7	172	2	T34464	hypothetical protei
62	34	55.7	235	2	T34464	nerve growth fact
63	34	55.7	260	2	AE0746	urosporophylogen-E
64	34	55.7	309	2	AE0746	motility protein E
65	34	55.7	315	2	T74480	conserved hypothea
66	34	55.7	332	2	T51259	hypothetical protei
67	34	55.7	336	2	T30281	occlusion-derived
68	34	55.7	393	2	S34591	BDI protein - yeast
69	34	55.7	435	2	UC7157	alpha-amyrase (EC
70	34	55.7	494	2	AD3235	1-sorbose dehydrog
71	34	55.7	513	2	T30793	A-type inclusion b
72	34	55.7	545	2	AH2430	CTP synthase (lim
73	34	55.7	548	2	CH4352	Lysyl-tRNA synthet
74	34	55.7	661	2	F90360	hypothetical protei
75	34	55.7	704	2	T31227	tRNA protein homol
76	34	55.7	705	2	S51396	glycogen(starch) s
77	34	55.7	759	2	F70539	probable 5-methylit
78	34	55.7	760	2	CH7029	hypothetical protei
79	34	55.7	1007	2	H72734	hypothetical protei
80	34	55.7	1166	2	F96598	protein F20N2.4 [J
81	33.5	54.9	175	2	F73545	hypothetical protei
82	33	54.1	109	2	CH4357	hypothetical protei
83	33	54.1	123	2	S30532	ig heavy chain V r
84	33	54.1	198	2	AE0161	probable permease
85	33	54.1	208	2	H61254	30S ribosomal prot
86	33	54.1	224	2	E72704	hypothetical protei
87	33	54.1	224	2	A65394	hypothetical protei
88	33	54.1	228	2	S38382	SEB4 protein - hu
89	33	54.1	229	2	S38383	SEB4 protein - hu
90	33	54.1	237	2	S38384	SEB4 protein - hu
91	33	54.1	244	2	T15647	hypothetical protei
92	33	54.1	247	2	CH82307	tRNA (guanine-N1-)
93	33	54.1	247	2	T17677	hypothetical protei
94	33	54.1	248	2	T33034	hypothetical protei
95	33	54.1	272	2	H86153	probable chitinase
96	33	54.1	283	2	G36979	uncaracterized pr
97	33	54.1	306	2	UC4347	urotophylin-III C
98	33	54.1	308	1	CE08CB	chemotaxis protein
99	33	54.1	308	2	G39953	chemotaxis protein
100	33	54.1	308	2	CH5802	hypothetical protei

ALIGNMENTS

RESULT 1

ALBHB

alpha-amylase (EC 3.2.1.1) B precursor 6-4 - barley
N:Alternate names: 1,4-alpha-D-glucan glucanohydrolase; alpha-amylase 2

C:Species: Hordeum vulgare (barley)

C>Date: 30-Jun-1987 #sequence_revision 01-Sep-1995 #text_change 18-Jun-1999

C:Accession: A11960; A00847; J0405; A26267; A24457; A30759

R:Khurshed, B.; Rogers, J.C.

J: Biol. Chem. 263, 18953-18960, 1988

A:Title: Barley alpha-amylase genes. Quantitative comparison of steady-state mRNA levels

A:Reference number: A92700; MUID:8906691; PMID:3264283

A:Accession: A11960

A:Molecule type: DNA

A:Residues: 1-427 <KHU>

A:Cross-references: GB:J04262

A:Experimental source: cv. Himalaya; gene Amy6-4

R:Rogers, J.C.

J: Biol. Chem. 260, 3731-3738, 1985

A:Title: Two barley alpha-amylase gene families are regulated differently in aleurone cell

A:Reference number: A00847; MUID:85131184; PMID:3871776

A:Accession: A00847

A:Molecule type: mRNA

A:Residues: 1-133,'D',135-194,'HRL',198-424,'Q',426-427 <ROG>

A:Experimental source: seed

R:Rahmatullah, R.J.; Huang, J.K.; Clark, K.L.; Reeck, G.R.; Chandra, G.R.; Muthukrishnan

Plant Mol. Biol. 12, 119-121, 1989

A:Title: Nucleotide and predicted amino acid sequences of two different genes for high-T

A:Reference number: J0405

A:Accession: J0405

A:Molecule type: DNA

A:Residues: 1-133,'D',135-424,'Q',426-427 <RAH>

A:Cross-references: EMBL:X15226; NID:q18894; PDB:CAA33299.1; PID:q295804

A:Experimental source: gene Amy152

R:Chandler, P.M.; Zwart, J.A.; Jacobsen, J.V.; Haggins, T.J.V.; Ingalls, A.S.

Plant Mol. Biol. 3, 407-418, 1984

A:Title: The effects of gibberellic acid and abscisic acid on alpha-amylase mRNA levels

A:Reference number: A26267

A:Accession: A26267

A:Molecule type: mRNA

A:Residues: 1-133,'V',135-184,'A',186-366,'GA' <CHM>

A:Experimental source: cv. Himalaya

A>Note: The authors translated the codon GTC for residue 134 as Gly

R:Svensson, B.; Mundy, J.; Gibson, R.M.; Svendsen, I.

Carlsberg Res. Commun. 50, 15-22, 1985

A:Title: Partial amino acid sequences of alpha-amylase isozymes from barley malt.

A:Reference number: A24457

A:Accession: A24457

A:Molecule type: protein

A:Residues: 25-59,'X',61-67,'HX',70-85,'X',87-92,'E',94,146-165,228-251,297-303,'X',305-

C:Comment: The mRNA of this isozyme (B) is present at very low levels in unstimulated al-

ed by the embryo during germination.

C:Genetics:

A:Gene: Amy2-2

A:Map position: 6

A:Introns: 29/3; 344/3

A>Note: multigene family on chromosome 6 encodes type B alpha-amylases; type A alpha-amyl

C:Function:

A:Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds

A:Pathway: glycogen/starch degradation

C:Superfamily: wheat alpha-amylase; alpha-amylase core homology

C:Keywords: aleurone cell; blocked amino end; calcium binding; germination; glycosidase;

F:1-24/Domain: signal sequence #status predicted <SIG>

F:25-427/Product: alpha-amylase #status experimental <MAT>

F:170-316/Domain: alpha-amylase core homology <AMY>

F:25/Modified site: blocked amino end (Gln) (in mature form) (probably pyrrolidone carb

F:203,228,313/Active site: Asp, Glu, Asp #status predicted

Query Match 100.0%; Score 61; DB 1; Length 427;

Best Local Similarity 100.0%; Pred. No. 0.0011; Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRDDPRYADG 10

Db 148 CRDDPRYADG 157

RESULT 2

J0406

alpha-amylase (EC 3.2.1.1) B precursor (gene Amy56 and others) - barley

N:Alternate names: 1,4-alpha-D-glucan glucanohydrolase

C:Species: Hordeum vulgare (barley)

C>Date: 17-Apr-1993 #sequence_revision 21-Jan-1997 #text_change 18-Jun-1999

C:Accession: J0406; B30759; S06275; B31960; B21826

R:Rahmatullah, R.J.; Huang, J.K.; Clark, K.L.; Reeck, G.R.; Chandra, G.R.; Muthukrishnan

Plant Mol. Biol. 12, 119-121, 1989

A:Title: Nucleotide and predicted amino acid sequences of two different genes for hig

A:Reference number: J0405

A:Accession: J0406

A:Molecule type: DNA

A:Residues: 1-429 <RAH>

A:Cross-references: EMBL:X15227; NID:q18899; PDB:CAA33299.1; PID:q295805

A:Experimental source: gene Amy56 for alpha-amylase

A:Genetics: A56

R:Rogers, J.C.

submitted to GenBank, September 1988

A:Reference number: A94535

A:Accession: B30759

A>Status: not compared with conceptual translation

A:Molecule type: DNA

A:Residues: 1-104,'G',106-154,'A',156-160,'PD',163,'G',167-196,'V',198-342,'T',344-39

A:Cross-references: GB:J04202; NID:q166984; PDB:AAA98615.1; PID:q166985

A:Experimental source: cv. Himalaya gene Amy46 for alpha-amylase B

A:Genetics: A46

R:Knox, C.A.P.; Southeyanon, B.; Chandra, G.R.; Muthukrishnan, S.

Plant Mol. Biol. 9, 3-17, 1987

A:Title: Structure and organization of two divergent alpha-amylase genes from barley.

A:Reference number: S06275

A:Accession: S06275

A:Molecule type: DNA

A:Residues: 1-11,'L',14-32,'S',34-57,'T',59-79,'Y',81-139,'R',141-160,'PA',163-164,'

A:Cross-references: EMBL:M17125; NID:q166978; PDB:AAA32926.1; PID:q166979

A:Experimental source: cv. Sundance gene for alpha-amylase 1 precursor (clone p141.11

A:Genetics: A41

A>Note: the authors translated the codon TCG for residue 33 as Trp

R:Khurshed, B.; Rogers, J.C.

J: Biol. Chem. 263, 18953-18960, 1988

A:Title: Barley alpha-amylase genes. Quantitative comparison of steady-state mRNA lev

A:Reference number: A92700; MUID:8906691; PMID:3264283

A:Accession: B31960

A>Status: not compared with conceptual translation

A:Molecule type: DNA

A:Residues: 1-51 <KHU>

A:Experimental source: strain Himalaya gene Amy46 for alpha-amylase B precursor

R:Huang, J.K.; Sweigle, M.; Dandekar, A.M.; Muthukrishnan, S.

J. Mol. Appl. Genet. 2, 579-588, 1984

A:Reference number: A92837; MUID:85159405; PMID:6335720

A:Accession: B21826

A:Molecule type: mRNA

A:Residues: 379-389,'T',391-392,'D',394-429 <HUA>

A:Cross-references: GB:K02636; NID:q166992; PDB:AAA22932.1; PID:q166993

A:Experimental source: cv. Himalaya aleurone cell mRNA (clone 96 for alpha-amylase B)

C:Genetics: <A56>

A:Gene: Amy56

A:Introns: 29/3; 346/3

C:Genetics: <A46>

A:Gene: Amy46

C:Genetics: <A41>

A:Gene: Amy1

A:Map position: 6

A:Introns: 29/3; 346/3

C:Function:

A:Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds

A:Pathway: glycogen/starch degradation

C:Superfamily: wheat alpha-amylase; alpha-amylase core homology
 C:Keywords: aleurone cell; germination; glycosidase; hydrolase; polysaccharide degradat
 F:172-318/Domain: alpha-amylase core homology <AMT>
 F:205,230,315/Active site: Asp, Glu, Asp #status predicted

Query Match 91.8%; Score 56; DB 1; Length 429;
 Best Local Similarity 90.0%; Pred. No. 0.0096; Indels 0; Gaps 0;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 CRDDRPYADG 10
 148 CRDDRPYDGS 157

RESULT 3

alpha-amylase (EC 3.2.1.1) precursor - black gram
 S10514
 C:Species: Vigna mungo (black gram)
 C:Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 22-Jun-1999
 C:Accession: S10514; S61336; S40201; S61334
 R:Yamauchi, D.; Minamikawa, T.
 Nucleic Acids Res. 18, 4250, 1990
 A:Title: Nucleotide sequence of cDNA for alpha-amylase from cotyledons of germinating Vi
 A:Reference number: S10514; MUID:90332425; PMID:2377468
 A:Accession: S10514
 A:Molecule type: mRNA
 A:Residues: 1-421 <YAM>
 A:Cross-references: EMBL:X53049; NID:g22059; PIDN:CAA37217.1; PID:g22060
 A:Accession: S61336
 A:Molecule type: protein
 A:Residues: 24-31 <YAM>
 R:Yamauchi, H.; Yamauchi, D.; Wada, S.; Minamikawa, T.
 submitted to the EMBL Data Library, June 1993
 A:Description: Nucleotide sequence of the alpha-amylase gene from Vigna mungo.
 A:Reference number: S40201
 A:Accession: S40201
 A:Molecule type: DNA
 A:Residues: 1-421 <YAM>
 A:Cross-references: EMBL:X73301; NID:g437944; PIDN:CAA31734.1; PID:g437945
 C:Genetic references: EMBL:X73301; NID:g437944; PIDN:CAA31734.1; PID:g437945
 A:Insertions: 28/3; 72/1; 340/3
 C:Function:
 A:Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
 A:Pathway: glycogen/starch degradation
 C:Superfamily: wheat alpha-amylase; alpha-amylase core homology
 C:Keywords: glycosidase; hydrolase; polysaccharide degradation; seed
 F:1-23/Domain: signal sequence #status predicted <SIG>
 F:24-421/Product: alpha-amylase #status experimental <AMT>
 F:168-312/Domain: alpha-amylase core homology <AMT>
 F:201,226,309/Active site: Asp, Glu, Asp #status predicted

Query Match 72.1%; Score 44; DB 2; Length 421;
 Best Local Similarity 70.0%; Pred. No. 1.8;
 Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 1 CRDDRPYADG 10
 146 CRDDRPYDGS 155

RESULT 4

alpha-amylase (EC 3.2.1.1) 2 precursor (clone p155.3) - barley
 S07040
 C:Species: Hordeum vulgare (barley)
 C:Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 22-Jun-1999
 C:Accession: S07040
 R:Knorr, C.A.P.; Sonthayanon, B.; Chandra, G.R.; Muthukrishnan, S.
 Plant Mol Biol. 9, 3-17, 1987
 A:Title: Structure and organization of two divergent alpha-amylase genes from barley.
 A:Reference number: S06275
 A:Accession: S07040
 A:Molecule type: DNA
 A:Residues: 1-437 <KNO>

A:Cross-references: EMBL:M17127; NID:g166982; PIDN:AAA32928.1; PID:g166983
 C:Genetics:
 A:Gene: amy2
 A:Map position: 1
 A:Insertions: 29/3; 74/1; 345/3
 C:Function:
 A:Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
 A:Pathway: glycogen/starch degradation
 C:Superfamily: wheat alpha-amylase; alpha-amylase core homology
 C:Keywords: glycosidase; hydrolase; polysaccharide degradation
 F:170-317/Domain: alpha-amylase core homology <AMT>
 F:203,228,314/Active site: Asp, Glu, Asp #status predicted

Query Match 72.1%; Score 44; DB 2; Length 437;
 Best Local Similarity 70.0%; Pred. No. 1.8;
 Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 1 CRDDRPYADG 10
 148 CRDDRPYDGS 157

RESULT 5

alpha-amylase (EC 3.2.1.1) precursor - barley
 S10013
 C:Species: Hordeum vulgare (barley)
 C:Date: 03-Aug-1984 #sequence_revision 03-Aug-1984 #text_change 18-Jun-1999
 C:Accession: A00846; S65602
 R:Rogers, J.C.; Millman, C.
 J. Biol. Chem. 258, 8169-8174, 1983
 A:Title: Isolation and sequence analysis of a barley alpha-amylase cDNA clone.
 A:Reference number: A00846; MUID:83238423; PMID:6150808
 A:Accession: A00846
 A:Molecule type: mRNA
 A:Residues: 1-438 <ROG>
 A:Cross-references: GB:J01236; NID:g166986; PIDN:AAA32929.1; PID:g166987
 R:Yamauchi, H.; Yamauchi, D.; Wada, S.; Minamikawa, T.
 submitted to the EMBL Data Library, June 1993
 A:Description: Nucleotide sequence of the alpha-amylase gene from Vigna mungo.
 A:Reference number: S40201
 A:Accession: S40201
 A:Molecule type: DNA
 A:Residues: 1-421 <YAM>
 A:Cross-references: EMBL:X73301; NID:g437944; PIDN:CAA31734.1; PID:g437945
 C:Genetic references: EMBL:X73301; NID:g437944; PIDN:CAA31734.1; PID:g437945
 A:Insertions: 28/3; 72/1; 340/3
 C:Function:
 A:Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
 A:Pathway: glycogen/starch degradation
 C:Superfamily: wheat alpha-amylase; alpha-amylase core homology
 C:Keywords: glycosidase; hydrolase; polysaccharide degradation
 F:1-24/Domain: signal sequence #status predicted <SIG>
 F:25-438/Product: alpha-amylase #status experimental <AMT>
 F:171-316/Domain: alpha-amylase core homology <AMT>
 F:204,229,315/Active site: Asp, Glu, Asp #status experimental

Query Match 72.1%; Score 44; DB 1; Length 438;
 Best Local Similarity 70.0%; Pred. No. 1.8;
 Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 1 CRDDRPYADG 10
 149 CRDDRPYDGS 158

RESULT 6

alpha-amylase (EC 3.2.1.1) 1 precursor (clone lambda-OSq2) - rice
 S10013
 C:Species: Oryza sativa (rice)
 C:Date: 21-Nov-1993 #sequence_revision 17-Nov-1995 #text_change 22-Jun-1999
 C:Accession: S10013
 R:Huang, N.; Sutcliffe, T.D.; Lites, J.C.; Rodriguez, R.L.
 Plant Mol Biol. 14, 655-668, 1990
 A:Title: Classification and characterization of the rice alpha-amylase multigene faml

A:Reference number: S10013; MUID:91346657; PMID:2102847
 A:Accession: S10013
 A:Molecule type: DNA
 A:Residues: 1-428 <HQA>
 A:Cross-references: EMBL:X16509; NID:920166; PIDN:CAA34516.1; PID:920167
 A:Experimental source: var. M202
 C:Genetics:
 A:Introns: 30/3; 75/1; 345/3
 C:Function:
 A:Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
 A:Pathway: glycogen/starch degradation
 C:Superfamily: wheat alpha-amylase; alpha-amylase core homology
 C:Keywords: glycosidase; hydrolase; polysaccharide degradation
 F:170-317/Domain: alpha-amylase core homology <AMT>

Query Match
 Best Local Similarity 68.0%; Score 41.5; DB 2; Length 428;
 Matches 8; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

OY 1 CRDDRPYADG 10
 |||||
 Db 149 CRDD-PYGDG 157

RESULT 7
 S12775
 alpha-amylase (EC 3.2.1.1) precursor (clone POS103) - rice
 C:Species: Oryza sativa (rice)
 C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 22-Jun-1999
 C:Accession: S12775
 R:O'Neill, S.D.; Kumagai, M.H.; Majumdar, A.; Huang, N.; Sutcliffe, T.D.; Rodriguez, R.L.
 Mol. Gen. Genet. 221, 235-244, 1990
 A:Title: The alpha-amylase genes in Oryza sativa: characterization of cDNA clones and m
 A:Reference number: S12775; MUID:90318322; PMID:2370848
 A:Accession: S12775
 A:Molecule type: mRNA
 A:Residues: 1-434 <ONE>
 A:Cross-references: EMBL:M24286; NID:9169752; PIDN:AAA33885.1; PID:9169753
 C:Function:
 A:Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
 A:Pathway: glycogen/starch degradation
 C:Superfamily: wheat alpha-amylase; alpha-amylase core homology
 C:Keywords: glycosidase; hydrolase; polysaccharide degradation
 F:176-323/Domain: alpha-amylase core homology <AMY>
 F:209,234,320/Active site: Asp, Glu, Asp #status predicted

Query Match
 Best Local Similarity 68.0%; Score 41.5; DB 2; Length 434;
 Matches 8; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

OY 1 CRDDRPYADG 10
 |||||
 Db 155 CRDD-PYGDG 163

RESULT 8
 S04123
 hypothetical protein 151 - Rhizobium meliloti
 C:Species: Rhizobium meliloti
 C:Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 08-Oct-1999
 C:Accession: S04123; S32840; S39987
 R:Batut, J.; Davearan-Mingot, M.L.; David, M.; Jacobs, J.; Garnerone, A.M.; Kahn, D.
 EMBO J. 8, 1279-1286, 1989
 A:Title: flxK, a gene homologous with fnr and cnp from Escherichia coli, regulates nitro
 A:Reference number: S04122; MUID:89305532; PMID:2663474
 A:Accession: S04123
 A:Molecule type: DNA
 A:Residues: 1-151 <BAT>
 A:Cross-references: EMBL:X15079; NID:948690; PIDN:CAA33184.1; PID:948692
 R:Kahn, D.D.
 submitted to the EMBL data library, March 1993
 A:Reference number: S32837
 A:Accession: S32840

A:Molecule type: DNA
 A:Residues: 1-151 <KAR>
 A:Cross-references: EMBL:Z21854; NID:949403; PIDN:CAA79900.1; PID:949407

Query Match
 Best Local Similarity 67.2%; Score 41; DB 2; Length 151;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 CRDDRPY 7
 |||||
 Db 26 CRDDPY 32

RESULT 9
 B95345
 hypothetical protein Sma1223 [imported] - Sinorhizobium meliloti (strain 1021) magap1
 C:Species: Sinorhizobium meliloti
 C:Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 30-Sep-2001
 C:Accession: B95345
 R:Barnett, M.J.; Fisher, R.F.; Jones, T.; Komp, C.; Abola, A.P.; Barloy-Hubler, F.; B
 .; Kalman, S.; Keating, D.H.; Palm, C.; Beck, M.C.; Surzycki, R.; Wells, D.H.; Yen, K
 .; Proc. Natl. Acad. Sci. U.S.A. 98, 9883-9888, 2001
 A:Title: Nucleotide sequence and predicted functions of the entire Sinorhizobium meli
 A:Reference number: A95262; MUID:21396509; PMID:11481432
 A:Accession: B95345
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-151 <KUR>
 A:Cross-references: GB:AEO06469; PIDN:AAK65324.1; PID:914523781; GSPDB:GN00165
 A:Experimental source: strain 1021, megaplasmid pSymA
 R:Galibert, F.; Finan, T.M.; Long, S.R.; Publer, A.; Abola, P.; Ampe, F.; Barloy-Hub
 pella, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.
 L.; Hyman, R.W.; Jones, T.
 Science 293, 668-672, 2001
 A:Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelau
 hebaull, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh,
 A:Title: The composite genome of the legume symbiont Sinorhizobium meliloti.
 A:Reference number: A96039; MUID:21368234; PMID:11474104
 A:Contents: annotation
 C:Genetics:
 A:Gene: Sma1223
 A:Genome: plasmid

Query Match
 Best Local Similarity 67.2%; Score 41; DB 2; Length 151;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 CRDDRPY 7
 |||||
 Db 26 CRDDPY 32

RESULT 10
 T03440
 probable chitinase (EC 3.2.1.14) - rice (fragment)
 C:Species: Oryza sativa (rice)
 C:Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 21-Jan-2000
 C:Accession: T03440
 R:Yun, C.H.; Lee, M.C.; Lee, J.S.; Yun, K.J.; Eun, M.Y.
 submitted to the EMBL Data Library, April 1997
 A:Description: isolation and characterization of a rice chitinase cDNA clone from ric
 A:Reference number: Z14947
 A:Accession: T03440
 A>Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-278 <YUN>
 A:Cross-references: EMBL:AF001501; NID:92109456; PID:92109457
 A:Experimental source: cv. IR36
 C:Superfamily: plant chitinase; plant chitinase homology
 C:Keywords: glycosidase; hydrolase; polysaccharide degradation
 F:54-276/Domain: plant chitinase homology <PCH>

Query Match
 Best Local Similarity 67.2%; Score 41; DB 2; Length 278;

Best Local Similarity 60.0%; Pred. No. 4.3;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 CRDPRYADG 10
|||||
DB 269 CRDCKPYGGG 278

RESULT 11

T09942
alpha-amylase (EC 3.2.1.1) precursor - southern Asian dodder (fragment)
N:Alternate names: alpha-1,4-glucan-4-glucanohydrolase
C:Species: Cuscuta reflexa (southern Asian dodder)
C>Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 21-Jan-2000
C:Accession: T09942
R:Ramachandiran, S.; Srinivasa, B.; Mahadevan, S.
Submitted to the EMBL Data Library, February 1994
A:Description: Molecular cloning and nucleotide sequence of detachment induced alpha amy
A:Reference number: 216900
A:Accession: T09942
A>Status: Preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-423 <RAM>
A:Cross-references: EMBL:U06754; NID:g458455; PID:g458456
A:Genetics:
A:Gene: AMY2
C:Function:
A:Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
C:Superfamily: wheat alpha-amylase; alpha-amylase core homology
C:Keywords: glycosidase; hydrolase; polysaccharide degradation
F:165-309/Domain: alpha-amylase core homology <AMY>

Query Match 67.2%; Score 41; DB 2; Length 423;
Best Local Similarity 60.0%; Pred. No. 6.6;

Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 CRDPRYADG 10
|||||
DB 143 CRDPTQISDG 152

RESULT 12

T4216
Chromosome condensation protein homolog Dpy-27 - Caenorhabditis elegans
N:Alternate names: protein R13G10.1
C:Species: Caenorhabditis elegans
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 02-Jun-2000
C:Accession: T4216; A55095
R:Gardner, A.
Submitted to the EMBL Data Library, August 1994
A:Reference number: 219857
A:Accession: T4216
A>Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1469 <NLL>
A:Cross-references: EMBL:Z35602; PIDN:CAA84669.1; GSPDB:GN00021; CESP:R13G10.1
A:Experimental source: clone R13G10
R:Chuang, P.T.; Albertson, D.G.; Meyer, B.J.
Cell 79, 459-474, 1994
A:Title: Dpy-27: a chromosome condensation protein homolog that regulates Caenorhabditis
A:Reference number: A55095; MUID:95042743; PMID:7954812
A:Accession: A55095
A>Status: Preliminary; nucleic acid sequence not shown
A:Molecule type: DNA
A:Residues: 1-1132; C: 1134-1469 <CHD>
A:Cross-references: GB:J35274; NID:9529384; PIDN:AAA62647.1; PID:9529385
A:Note: authors translated the codon GAT for residue 1133 as GAT
C:Genetics:
A:Gene: CESP:R13G10.1
A:Map position: 3
A:Introns: 142/3; 176/3; 296/2; 548/2; 627/3; 697/2; 847/3; 993/3; 1086/2; 1202/3; 1383/
C:Superfamily: chromosome segregation protein SMCI

Query Match 67.2%; Score 41; DB 2; Length 1469;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 DDRPYAD 9
|||||
DB 13 DDRPYAD 19

RESULT 13

AE0281
two-component regulatory system, response regulator protein rsta [Imported] - Yersinia
C:Species: Yersinia pestis
C>Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Nov-2001
R:Parkhill, J.; Wren, B.W.; Thomson, N.R.; Tiltball, R.W.; Holden, M.T.G.; Prentice, M.
deno-Parraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.
11, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrel
Nature 413, 523-527, 2001
A:Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A:Reference number: AB0001; MUID:21470413; PMID:11586360
A:Accession: AE0281
A>Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-248 <YUR>
A:Cross-references: GB:AL590842; PIDN:CA91113.1; PID:g15980304; GSPDB:GN00175
C:Genetics:
A:Gene: rsta
C:Superfamily: ompr protein; response regulator homology

Query Match 65.6%; Score 40; DB 2; Length 248;
Best Local Similarity 70.0%; Pred. No. 6;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 CRDPRYADG 10
|||||
DB 64 CRDPRYADG 73

RESULT 14

JQ1527
alpha-amylase (EC 3.2.1.1) 2A - rice
C:Species: Oryza sativa (rice)
C>Date: 17-Aug-1992 #sequence_revision 17-Aug-1992 #text_change 22-Jun-1999
C:Accession: JQ1527
R:Huang, N.; Reihl, S.J.; Rodriguez, R.L.
Gene 111, 223-228, 1992
A:Title: Rany2A: a novel alpha-amylase-encoding gene in rice.
A:Reference number: JQ1527; MUID:92175526; PMID:1541400
A:Accession: JQ1527
A:Molecule type: DNA
A:Residues: 1-443 <HUA>
A:Cross-references: GB:M74177; NID:g169768; PIDN:AAA33894.1; PID:g169769
C:Comment: Rice alpha-amylases are encoded by three multigene families, Amy1, Amy2
C:Genetics:
A:Gene: RANY2A
A:Introns: 27/3; 71/1; 345/3
A:Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
A:Pathway: glycogen/starch degradation
C:Superfamily: wheat alpha-amylase; alpha-amylase core homology
C:Keywords: glycosidase; hydrolase; polysaccharide degradation
F:108-311/Domain: alpha-amylase core homology <AMY>
F:202,228,314/Active site: Asp, Glu, Asp #status predicted

Query Match 65.6%; Score 40; DB 2; Length 443;
Best Local Similarity 60.0%; Pred. No. 11;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 CRDPRYADG 10
|||||
DB 146 CRDPTQISDG 155

RESULT 15
S19990
alpha-amylase (EC 3.2.1.1) - rice
C:Species: Oryza sativa (rice)
C>Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 22-Jun-1999
C:Accession: S19990
R:Goldman, S.; Mawal, Y.; Wu, R.
submitted to the EMBL Data Library, February 1992
A:Reference number: S19990
A:Accession: S19990
A:Molecule type: mRNA
A:Residues: 1-445 <GOL>
A:Cross-references: EMBL:X64619; NID:g20172; PIDN:CAA45903.1; PID:g20173
C:Function:
A:Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
A:Pathway: glycogen/starch degradation
C:Superfamily: wheat alpha-amylase; alpha-amylase core homology
C:Keywords: glycosidase; hydrolase; polysaccharide degradation
F:168-317/domain: alpha-amylase core homology <AMY>
F:202,228,314/Active site: Asp, Glu, Asp #status predicted

Query Match 65.6%; Score 40; DB 2; Length 445;
Best Local Similarity 60.0%; Pred. No. 11;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 1 CRDDPYADG 10
1111 :111
Db 146 CRDDPYADG 155

RESULT 16
H70971
hypothetical protein RV3369 - Mycobacterium tuberculosis (strain H37RV)
C:Species: Mycobacterium tuberculosis
C>Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000
C:Accession: H70971
R:Cole, S.T.; Brosch, R.; Parkhill, J.; Garner, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holtroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, K.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A:Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A:Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
A:Reference number: A70500; MUID:96295987; PMID:9634230
A:Accession: H70971
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-144 <COL>
A:Cross-references: GB:AL009198; GB:AL123456; NID:g3242262; PIDN:CAA15754.1; PID:g266164
A:Experimental source: strain H37RV
C:Genetics:
A:Gene: RV3369
C:Superfamily: Mycobacterium tuberculosis hypothetical protein RV3369

Query Match 63.9%; Score 39; DB 2; Length 144;
Best Local Similarity 85.7%; Pred. No. 5.4;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 CRDDPY 7
1111 11
Db 101 CRDDPY 107

RESULT 17
A87358
hypothetical protein CC0876 [imported] - Caulobacter crescentus
C:Species: Caulobacter crescentus
C>Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 20-Apr-2001
C:Accession: A87358
R:Nierman, W.C.; Felblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.; B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.

Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A:Title: Complete Genome Sequence of *Caulobacter crescentus*.
A:Reference number: A87249; MUID:21173698; PMID:11259647
A:Accession: A87358
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-370 <STO>
A:Cross-references: GB:AE005673; NID:g13422137; PIDN:AAK22861.1; GSPDB:GN00148
C:Genetics:
A:Gene: CC0876

Query Match 63.9%; Score 39; DB 2; Length 370;
Best Local Similarity 77.8%; Pred. No. 14;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 2 RDDRPRADG 10
1111 111
Db 234 RDDRPRADG 242

RESULT 18
AB2711
30S ribosomal protein S6 [imported] - *Agrobacterium tumefaciens* (strain C58, Dupont)
C:Species: *Agrobacterium tumefaciens*
C>Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 18-Nov-2002
C:Accession: AB2711
R:Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chan, L.; Wood, G.E.; Chen, Y.; Woo, erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutayavin, T.; Levy, R.; Li, M.; McCl, science 294, 2317-2323, 2001
A:Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kam ster, E.W.
A:Title: The genome of the Natural Genetic Engineer *Agrobacterium tumefaciens* C58.
A:Reference number: AB2577; MUID:21608550; PMID:11743193
A:Accession: AB2711
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-153 <KUR>
A:Cross-references: GB:AE008688; PIDN:AAI42104.1; PID:g17739486; GSPDB:GN00186
A:Experimental source: strain C58 (Dupont)
C:Genetics:
A:Gene: rpsF
A:Map position: circular chromosome
C:Superfamily: *Escherichia coli* ribosomal protein S6

Query Match 62.3%; Score 38; DB 2; Length 153;
Best Local Similarity 77.8%; Pred. No. 8.8;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 RDDRPRADG 10
1111 11
Db 109 RDDRPRADG 117

RESULT 19
J01648
SHL2 protein - human herpesvirus 6
C:Species: human herpesvirus 6
C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 20-Jun-2000
C:Accession: J01648
R:Efsthion, S.; Lawrence, G.L.; Brown, C.M.; Barrell, B.G.
J. Gen. Virol. 73, 1661-1671, 1992
A:Title: Identification of homologues to the human cytomegalovirus US22 gene family 1
A:Reference number: J01647; MUID:92333249; PMID:1321206
A:Accession: J01648
A:Molecule type: DNA
A:Residues: 1-373 <EPS>
A:Cross-references: DDBJ:D10082; NID:g221456; PIDN:BA00977.1; PID:g221458
A:Experimental source: strain 01102
C:Superfamily: human herpesvirus 6 SHL2 protein

Query Match 62.3%; Score 38; DB 2; Length 373;
Best Local Similarity 66.7%; Pred. No. 21;

Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 CRDPRVAD 9
|||: |||

DB 90 CRDENEYAD 98

RESULT 20

T43962
hypothetical protein U3 [imported] - human herpesvirus 6 (strain HST)
C:Species: human herpesvirus 6
A:Variety: strain HST
C:Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 21-Jul-2000
C:Accession: T43962
R:Issigawa, Y.; Mukai, T.; Nakano, K.; Kagawa, M.; Chen, J.; Mori, Y.; Sunagawa, T.; Kawa
J. Virol. 73, 8053-8063, 1999
A:Title: Comparison of the complete DNA sequences of human herpesvirus 6 variants A and
A:Reference number: 222732; MUID:99412319; PMID:10462554
A:Accession: T43962
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-386 <1386>
A:Cross-references: EMBL:AB021506; NID:g4995977; PIDN:BA18223.1; PID:g4995990
A:Experimental source: strain HST; pop. variant B
C:Genetics:
A:Note: U3
C:Superfamily: human herpesvirus 6 SHL2 protein

Query Match 62.3%; Score 38; DB 2; Length 386;
Best Local Similarity 66.7%; Pred. No. 22;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 CRDPRVAD 9
|||: |||

DB 103 CRDENEYAD 111

RESULT 21

T44151
hypothetical protein U3 [imported] - human herpesvirus 6 (strain Z29)
C:Species: human herpesvirus 6
A:Variety: strain Z29
C:Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 20-Jun-2000
C:Accession: T44151
R:Dominger, G.; Dambaugh, T.R.; Stamey, F.R.; Dewhurst, S.; Inoue, N.; Pellett, P.E.
J. Virol. 73, 8040-8052, 1999
A:Title: Human herpesvirus 6B genome sequence: coding content and comparison with human
A:Reference number: 222734; MUID:99412318; PMID:10462553
A:Accession: T44151
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-386 <DNA>
A:Cross-references: EMBL:AF157706; PIDN:ADA9622.1
A:Experimental source: strain Z29; variant B
C:Genetics:
A:Note: U3
C:Superfamily: human herpesvirus 6 SHL2 protein

Query Match 62.3%; Score 38; DB 2; Length 386;
Best Local Similarity 66.7%; Pred. No. 22;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 CRDPRVAD 9
|||: |||

DB 103 CRDENEYAD 111

RESULT 22

S12625
alpha-amylase (EC 3.2.1.1) 3D - rice
C:Species: Oryza sativa (rice)
C:Date: 04-Dec-1992 #sequence_revision 04-Dec-1992 #text_change 22-Jun-1999
C:Accession: S12625; S12776; S15054; J10945

R:Huang, N.; Koizumi, N.; Reini, S.; Rodriguez, R.L.
Nucleic Acids Res. 18, 7007-7014, 1990
A:Title: Structural organization and differential expression of rice alpha-amylase ge
A:Reference number: J10945; MUID:91088278; PMID:2263460
A:Accession: S12625
A:Molecule type: DNA
A:Residues: 1-435 <HUA>

A:Cross-references: EMBL:M59351; NID:9169770; PIDN:AAA3895.1; PID:9169771
R:O'Neill, S.D.; Kumagai, M.H.; Majumdar, A.; Huang, N.; Sutcliffe, T.D.; Rodriguez, R
Mol. Gen. Genet. 221, 235-244, 1990
A:Title: The alpha-amylase genes in Oryza sativa: characterization of cDNA clones and
A:Reference number: S12775; MUID:90318322; PMID:2370848
A:Accession: S12776
A:Molecule type: mRNA
A:Residues: 1-435 <ONE>
A:Cross-references: EMBL:M24287
R:O'Neill, S.D.; Kumagai, M.H.; Majumdar, A.; Huang, N.; Sutcliffe, T.D.; Rodriguez, R L
submitted to the EMBL Data Library April 1989
A:Description: The alpha-amylase genes in Oryza sativa: Characterization of cDNA clon
A:Reference number: S15054
A:Accession: S15054
A:Molecule type: mRNA
A:Residues: 1-72, 'R', 75-136, 'R', 138-435 <ON2>
A:Cross-references: EMBL:M24287; NID:9169754; PIDN:AAA3886.1; PID:9169755
C:Genetics:
A:Insertions: 30/3; 342/3
C:Function:
A:Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
A:Pathway: glycogen/starch degradation
C:Superfamily: wheat alpha-amylase; alpha-amylase core homology
C:Keywords: glycosidase; hydrolase; polysaccharide degradation
F:170-314/Domain: alpha-amylase core homology <AMY>
F:203,228,311/Active site: Asp, Glu, Asp #status predicted

Query Match 62.3%; Score 38; DB 2; Length 435;
Best Local Similarity 60.0%; Pred. No. 25;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 1 CRDPRVAD 10
|||: |||

DB 148 CSDPTOYSDS 157

RESULT 23

S71804
receptor-like serpentine protein smoothened - fruit fly (Drosophila melanogaster)
C:Species: Drosophila melanogaster
C:Date: 19-Mar-1998 #sequence_revision 17-Apr-1998 #text_change 17-Apr-1998
C:Accession: S71804
R:van den Heuvel, M.; Ingham, P.W.
Nature 382, 547-551, 1996
A:Title: smoothened encodes a receptor-like serpentine protein required for hedgehog
A:Reference number: S71804; MUID:96320560; PMID:8700230
A:Accession: S71804
A:Status: preliminary; nucleic acid sequence not shown; not compared with conceptual
A:Molecule type: mRNA
A:Residues: 1-1024 <VAN>
A:Note: Intron-exon boundaries were confirmed by sequencing fragments of the genomic

Query Match 62.3%; Score 38; DB 2; Length 1024;
Best Local Similarity 66.7%; Pred. No. 158;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 2 RDRPRVAD 10
|||: |||

DB 56 RDKPWFDS 64

RESULT 24

A26311
nerve growth factor beta chain precursor - chicken (fragment)
C:Species: Gallus gallus (chicken)
C:Date: 05-Oct-1988 #sequence_revision 05-Oct-1988 #text_change 21-Jul-2000

C:Accession: A26311; A24857; S00127; S12532
 R:Ebdendal, T.; Larhammar, D.; Persson, H.
 EMBL J. 5, 1483-1487, 1986
 A:Title: Structure and expression of the chicken beta nerve growth factor gene.
 A:Reference number: A26311; MUID:86300646; PMID:3017695
 A:Accession: A26311
 A:Molecule type: mRNA
 A:Residues: 1-243 <EBE>
 C:Cross-references: GB:X04003; NID:963697; PIDN:CAA27633.1; PID:G1334740
 R:Wion, D.; Perret, C.; Frechin, N.; Keller, A.; Behar, G.; Brachet, P.; Auffray, C.
 FEBS Lett. 203, 82-86, 1986
 A:Title: Molecular cloning of the avian beta-nerve growth factor gene: transcription in
 A:Reference number: A24857; MUID:86248129; PMID:3720959
 A:Accession: A24857
 A:Molecule type: DNA
 A:Residues: 118-243 <MIO>
 A:Cross-references: GB:D00010; GB:N00010; GB:X04067; NID:9222840; PIDN:BA00008.1; PID:9
 R:Meier, R.; Becker-Andre, M.; Goetz, R.; Heumann, R.; Shaw, A.; Thoenen, H.
 EMBL J. 5, 1489-1493, 1986
 A:Title: Molecular cloning of bovine and chick nerve growth factor (NGF): delineation of
 A:Reference number: A26312; MUID:86300647; PMID:2427334
 A:Accession: S00127
 A:Status: preliminary; not compared with conceptual translation
 A:Molecule type: DNA
 A:Residues: 121-243 <MET>
 A:Cross-references: GB:M26810; NID:9212446; PIDN:AAA48984.1; PID:9212447
 R:Ibanez, C.F.; Halboeck, F.; Ebdendal, T.; Persson, H.
 EMBL J. 9, 1477-1483, 1990
 A:Title: Structure-function studies of nerve growth factor: functional importance of his
 A:Reference number: S12532; MUID:90228346; PMID:2338722
 A:Accession: S12532
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 126-243 <IBA>
 C:Superfamily: nerve growth factor beta chain
 C:Keywords: growth factor
 F:1-125/Domain: signal sequence #status predicted <SIG>
 F:126-243/Product: nerve growth factor beta chain #status predicted <MAT>
 Query Match 60.7%; Score 37; DB 2; Length 243;
 Best Local Similarity 60.0%; Pred. No. 22;
 Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 OY 1 CRDPRYADG 10
 Db 182 CRDPRVSSG 191
 RESULT 25
 C47031
 orf1 3' of bah - Streptomyces hygroscopicus
 C:Species: Streptomyces hygroscopicus
 C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
 C:Accession: C47031
 R:Raibaud, A.; Zalacain, M.; Holt, T.G.; Tizard, R.; Thompson, C.J.
 J. Bacteriol. 173, 4454-4463, 1991
 A:Title: Nucleotide sequence analysis reveals linked N-acetyl hydrolase, thioesterase, t
 A:Reference number: A47031; MUID:91294191; PMID:2066341
 A:Accession: C47031
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-253 <RAI>
 A:Cross-references: GB:M64783; NID:9153172; PIDN:AAA9278.1; PID:9153174
 A>Note: sequence extracted from NCBI backbone (NCBIN:41300, NCBI:41305)
 C:Superfamily: oleoyl-[acyl-carrier-protein] hydrolase; oleoyl-[acyl-carrier-protein] hy
 F:16-228/Domain: oleoyl-[acyl-carrier-protein] hydrolase homology <ACPh>
 Query Match 60.7%; Score 37; DB 1; Length 253;
 Best Local Similarity 66.7%; Pred. No. 22;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 OY 2 RDDRPRYADG 10

Db 124 KTERPYGDG 132
 RESULT 26
 T11610
 Probable cinnamyl-alcohol dehydrogenase (EC 1.1.1.195) CPRD14 - cowpea
 C:Species: Vigna unguiculata (cowpea)
 C>Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 21-Jul-2000
 C:Accession: T11610
 R:Uchi, S.; Yamaguchi-Shinozaki, K.; Urao, T.; Terao, T.; Shinozaki, K.
 Plant Cell Physiol. 37, 1073-1082, 1996
 A:Title: Novel drought-inducible genes in the highly drought-tolerant cowpea:cloning
 A:Reference number: Z17294; MUID:97185229; PMID:9032963
 A:Accession: T11610
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-325 <UCG>
 A:Cross-references: EMBL:D83971; NID:91854444; PIDN:BA12161.1; PID:91854445
 A:Experimental source: strain IT84S-2246-4
 C:Superfamily: dihydrokaempferol 4-reductase
 C:Keywords: oxidoreductase
 Query Match 60.7%; Score 37; DB 2; Length 325;
 Best Local Similarity 85.7%; Pred. No. 29;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 OY 1 CRDPRY 7
 Db 279 CVDDRPY 285
 RESULT 27
 T29442
 hypothetical protein F08F3.3 - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Dec-2002
 C:Accession: T29442
 R:Blanchard, M.; Bradshaw, H.
 submitted to the EMBL data library, July 1996
 A:Description: The sequence of C. elegans cosmid F08F3.
 A:Reference number: Z20620
 A:Accession: T29442
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-463 <BLA>
 A:Cross-references: EMBL:U64847; PIDN:AAB04874.1; GSPDB:GN00023; CESP:F08F3.3
 A:Experimental source: strain Bristol N2; clone F08F3
 C:Genetics:
 A:Gene: CESP:F08F3.3
 A:Map position: 5
 A:Insertions: 18/3; 167/3; 266/3; 362/2; 442/3
 C:Superfamily: human erythrocyte membrane protein Rhd
 Query Match 60.7%; Score 37; DB 2; Length 463;
 Best Local Similarity 77.8%; Pred. No. 41;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 OY 2 RDDRPRYADG 10
 Db 420 RDDEYYADG 428
 RESULT 28
 F87317
 hypothetical protein CC0551 [imported] - Caulobacter crescentus
 C:Species: Caulobacter crescentus
 C>Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 20-Apr-2001
 C:Accession: F87317
 R:Nierman, W.C.; Feldblum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg,
 B.; Laub, M.T.; Deboy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Ko
 n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C
 Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001

A:Title: Complete Genome Sequence of *Caulobacter crescentus*.
A:Reference number: A87249; MUID:21173698; PMID:11259647
A:Accession: F87317
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1521 (SNC)
A:Cross-references: GB:AF005673; NID:g13421742; PIDN:AAK22538.1; GSPDB:GN00148
C:Genetic: CC0551
A:Gene: CC0551

Query Match 60.7%; Score 37; DB 2; Length 521;
Best Local Similarity 85.7%; Pred. No. 46;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 RODRPA 8
Db 107 KODRPA 113

RESULT 29

S71008
Propionyl-CoA carboxylase beta chain homolog - *Saccharopolyspora erythraea*
C:Species: *Saccharopolyspora erythraea*
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 16-Jun-2000
C:Accession: S71008
R:Donadio, S.; Staver, M.J.; Katz, L.
Mol. Microbiol. 19, 977-984, 1996
A:Title: Erythromycin production in *Saccharopolyspora erythraea* does not require a function
A:Reference number: S71005; MUID:96249691; PMID:8830278
A:Accession: S71008
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-546 <DON>
A:Cross-references: EMBL:X92557; NID:g1177651; PIDN:CAA63310.1; PID:g1177652
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1995
C:Genetics:
A:Gene: pccB
C:Superfamily: propionyl-CoA carboxylase beta chain

Query Match 60.7%; Score 37; DB 1; Length 546;
Best Local Similarity 85.7%; Pred. No. 48;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 DRPYADG 10
Db 87 DRPYDG 93

RESULT 30

C84976
tRNA (guanine-N1)-methyltransferase (EC 2.1.1.31) [imported] - *Buchnera* sp. (strain AP6)
C:Species: *Buchnera* sp.
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 23-Mar-2001
C:Accession: C84976
R:Shigenobu, S.; Watanabe, H.; Hattori, M.; Sakaki, Y.; Ishikawa, H.
Nature 407, 81-86, 2000
A:Title: Genome sequence of the endocellular bacterial symbiont of aphids *Buchnera* sp. A
A:Reference number: A84930; MUID:2045173; PMID:10993077
A:Accession: C84976
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-237 <SNC>
A:Cross-references: GB:AP000398; GSPDB:GN00144
A:Experimental source: strain AP6
C:Genetics:
A:Gene: tmd; BU396
C:Superfamily: tRNA (guanine-N1) methyltransferase
C:Keywords: methyltransferase; S-adenosylmethionine

Query Match 59.0%; Score 36; DB 2; Length 237;
Best Local Similarity 75.0%; Pred. No. 33;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 DRPYADG 10
Db 59 DRPYGCG 66

Search completed: August 29, 2003, 18:48:29
Job time: 11.2857 secs

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Om protein - protein search, using sw model

Run on: August 29, 2003, 18:39:11 ; Search time 6.57143 Seconds

(without alignments)
71.562 Million cell updates/sec

```
Title: US-09-830-876-2
Perfect score: 61
Sequence: 1 CRDDRPYADG 10
```

Scoring table: BLOSUM62

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Post-processing: Minimum Match 0%

Listing first 100 summaries

Database : SwissProt_41:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

Result No	Score	Query Match	Length	DB	ID	Description
1	61	100.0	368	1	AMY3_HORVU	P04747 hordenum vultu
2	61	100.0	427	1	AMY2_HORVU	P04063 hordenum vultu
3	56	91.8	429	1	AMY6_HORVU	P04750 hordenum vultu
4	44	72.1	421	1	AMY4_VIGMU	P17859 viona munggoi
5	44	72.1	438	1	AMY1_HORVU	P00693 hordenum vultu
6	41.5	68.0	428	1	AMY1_ORSEA	P17654 oryza sativa
7	41	67.2	151	1	Y4G6_RHME	P13486 rhizobium n
8	41	67.2	1466	1	DP27_CAEEL	P48996 caenorhabditis
9	40	65.6	443	1	AM2A_ORSEA	P27935 oryza sativa
10	40	65.6	445	1	AMC2_ORSEA	P27941 oryza sativa
11	38	62.3	149	1	RS6_RHME	G92947 rhizobium n
12	38	62.3	153	1	RS6_AGRFS	O08697 agrobacterium
13	38	62.3	373	1	VU3_HSVGU	O01350 human herpes
14	38	62.3	435	1	AM3D_ORSEA	P27933 oryza sativa
15	38	62.3	1036	1	SMO_DROME	P16882 drosophila
16	38	62.3	3255	1	POLG_LAME	P69876 h1 genome pc
17	37	60.7	243	1	NGF_CHICK	P05200 gallus galli
18	37	60.7	546	1	PCCB_SAGER	P53303 saccharopopo
19	36.5	59.8	519	1	IRX4_HUMAN	P78413 homo sapiens
20	36	59.0	237	1	TRMD_BUCAI	P54746 buchnera apt
21	36	59.0	245	1	TRMD_PASMU	O93611 pasteurella
22	36	59.0	246	1	TRMD_HAEIN	O83912 haemophilus
23	36	59.0	246	1	TRMD_YERPE	P48919 yersinia pestis
24	36	59.0	249	1	TRMD_VIBVU	O83918 vibrio vuln
25	36	59.0	250	1	TRMD_BUCBP	P59518 buchnera apt
26	36	59.0	255	1	TRMD_ECOLI	P07020 escherichia
27	36	59.0	255	1	TRMD_SALTI	O84415 salmonella
28	36	59.0	255	1	TRMD_SALTY	P36245 salmonella
29	36	59.0	255	1	TRMD_SERMA	P36245 serrattia m
30	36	59.0	262	1	TRMD_BUCAP	O8K914 buchnera apt
31	36	59.0	262	1	TRMD_RALSO	O8K908 ralstonia s
32	36	59.0	423	1	YVW2_CAEEL	O11076 caenorhabditis
33	36	59.0	440	1	AM3A_ORSEA	P27932 oryza sativa

ALIGNMENTS

34	36	59.0	539.1	YQOI_RHISM
35	57.4	85.1	1	YPBS_BACSU
36	57.4	165.1	1	UBC7_YEAST
37	55.4	226.1	1	NDUM_RAT
38	57.4	227.1	1	NDUM_MOUSE
39	55.4	659.1	1	VEL1_HPV03
40	57.4	660.1	1	VEL1_HPV29
41	35	57.4	662.1	VEL1_HPV28
42	34	55.7	197.1	HANI_XENLA
43	34	55.7	231.1	NCF_XENLA
44	34	55.7	276.1	METD_PASMU
45	34	55.7	300.1	NOTB_SALTU
46	34	55.7	393.1	MNIO_TASTY
47	34	55.7	353.1	PIRG_METKA
48	34	55.7	345.1	PIRG_ANASP
49	34	55.7	348.1	SVK_HALNI
50	34	55.7	354.1	PIRG_RALSO
51	34	55.7	759.1	GSX2_YEAST
52	34	55.7	794.1	METE_MYCTU
53	34	55.7	760.1	METE_MYCLE
54	34	55.7	1310.1	CYNA_MOUSE
55	34	55.7	1433.1	REST_CHICK
56	34	54.1	200.1	RS4_OCEIH
57	33	54.1	208.1	RS4_CAMJE
58	33	54.1	216.1	RNP1_HUMAN
59	33	54.1	237.1	RNP1_MOUSE
60	33	54.1	247.1	TRMD_VIBCH
61	33	54.1	308.1	NOTB_ECOLI
62	33	54.1	319.1	ERA_TREPA
63	33	54.1	334.1	YHOS_YEAST
64	33	54.1	394.1	VIEA_PFGAV
65	33	54.1	433.1	AMV3_WHEAT
66	33	54.1	437.1	AMK3_OYRSA
67	33	54.1	437.1	AMK3_OYRSA
68	33	54.1	438.1	AM3B_OYRSA
69	33	54.1	414.1	Y143_MYCTU
70	33	54.1	574.1	MIG1_CANAU
71	33	54.1	2192.1	HUMAN
72	33	54.1	778.1	DEGI_CAREL
73	33	838.1	1	L100_ADEP3
74	33	939.1	1	ARI1_STRILI
75	33	960.1	1	CAP2_MESCR
76	33	964.1	1	CAP1_TBAC
77	33	966.1	1	CAP1_MESCR
78	33	967.1	1	CAP1_ARATH
79	33	54.1	997.1	ATA2_CANFA
80	33	54.1	997.1	ATA2_FELCA
81	33	54.1	998.1	RPOO_BOOLV
82	33	54.1	1044.1	ATA2_MOUSE
83	32.5	53.3	122.1	YCG3_ECOLI
84	32.5	53.3	515.1	IRX4_MOUSE
85	32	52.5	98.1	YOME_RAT
86	32	52.5	135.1	Y195_MERTH
87	32	52.5	155.1	VEB6_HPV56
88	32	52.5	202.1	TEFN_HUMAN
89	32	52.5	203.1	TEFN_MOUSE
90	32	52.5	209.1	RS4_THEMA
91	32	52.5	218.1	YOB1_NYPOP
92	32	52.5	249.1	TRMD_NEIMA
93	32	52.5	249.1	TRMD_NEIMB
94	32	52.5	253.1	TRMD_PSEAE
95	32	52.5	253.1	TRMD_XANAC
96	32	52.5	253.1	TRMD_XANCP
97	32	52.5	264.1	TRMD_XYLPA
98	32	52.5	260.1	DR3E_PSECT
99	32	52.5	306.1	BSS4_MOUSE
100	32	52.5	324.1	BGG2_MOUSE

AMY2_HORVU STANDARD; PRT; 368 AA.

AC P04747;
 DT 13-AUG-1987 (Rel. 05, Created)
 DT 13-AUG-1987 (Rel. 05, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Alpha-amylase type B isozyme precursor (EC 3.2.1.1) (1,4-alpha-D-glucan glucanohydrolase) (Clone PHV19) (Fragment).
 GN AMYL.3.
 OS Hordeum vulgare (Barley).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae; OC Triticeae; Hordeum.
 OX NCBI_TaxID=4513;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Chandler P.M., Zwar J.A., Jacobsen J.V., Higgins T.J.V., Inglis A.S.;
 RT "The effects of gibberellic acid and abscisic acid on alpha-amylase mRNA levels in barley aleurone layers studies using an alpha amylase cDNA clone.";
 RL Plant Mol. Biol. 3:407-418(1984).
 CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic linkages in oligosaccharides and polysaccharides.
 CC -1- COFACTOR: BINDS A CALCIUM ION REQUIRED FOR ITS ACTIVITY.
 CC -1- DEVELOPMENTAL STAGE: PRODUCTION OF ALPHA-AMYLASE IS HORMONALLY REGULATED. GERMINATING EMBRYOS PRODUCE THE HORMONE GIBBERELLIC ACID, WHICH WITHIN 10 HOURS STIMULATES THE ALEURONE CELLS COVERING THE ENDOSPERM OF THE SEED TO PRODUCE ALPHA-AMYLASE. THE ENZYME THEN DEGRADES THE STARCH WITHIN THE ENDOSPERM FOR USE BY THE DEVELOPING PLANT EMBRYO.
 CC -1- MISCELLANEOUS: THERE ARE AT LEAST 4 TYPES OF ALPHA-AMYLASE IN BARLEY.
 CC -1- MISCELLANEOUS: TYPE B ISOZYME MRNA IS UNDETECTABLE IN UNSTIMULATED CELLS AND INCREASES A HUNDRED-FOLD AFTER STIMULATION WITH GIBBERELLIC ACID.
 CC -1- SIMILARITY: BELONGS TO FAMILY 13 OF GLYCOSYL HYDROLASES, ALSO KNOWN AS THE ALPHA-AMYLASE FAMILY.
 CC -----
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 CC -----
 DR EMBL; K02638; AAA32933.1; -;
 DR HSSP; P04063; IAVA.
 DR InterPro: IPR006589; ALP_ami1_cat_sub.
 DR InterPro: IPR006047; Alpha_ami1_cat.
 DR Pfam; PF00128; alpha-amylase; 1.
 DR SMART; SM00642; Amy; 1.
 KW Hydrolyase; Glycosidase; Carbohydrate metabolism; Seed; Germination;
 KW Calcium; Multigene family; Signal.
 FT SIGNAL 1 24
 FT CHAIN 25 >368 ALPHA-AMYLASE TYPE B ISOZYME.
 FT ACT_SITE 203 203 BY SIMILARITY.
 FT ACT_SITE 228 228 BY SIMILARITY.
 FT ACT_SITE 313 313 BY SIMILARITY.
 FT NON_TER 368 368
 FT SEQUENCE 368 AA; 40787 MW; A237EF55793BA93B CRC64;
 Query Match 100.0%; Score 61; DB 1; Length 368;
 Best Local Similarity 100.0%; Pred. No. 0.00079;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 2
 AMY2_HORVU

AMY2_HORVU STANDARD; PRT; 427 AA.

AC P04063;
 DT 01-NOV-1986 (Rel. 03, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Alpha-amylase type B isozyme precursor (EC 3.2.1.1) (1,4-alpha-D-glucan glucanohydrolase) (AMY2-2) (High pi alpha-amylase).
 GN AMYL.2.
 OS Hordeum vulgare (Barley).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae; OC Triticeae; Hordeum.
 OX NCBI_TaxID=4513;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Rahmatullah R.J., Huang J.K., Clark K.L., Reeck G.R.,
 RA Chandra G.R., Muthukrishnan S.;
 RT "Nucleotide and predicted amino acid sequences of two different genes for high-pi alpha-amylases from barley.";
 RL Plant Mol. Biol. 12:119-121(1989).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=85131184; PubMed=3871776;
 RA Rogers J.C.;
 RT "Two barley alpha-amylase gene families are regulated differently in aleurone cells.";
 RL J. Biol. Chem. 260:3731-3738(1985).
 RN [3]
 RP X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS).
 RX MEDLINE=94254083; PubMed=8196040;
 RA Kadziola A., Abe J.-I., Svensson B., Haser R.;
 RT "Crystal and molecular structure of barley alpha-amylase.";
 RL J. Mol. Biol. 239:104-121(1994).
 RN [4]
 RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS) OF COMPLEX WITH BASI.
 RC STRAIN-CV. Mennet;
 RX MEDLINE=98298441; PubMed=9634702;
 RA Vallee F., Kadziola A., Bourne Y., Juy M., Rodenburg K.W.,
 RA Svensson B., Haser R.;
 RT "Barley alpha-amylase bound to its endogenous protein inhibitor BASI: crystal structure of the complex at 1.9-A resolution.";
 RL Structure 6:649-659(1998).
 CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic linkages in oligosaccharides and polysaccharides.
 CC -1- COFACTOR: BINDS A CALCIUM ION REQUIRED FOR ITS ACTIVITY.
 CC -1- DEVELOPMENTAL STAGE: PRODUCTION OF ALPHA-AMYLASE IS HORMONALLY REGULATED. GERMINATING EMBRYOS PRODUCE THE HORMONE GIBBERELLIC ACID, WHICH WITHIN 10 HOURS STIMULATES THE ALEURONE CELLS COVERING THE ENDOSPERM OF THE SEED TO PRODUCE ALPHA-AMYLASE. THE ENZYME THEN DEGRADES THE STARCH WITHIN THE ENDOSPERM FOR USE BY THE DEVELOPING PLANT EMBRYO.
 CC -1- INDUCTION: TYPE B ISOZYME MRNA IS UNDETECTABLE IN UNSTIMULATED CELLS AND INCREASES A HUNDRED-FOLD AFTER STIMULATION WITH GIBBERELLIC ACID.
 CC -1- MISCELLANEOUS: THERE ARE AT LEAST 4 TYPES OF ALPHA-AMYLASE IN BARLEY.
 CC -1- SIMILARITY: BELONGS TO FAMILY 13 OF GLYCOSYL HYDROLASES, ALSO KNOWN AS THE ALPHA-AMYLASE FAMILY.
 CC -----
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 CC -----
 DR EMBL; X15226; CAA33298.1; -;
 DR EMBL; K02637; AAA8790.1; -;
 DR PIR; A31960; ALBHB.
 DR PDB; IAMY; 13-MAY-95.
 DR PDB; IAVA; 16-MAR-99.
 DR PDB; IBC9; 15-JUN-99.

InterPro: IPR006589; Alp_amiL_cat.sub.
 DR InterPro: IPR006047; Alpha_amiL_cat.
 DR InterPro: IPR006046; Glyco_hydro_13.
 DR Pfam: PR00128; alpha-amyLase; 1.
 DR PRINTS: PR00110; ALPHAAMYLASE.
 DR SMART: SM00642; Amy; 1.
 KM Hydrolyase; glycosidase; Carbohydrate metabolism; Seed; Germination;
 KM Calcium; Multigene family; Signal; 3D-structure.
 FT SIGNAL 1 24
 FT CHAIN 25 427
 FT ACT_SITE 203 203
 FT ACT_SITE 228 228
 FT ACT_SITE 313 313
 FT ACT_SITE 134 134
 FT CONFLICT 195 197
 FT CONFLICT 425 425
 FT CONFLICT 27 29
 FT STRAND 33 34
 FT TURN 35 37
 FT HELIX 39 40
 FT TURN 42 47
 FT HELIX 48 49
 FT TURN 50 56
 FT HELIX 57 57
 FT STRAND 60 63
 FT STRAND 69 69
 FT TURN 72 73
 FT TURN 77 77
 FT STRAND 80 81
 FT TURN 84 85
 FT TURN 87 88
 FT HELIX 91 104
 FT TURN 105 105
 FT STRAND 107 112
 FT STRAND 116 116
 FT STRAND 121 122
 FT TURN 124 125
 FT STRAND 128 130
 FT TURN 139 140
 FT TURN 144 146
 FT HELIX 147 147
 FT STRAND 149 150
 FT TURN 152 154
 FT STRAND 155 155
 FT TURN 168 169
 FT STRAND 172 173
 FT TURN 175 176
 FT HELIX 178 193
 FT TURN 194 195
 FT STRAND 199 202
 FT TURN 203 204
 FT HELIX 205 207
 FT TURN 210 220
 FT STRAND 224 227
 FT STRAND 235 235
 FT TURN 238 238
 FT TURN 241 241
 FT HELIX 246 260
 FT TURN 261 262
 FT STRAND 265 268
 FT HELIX 270 279
 FT TURN 280 282
 FT HELIX 284 287
 FT TURN 290 291
 FT HELIX 297 299
 FT TURN 300 300
 FT HELIX 302 304
 FT STRAND 305 308
 FT TURN 312 314
 FT TURN 316 318
 FT HELIX 325 327
 FT HELIX 328 337
 FT STRAND 341 345

ALPHA-AMYLASE TYPE B ISOZYME.
 G -> D (IN REF. 1).
 IGF -> HRL (IN REF. 2).
 E -> Q (IN REF. 1).

FT HELIX 346 350
 FT TURN 351 351
 FT HELIX 355 357
 FT TURN 368 369
 FT TURN 372 373
 FT STRAND 376 382
 FT TURN 383 384
 FT STRAND 385 390
 FT TURN 391 393
 FT STRAND 394 398
 FT HELIX 405 407
 FT STRAND 412 418
 FT TURN 419 420
 FT STRAND 421 427
 SO SEQUENCE 427 AA; 47355 MW; 957C0B16621BF748 CRC64;

Query Match 100.0%; Score 61; DB 1; Length 427;
 Best local similarity 100.0%; Pred. No. 0.0092;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CRDDREYADG 10
 |||||
 Db 148 CRDDREYADG 157

RESULT 3
 ID ANY6_HORVU STANDARD: PRT: 429 AA.
 AC P04750.
 DT 13-AUG-1987 (Rel. 05, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE Alpha-amyLase type B isozyme precursor (EC 3.2.1.1) (1,4-alpha-D-
 DE glucan glucanohydrolase) (Clones GRAM56 and 963).
 GN AmyL.6.
 OS Hordeum vulgare (Barley).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
 OC Triticaceae; Hordeum.
 OC NCBI_Taxid=4513;
 RN [1]
 RP SEQUENCE FROM N.A. (CLONE GRAM56).
 RA Rahmatullah R.J., Huang J.-K., Clark K.L., Reeck G.R.,
 RA Chandra G.R., Muthukrishnan S.;
 RT "Nucleotide and predicted amino acid sequences of two different genes
 RT for high-pI alpha-amyLases from barley."
 RL Plant Mol. Biol. 12:119-121(1989).
 RN [2]
 RP SEQUENCE OF 380-429 FROM N.A. (CLONE 963).
 RX MEDLINE=65159405; Pubmed=6335720.
 RA Huang J.-K., Swegle M., Dandekar A.M., Muthukrishnan S.;
 RT "Expressio" and regulation of alpha-amyLase gene family in barley
 RT aleurones."
 RL J. Mol. Appl. Genet. 2:579-588(1984).
 CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic
 CC linkages in oligosaccharides and polysaccharides.
 CC -1- COFACTOR: BINDS A CALCIUM ION REQUIRED FOR ITS ACTIVITY.
 CC -1- DEVELOPMENTAL STAGE: PRODUCTION OF ALPHA-AMYLASE IS HORMONALLY
 CC REGULATED. GERMINATING EMBRYOS PRODUCE THE HORMONE GIBBERELLIC
 CC ACID, WHICH WITHIN 10 HOURS STIMULATES THE ALEURONE CELLS COVERING
 CC THE ENDOSPERM OF THE SEED TO PRODUCE ALPHA-AMYLASE. THE ENZYME
 CC THEN DEGRADES THE STARCH WITHIN THE ENDOSPERM FOR USE BY THE
 CC DEVELOPING PLANT EMBRYO.
 CC -1- MISCELLANEOUS: THERE ARE AT LEAST 4 TYPES OF ALPHA-AMYLASE IN
 CC BARLEY.
 CC -1- MISCELLANEOUS: TYPE B ISOZYME MRNA IS UNDETECTABLE IN UNSTIMULATED
 CC CELLS AND INCREASES A HUNDRED-FOLD AFTER STIMULATION WITH
 CC GIBBERELLIC ACID.
 CC -1- SIMILARITY: BELONGS TO FAMILY 13 OF GLYCOSYL HYDROLASES, ALSO
 CC KNOWN AS THE ALPHA-AMYLASE FAMILY.
 CC -----
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 DR EMBL: X15227; CAA33229.1; -
 DR EMBL: K02636; AAA32932.1; -
 DR PIR: J0406; J0406.
 DR HSSP: P04063; IAVA.
 DR InterPro: IPR006589; Alp_amy1_cat_sub.
 DR InterPro: IPR006047; Alpha_amy1_cat.
 DR Pfam: PF00128; alpha-amy1ase; 1.
 DR SMART: SM00642; Amy; 1.
 KW Hydroxylase; Glycosidase; Carbohydrate metabolism; Seed; Germination;
 KW Calcium; Multigene family; Signal.
 FT SIGNAL 1 24
 FT CHAIN 25 429 ALPHA-AMYLAASE TYPE B ISOZYME.
 FT ACT_SITE 205 205 BY SIMILARITY.
 FT ACT_SITE 315 315 BY SIMILARITY.
 SQ SEQUENCE 429 AA; 47937 MW; 1C924CA6319D5262 CRC64;

Query Match 91.8%; Score 56; DB 1; Length 429;
 Best Local Similarity 90.0%; Pred. No. 0.0075;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 CRDDRPYADG 10
 Db 148 CRDDRPYDGD 157

RESULT 4
 ID AMYA_VIGNU STANDARD; PRT; 421 AA.
 AC P17859;
 DT 01-AUG-1990 (Rel. 15, Created)
 DT 01-AUG-1990 (Rel. 15, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Alpha-amy1ase precursor (EC 3.2.1.1) (1,4-alpha-D-glucan
 DE glucanohydrolase).
 GN AMY1.1.
 OS Vigna mungo (Rice bean) (Black gram).
 CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 CC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 CC eucosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Vigna.
 CC NCBI_TaxID=3915;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Cotyledon;
 RX MEDLINE=90332425; PubMed=2377468;
 RA Yamauchi D., Minamikawa T.;
 RT "Nucleotide sequence of cDNA for alpha-amy1ase from cotyledons of
 RT germinating Vigna mungo seeds.";
 RL Nucleic Acids Res. 18:4250-4250(1990).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94120017; PubMed=8290640;
 RA Takeuchi H., Yamauchi D., Wada S., Minamikawa T.;
 RT "Nucleotide sequence of the alpha-amy1ase gene from Vigna mungo.";
 RL Plant Physiol. 103:1459-1459(1993).
 CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic
 CC linkages in oligosaccharides and polysaccharides.
 CC -1- COFACTOR: BINDS A CALCIUM ION REQUIRED FOR ITS ACTIVITY.
 CC -1- SIMILARITY: BELONGS TO FAMILY 13 OF GLYCOSYL HYDROLASES, ALSO
 CC KNOWN AS THE ALPHA-AMYLAASE FAMILY.
 CC -----
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CC EMBL: X53049; CAA37217.1; -
 DR EMBL: X73301; CAA51734.1; -
 DR PIR: S10514; S10514.
 DR HSSP: P04063; IAVA.
 DR InterPro: IPR006589; Alp_amy1_cat_sub.
 DR InterPro: IPR006047; Alpha_amy1_cat.
 DR InterPro: IPR006046; Glyco_hydro_13.
 DR Pfam: PF00128; alpha-amy1ase; 1.
 DR PRINTS: PR00110; ALPHAAMYLAASE.
 KW Hydroxylase; Glycosidase; Carbohydrate metabolism; Calcium; signal.
 KW SMART: SM00642; Amy; 1.
 FT SIGNAL 1 23
 FT CHAIN 24 421 PROBABLE.
 FT ACT_SITE 201 201 ALPHA-AMYLAASE.
 FT ACT_SITE 309 309 BY SIMILARITY.
 FT METAL 113 113 BY SIMILARITY.
 FT METAL 172 172 CALCIUM (BY SIMILARITY).
 SQ SEQUENCE 421 AA; 46888 MW; 15CA0DABA3DB4656 CRC64;

Query Match 72.1%; Score 44; DB 1; Length 421;
 Best Local Similarity 70.0%; Pred. No. 1.1;
 Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 CRDDRPYADG 10
 Db 146 CRDDTATSDG 155

RESULT 5
 ID AMYL_HORVU STANDARD; PRT; 438 AA.
 AC P00653;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Alpha-amy1ase type A isozyme precursor (EC 3.2.1.1) (1,4-alpha-D-
 DE glucan glucanohydrolase) (AMY1) (low pI alpha-amy1ase).
 GN AMY1.1.
 OS Hordeum vulgare (Barley).
 CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 CC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
 CC Triticeae; Hordeum.
 CC NCBI_TaxID=4513;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Himalaya;
 RX MEDLINE=83238423; PubMed=6190808;
 RA Rogers J.C., Millman C.;
 RT "Isolation and sequence analysis of a barley alpha-amy1ase cDNA
 RT clone.";
 RL J. Biol. Chem. 258:8169-8174(1983).
 CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic
 CC linkages in oligosaccharides and polysaccharides.
 CC -1- COFACTOR: BINDS A CALCIUM ION REQUIRED FOR ITS ACTIVITY.
 CC -1- SUBCELLULAR LOCATION: Extracellular.
 CC -1- DEVELOPMENTAL STAGE: PRODUCTION OF ALPHA-AMYLAASE IS HORMONALLY
 CC REGULATED. GERMINATING EMBRYOS PRODUCE THE HORMONE GIBBERELLIC
 CC ACID, WHICH WITHIN 10 HOURS STIMULATES THE ALBURNONE CELLS COVERING
 CC THE ENDOSPERM OF THE SEED TO PRODUCE ALPHA-AMYLAASE. THE ENZYME
 CC THEN DEGRADES THE STARCH WITHIN THE ENDOSPERM FOR USE BY THE
 CC DEVELOPING PLANT EMBRYO.
 CC -1- MISCELLANEOUS: THERE ARE AT LEAST 4 TYPES OF ALPHA-AMYLAASE IN
 CC BARLEY.
 CC -1- SIMILARITY: BELONGS TO FAMILY 13 OF GLYCOSYL HYDROLASES, ALSO
 CC KNOWN AS THE ALPHA-AMYLAASE FAMILY.
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CC -----
CC EMBL: J01236; AAA32929.1;
CC PIR: A00846; ALBH.
CC HSSP: P04063; IAVA.
CC InterPro: IPR006589; Alp-amy1_cat_sub.
CC InterPro: IPR006047; Alpha-amy1_cat.
CC Pfam: PR00128; alpha-amy1ase; 1.
CC SMART: SM00642; Amy; 1.
CC Hydrolyase; Glycosidase; Carbohydrate metabolism; Seed; Germination;
CC Calcium; Multigene family; Signal.
CC SIGNAL
CC CHAIN 1 24
CC FT 23 438 ALPHA-AMYLASE TYPE A ISOZYME.
CC FT ACT_SITE 204 204 BY SIMILARITY.
CC FT ACT_SITE 229 229 BY SIMILARITY.
CC FT ACT_SITE 315 315 BY SIMILARITY.
CC FT ACT_SITE 315 315 BY SIMILARITY.
CC SEQUENCE 438 AA; 47796 MW; 2393FDC5180F51 CRC64;

Query Match 72.1%; Score 44; DB 1; Length 438;
Best Local Similarity 70.0%; Pred. No. 1.2;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 CRDDPRYADG 10
Db 149 CRDDPRYSDG 158

RESULT 6
AMY1_ORYSA STANDARD; PRT: 428 AA.
ID AMY1_ORYSA
AC P17654;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Alpha-amy1ase precursor (EC 3.2.1.1) (1,4-alpha-D-glucan
DE glucanohydrolase) (Isozyme 1B).
GN AMY1 OR AMY1A.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OC NCBI_TaxID=4550;
OX
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Japonica M202;
RX MEDLINE=91346657; PubMed=2102847;
RA Huang N., Sutcliffe T.D., Lites J.C., Rodriguez R.L.;
RT "Classification and characterization of the rice alpha-amy1ase
RT multi-gene family."
RL Plant Mol. Biol. 14:655-668(1990).
RN [2]
RP SEQUENCE FROM N.A. (CLONE POS103).
RC STRAIN=cv. Japonica M202;
RX MEDLINE=90318322; PubMed=2370848;
RA O'Neill S.D., Kumagai M.H., Majumdar A., Huang N., Sutcliffe T.D.,
RA Rodriguez R.L.;
RT "The alpha-amy1ase genes in Oryza sativa: characterization of cDNA
RT clones and mRNA expression during seed germination."
RL Mol. Gen. Genet. 221:235-244(1990).
CC -1- FUNCTION: IMPORTANT FOR BREAKDOWN OF ENDOSPERM STARCH DURING
CC GERMINATION
CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic
CC linkages in oligosaccharides and polysaccharides.
CC -1- COPACATOR: BINDS A CALCIUM ION REQUIRED FOR ITS ACTIVITY.
CC -1- SUBUNIT: Monomer.
CC -1- TISSUE SPECIFICITY: MORE ABUNDANT IN GERMINATING SEEDS, THAN IN
CC CALDUS, YOUNG ROOTS AND LEAVES.
CC -1- DEVELOPMENTAL STAGE: EXPRESSED AT A HIGH LEVEL DURING GERMINATION
CC IN THE ALBUKONES CELLS UNDER THE CONTROL OF THE PLANT HORMONE
CC GIBBERELIC ACID AND IN THE DEVELOPING GRAINS AT A LOW LEVEL.
CC -1- PFM: ONLY CEREAL AMYLASE KNOWN TO BE GLYCOSYLATED.
CC -1- SIMILARITY: BELONGS TO FAMILY 13 OF GLYCOSYL HYDROLASES, ALSO
CC KNOWN AS THE ALPHA-AMYLASE FAMILY.

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CC or send an email to license@lsb-sib.ch).
CC -----
CC EMBL: X16509; CAA34516.1;
CC EMBL: M24286; AAA33885.1; ALT_INIT.
CC PIR: S10013; S10013.
CC HSSP: P04063; IAVA.
CC Gramene; P17654;
CC InterPro: IPR006589; Alp-amy1_cat_sub.
CC InterPro: IPR006047; Alpha-amy1_cat.
CC InterPro: IPR006046; Glyco_hydro_13.
CC Pfam: PR00128; alpha-amy1ase; 1.
CC PRINTS: PR00110; ALPHA-AMYLASE.
CC SMART: SM00642; Amy; 1.
CC Hydrolyase; Glycosidase; Carbohydrate metabolism; Calcium; Signal;
CC Glycoprotein; Multigene family.
CC SIGNAL
CC CHAIN 1 25 PROBABLE.
CC FT 26 428 ALPHA-AMYLASE.
CC FT ACT_SITE 203 203 BY SIMILARITY.
CC FT ACT_SITE 314 314 BY SIMILARITY.
CC FT METAL 116 116 CALCIUM (BY SIMILARITY).
CC FT METAL 174 174 CALCIUM (BY SIMILARITY).
CC FT CARBOHYD 265 265 N-LINKED (GLUCNAC...) (PROBABLE).
CC SEQUENCE 428 AA; 47755 MW; 3B71403ACFC6A6 CRC64;

Query Match 68.0%; Score 41.5; DB 1; Length 428;
Best Local Similarity 80.0%; Pred. No. 3.3;
Matches 8; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

OY 1 CRDDPRYADG 10
Db 149 CRDD-PRYDGD 157

RESULT 7
YAG6_RHIME STANDARD; PRT: 151 AA.
ID YAG6_RHIME
AC P13486;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Hypothetical protein RA0666.
GN RA0666 OR SMA1223.
OS Rhizobium meliloti (Sinorhizobium meliloti).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Rhizobiaceae; Sinorhizobium/Ensifer group; Sinorhizobium.
OX NCBI_TaxID=382;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=89305532; PubMed=2663474;
RX Baitt J., Daverin-Milgou M.-L., David M., Jacobs J., Garnerone A.-M.,
RA Kahn D., Daverin-Milgou M.-L., David M., Jacobs J., Garnerone A.-M.,
RA "FixX", a gene homologous with fix and cnp from Escherichia coli,
RT regulates nitrogen fixation genes both positively and negatively in
RT Rhizobium meliloti.
RL EMBO J. 8:1279-1286(1989).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=1021;
RX MEDLINE=21396509; PubMed=11481432;
RA Barnett M.J., Fisher R.F., Jones T., Komp C., Abola A.P.,
RA Barlow-Hubler F., Bowser L., Capela D., Gilbert F., Gouzy J.,
RA Gurjal M., Hong A., Hultzer L., Hyman R.W., Kahn D., Kahn M.L.,
RA Kishan S., Keating D.H., Palm C., Peck M.C., Surzycki R., Wells D.H.,
RA Yeh K.-C., Davis R.W., Federspiel N.A., Long S.R.;
RT "Nucleotide sequence and predicted functions of the entire

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RT Sinorhizobium meliloti pSymA megaplasmid";
 RL Proc. Natl. Acad. Sci. U.S.A. 98:9883-9888(2001).
 CC -----
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 CC -----
 DR EMBL: X15079; CAA33184.1; -
 DR EMBL: Z21854; CAA79900.1; -
 DR EMBL: AE007255; AAK65324.1; -
 DR PIR: B95345; B95345.
 DR PIR: S04123; S04123.
 KW Hypothetical protein; Nitrogen fixation; Plasmid; Complete proteome.
 SO SEQUENCE 151 AA; 17013 MW; C646ED93410F1E09 CRC64;
 Query Match 67.2%; Score 41; DB 1; Length 151;
 Best Local Similarity 85.7%; Pred. No. 1.4;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 CRDDRPY 7
 Db 26 CRDDQPY 32
 RESULT 8
 DP27_CAEEL STANDARD; PRT; 1469 AA.
 AC PA8996;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Chromosome condensation protein dpy-27 (Dumpy-27 protein).
 OS Dpy-27 OR R13G10.1.
 GN Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditioidea;
 OC Rhabditidae; Pelodierinae; Caenorhabditis.
 OC NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A., FUNCTION, SUBCELLULAR LOCATION, AND MUTAGENESIS OF
 RP IYS-128.
 RC STRAIN-Bristol N2;
 RA MEDLINE=95042743; PubMed=7954812;
 RA Chuang P.-T., Albertson D.G., Meyer B.J.;
 RT "Dpy-27: a chromosome condensation protein homolog that regulates C.
 RT elegans dosage compensation through association with the X
 RT chromosome";
 RL Cell 79:459-474(1994).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-Bristol N2;
 RA Gardner A.;
 RL Submitted (Aug-1994) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SUBCELLULAR LOCATION.
 RP MEDLINE=96017644; PubMed=7588066;
 RA Hsu D.R., Chuang P.-T., Meyer B.J.;
 RT "Dpy-30, a nuclear protein essential early in embryogenesis for
 RT Caenorhabditis elegans dosage compensation";
 RL Development 121:3323-3334(1995).
 RN [4]
 RP FUNCTION, AND IDENTIFICATION IN A COMPLEX WITH DPY-26.
 RP MEDLINE=97094383; PubMed=8939870;
 RA Chuang P.-T., Lieb J.D., Meyer B.J.;
 RT "Sex-specific assembly of a dosage compensation complex on the
 RT nematode X chromosome";
 RL Science 274:1736-1739(1996).
 CC -1- FUNCTION: Involved in X dosage compensation chromosome. Required
 CC to reduce expression of both hermaphrodite X chromosomes. Its
 CC strong similarity with the condensin subunit smc4 suggests that it

CC may reduce the X-chromosome transcript level by condensing the
 CC chromatin structure during interphase cells.
 CC -1- SUBUNIT: Component of a complex containing dpy-26 and two
 CC unidentified proteins.
 CC -1- SUBCELLULAR LOCATION: Nuclear. Associates with chromatin after 30-
 CC cell stage. It specifically localizes to the X chromosomes of
 CC wild-type XX embryos, but remains diffusely distributed throughout
 CC the nuclei of male (XO) embryos. Dpy-26 is required for its X-
 CC chromosome specific association.
 CC -1- DEVELOPMENTAL STAGE: Expressed in embryos and early-staged larvae.
 CC -1- DOMAIN: Consists of two putative central coiled-coil regions
 CC flanked by putative globular regions at the N- and C-termini.
 CC -1- SIMILARITY: Belongs to the SMC family. SMC4 subfamily.
 CC -----
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 CC -----
 DR EMBL: U35274; AA62647.1; -
 DR EMBL: Z35602; CAA84669.1; -
 DR PIR: T24216; T24216.
 DR WormPep: R13G10.1; CE01052.
 DR InterPro: IPR003405; SMC_C.
 DR InterPro: IPR003395; SMC_N.
 DR Pfam: PF02483; SMC_C; 1.
 DR Pfam: PF02463; SMC_N; 1.
 KW DNA condensation; SMC_N; 1.
 DR NP_BIND 122 129
 FT DOMAIN 356 542
 FT DOMAIN 543 804
 FT DOMAIN 805 974
 FT DOMAIN 1016 1056
 FT DOMAIN 1159 1182
 FT DOMAIN 1245 1280
 FT MUTAGEN K->E, I: LOSS OF FUNCTION.
 SO SEQUENCE 1469 AA; 169618 MW; EF9043CA2AC23B06 CRC64;
 Query Match 67.2%; Score 41; DB 1; Length 1469;
 Best Local Similarity 100.0%; Pred. No. 15;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 3 DDRPYAD 9
 Db 13 DDRPYAD 19
 RESULT 9
 AM2A_ORYSA STANDARD; PRT; 443 AA.
 AC P27935;
 DT 01-AUG-1992 (Rel. 23, Created)
 DT 01-AUG-1992 (Rel. 23, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Alpha-amylase isozyme 2A precursor (EC 3.2.1.1) (1.4-alpha-D-glucan
 DE glucanohydrolase).
 GN AMY1.5 OR AMY2A.
 OS Oryza sativa (Rice).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Ehrhartoideae; Oryzaceae; Oryza.
 OC NCBI_TaxID=4530;
 RN [1]
 RP SEQUENCE FROM N.A.
 RP STRAIN=cv. Japonica M202;
 RC MEDLINE=92175526; PubMed=1541400;
 RA Huang N., Reini S.J., Rodriguez R.L.;
 RT "AMY2A: a novel alpha-amylase-encoding gene in rice";
 RL Gene 111:223-228(1992).
 CC -1- FUNCTION: IMPORTANT FOR BREAKDOWN OF ENDOSPERM STARCH DURING

CC GERMINATION.
CC CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic
CC linkages in oligosaccharides and polysaccharides.
CC -1- COFACTOR: BINDS A CALCIUM ION REQUIRED FOR ITS ACTIVITY.
CC -1- SUBUNIT: Monomer.
CC -1- DEVELOPMENTAL STAGE: EXPRESSED AT A HIGH LEVEL DURING GERMINATION
CC IN THE ALBURNONS CELLS UNDER THE CONTROL OF THE PLANT HORMONE
CC GIBBERELIC ACID AND IN THE DEVELOPING GRAINS AT A LOW LEVEL.
CC -1- SIMILARITY: BELONGS TO FAMILY 13 OF GLYCOSYL HYDROLASES, ALSO
CC KNOWN AS THE ALPHA-AMYLASE FAMILY.
CC -----
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CC -----
CC EMBL: M74177; AAA3894.1; -
CC PIR: J01527; J01527.
CC HSSP: P04063; 1A7A.
CC Gramene: P27941.
CC InterPro: IPR006047; Alpha-amyl_cat.
CC Pfam: PF00128; alpha-amylase; 1.
CC KEGG: Glycosylase; Carbohydrate metabolism; Calcium; Signal;
CC Multigene family.
CC FT SIGNAL 1 21 POTENTIAL.
FT CHAIN 1 21 ALPHA-AMYLASE ISOZYME 2A.
FT ACT_SITE 202 202 BY SIMILARITY.
FT ACT_SITE 314 314 BY SIMILARITY.
FT METAL 113 113 CALCIUM (BY SIMILARITY).
FT METAL 172 172 CALCIUM (BY SIMILARITY).
SQ SEQUENCE 443 AA; 48527 MW; 783F9264404F67F6 CRC64;
Query Match 65.6%; Score 40; DB 1; Length 443;
Best Local Similarity 60.0%; Pred. No. 6.5;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
OY 1 CRDDRPYADG 10
Db 146 CRDDTGFSDG 155
RESULT 10
AMC2_ORYSA STANDARD; PRT; 445 AA.
AC P27941;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Alpha-amylase Isozyme C2 precursor (EC 3.2.1.1) (1,4-alpha-D-glucan
DE glucanohydrolase).
GN AMYL 8.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Eriophytidae; Oryzaceae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RA GOLDMAN S., MAWAL Y., WU R.;
RA Submitted (FEB-1992) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: IMPORTANT FOR BREAKDOWN OF ENDOSPERM STARCH DURING
CC GERMINATION.
CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic
CC linkages in oligosaccharides and polysaccharides.
CC -1- COFACTOR: BINDS A CALCIUM ION REQUIRED FOR ITS ACTIVITY.
CC -1- SUBUNIT: Monomer.
CC -1- DEVELOPMENTAL STAGE: EXPRESSED AT A HIGH LEVEL DURING GERMINATION
CC IN THE ALBURNONS CELLS UNDER THE CONTROL OF THE PLANT HORMONE
CC GIBBERELIC ACID AND IN THE DEVELOPING GRAINS AT A LOW LEVEL.

CC -1- SIMILARITY: BELONGS TO FAMILY 13 OF GLYCOSYL HYDROLASES, ALSO
CC KNOWN AS THE ALPHA-AMYLASE FAMILY.
CC -----
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CC -----
CC EMBL: X64619; CA45903.1; -
CC PIR: S19990; S19990.
CC HSSP: P04063; 1A7A.
CC Gramene: P27941.
CC InterPro: IPR006047; Alpha-amyl_cat.
CC Pfam: PF00128; alpha-amylase; 1.
CC KEGG: Glycosylase; Carbohydrate metabolism; Calcium; Signal;
CC Multigene family.
CC FT SIGNAL 1 21 POTENTIAL.
FT CHAIN 1 21 ALPHA-AMYLASE ISOZYME C2.
FT ACT_SITE 202 202 BY SIMILARITY.
FT ACT_SITE 314 314 BY SIMILARITY.
FT METAL 113 113 CALCIUM (BY SIMILARITY).
FT METAL 172 172 CALCIUM (BY SIMILARITY).
SQ SEQUENCE 445 AA; 49207 MW; DED23701E836ACDA CRC64;
Query Match 65.6%; Score 40; DB 1; Length 445;
Best Local Similarity 60.0%; Pred. No. 6.5;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
OY 1 CRDDRPYADG 10
Db 146 CRDDTGFSDG 155
RESULT 11
RS6_RHIME STANDARD; PRT; 149 AA.
AC Q92027;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE 30S ribosomal protein S6.
DE RPSF OR R01138 OR SMC00568
OS Rhizobium meliloti (Sinorhizobium meliloti).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Rhizobiaceae; Sinorhizobium/Ensifer group; Sinorhizobium.
OX NCBI_TaxID=382;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=1021;
RC MEDLINE=21396507; PubMed=11481430;
RA Capela D., Barloy-Hubler F., Gouzy J., Botte G., Ampe F., Batut J.,
RA Boistard P., Becker A., Boutry M., Cadieu E., Dreano S., Gloux S.,
RA Godrie T., Goffeau A., Kahn D., Kiss E., Lelaure V., Masuy D.,
RA Pohl T., Portetalle D., Puehler A., Purnelle B., Ramsperger U.,
RA Renard C., Thebaud P., Vandenbol M., Weidner S., Gallbert F.;
RT Analysis of the chromosome sequence of the legume symbiont
RT Sinorhizobium meliloti strain 1021.
RL Proc. Natl. Acad. Sci. U.S.A. 98:9877-9882(2001).
CC -1- FUNCTION: Binds together with S18 to 16S ribosomal RNA (by
CC similarity).
CC -1- SIMILARITY: BELONGS TO THE S6P FAMILY OF RIBOSOMAL PROTEINS.
CC -----
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DR EMBL: AL591786; CAC45717.1; -.
DR HAMAP: MF_00360; -. 1.
DR InterPro: IPR000529; Ribosomal_S6.
DR P1am; P001250; Ribosomal_S6; 1.
DR ProDom: PD003809; Ribosomal_S6; 1.
DR TIGRFAMs: TIGR00166; S6; 1.
DR PROSITE: PS01048; RIBOSOMAL_S6; FALSE NEG.
KW Ribosomal protein; rRNA-binding; Complete proteome.
SQ SEQUENCE 149 AA; 17274 MW; 15766B6EAE7FF18C CAC64;

Query Match      62.3%; Score 38; DB 1; Length 149;
Best Local Similarity 77.8%; Pred. No. 4.9;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      2 RDDRPVADG 10
        ||||| 11
Db      109 RDDRRRRDG 117

RESULT 12
RS6_AGR75 STANDARD; PRT; 153 AA.
AC O8UG67;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE 30S ribosomal protein S6.
PF P6F OR ATU1091 OR AGR_C_2022.
GN Agrobacterium tumefaciens (strain C58 / ATCC 33970).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Rhizobiaceae; Rhizobium/Agrobacterium group; Agrobacterium.
CX NCBI_TaxID=176299;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21608550; PubMed=11743193;
RA Wood D.W., Setubal J.C., Kaul R., Monks D.E., Kitajima J.P.,
RA Okura Y.K., Zhou Y., Chen L., Wood G.E., Almeida N.F. Jr., Woo L.,
RA Chen Y., Paulsen I.T., Eisen J.A., Karp P.D., Bovee D. St.,
RA Chapman P., Clendenning J., Deatherage G., Gillet W., Grant C.,
RA Kutayavin T., Levy R., Li M.-J., McClelland E., Palmieri A.,
RA Raymond C., Rouse G., Saenphimachak C., Wu Z., Romero P., Gordon D.,
RA Zhang S., Yoo H., Tao Y., Biddle P., Jung M., Krespan W., Perry M.,
RA Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M.,
RA Chumley F., Tingey S.V., Tomb J.-F., Gordon M.P., Olson M.V.,
RA Nester E.W.;
RT "The genome of the natural genetic engineer Agrobacterium tumefaciens
RL C58."
RL Science 294:2317-2323(2001).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=21608551; PubMed=11743194;
RA Goodner B., Hinkle G., Gattung S., Miller N., Blanchard M.,
RA Oucullo B., Goldman B.S., Cao Y., Askenazi M., Halling C., Mullin L.,
RA Houmlet K., Gordon J., Vaundin M., Iatchouk O., Epp A., Liu F.,
RA Wollam C., Allinger M., Doughy D., Scott C., Lappas C., Markelz B.,
RA Flanagan C., Crowell C., Gurnson J., Lomo C.C., Strub G.,
RA Cialo C., Slater S.;
RT "Genome sequence of the plant pathogen and biotechnology agent
RL Agrobacterium tumefaciens C58."
RL Science 294:2323-2328(2001).
CC -1- FUNCTION: Binds together with S18 to 16S ribosomal RNA (By
CC similarity).
CC -1- SIMILARITY: BELONGS TO THE S6P FAMILY OF RIBOSOMAL PROTEINS.
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CC
EMBL: AE009072; AAL42104.1; -.

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DR EMBL: AE008039; -; NOT_ANNOTATED_CD5.
DR PIR: AB2711; AB2711.
DR HAMAP: MF_00360; -; 1.
DR InterPro: IPR000529; Ribosomal_S6.
DR Pfam: PF01250; Ribosomal_S6; 1.
DR ProDom: PD003809; Ribosomal_S6; 1.
DR TIGRFAMs: TIGR00166; S6; 1.
DR PROSITE: PS01048; Ribosomal_S6; FALSE NEG.
KW Ribosomal protein; rRNA-binding; Complete proteome.
SQ SEQUENCE 153 AA; 17766 MW; 79C494057455977F CRC64;

Query Match      62.3%; Score 38; DB 1; Length 153;
Best Local Similarity 77.8%; Pred. No. 5;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 RDDRPPYADG 10
   ||||| 11
Db 109 RDDRPRRDG 117

RESULT 13
V03_HSV60 STANDARD; PRT; 373 AA.
AC Q01350;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE U3 protein.
GN U3 OR SHL2.
OS Human herpesvirus (type 6 / strain Uganda-1102) (HHV6).
OC Vitruvinae: dsDNA viruses, no RNA stage: Herpesviridae;
OC Betaherpesvirinae: Roseolovirus.
OX NCBI_TaxID=10370;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92333249; PubMed=1321206;
RT "Identification of homologues to the human cytomegalovirus US22 gene family in human herpesvirus 6";
RT J. Gen. Virol. 73:1661-1671(1992).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=95266321; PubMed=7747482;
RT Compels U.A., Nicholas J., Lawrence G., Jones M., Thomson B.J.,
RT Martin M.E., Efsthaliou S., Craxton M., Macaulay H.A.;
RT "The DNA sequence of human herpesvirus-6: structure, coding content, and genome evolution.";
RT Virology 209:29-51(1995).
CC -1- SIMILARITY: BELONGS TO THE US22 FAMILY. STRONGEST SIMILARITY TO
CC HUMAN CYTOMEGALOVIRUS UL24 PROTEIN.
CC -----
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CC
DR EMBL: X83413; CA58430.1; -.
DR EMBL: D10082; BAA00977.1; -.
DR PIR: J01648; J01648.
DR InterPro: IPR003360; US22.
DR Pfam: PF02393; US22; 1.
SQ SEQUENCE 373 AA; 43698 MW; 60A402E7236D274E CRC64;

Query Match      62.3%; Score 38; DB 1; Length 373;
Best Local Similarity 66.7%; Pred. No. 13;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 CRDDRPYAD 9
   |||| 111
Db 90 CRDENEYAD 98

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RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svitskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao O.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.W., Venter J.C.,
 RT "The genome sequence of *Drosophila melanogaster*.";
 Science 287:2185-2195(2000).
 CC -I- FUNCTION: SEGMENT POLARITY PROTEIN REQUIRED FOR CORRECT PATTERNING
 CC OF EVERY SEGMENT. G-PROTEIN-COUPLED RECEPTOR THAT ASSOCIATES WITH
 CC THE PATCHED PROTEIN (PTC) TO TRANSDUCE THE HEDGEHOG (HH) SIGNAL.
 CC THROUGH THE ACTIVATION OF AN INHIBITORY G-PROTEIN. IN THE ABSENCE
 CC OF HH, PTC REPRESENTS THE CONSTITUTIVE SIGNALING ACTIVITY OF SMO
 CC THROUGH FUSED (FU).
 CC -I- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -I- DEVELOPMENTAL STAGE: EXPRESSED AT ALL DEVELOPMENTAL STAGES, THOUGH
 CC THE LEVELS VARY.
 CC -I- SIMILARITY: BELONGS TO FAMILY FZ/SMO OF G-PROTEIN COUPLED
 CC RECEPTORS.
 CC -I- CAUTION: IT IS UNCERTAIN WHETHER MET-1, MET-9, MET-13 OR MET-14 IS
 CC THE INITIATOR.
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 CC -----
 DR EMBL: U87613; AAC33180.1; -;
 DR EMBL: AF030334; AAB84275.1; -;
 DR EMBL: AE003590; AAF51518.2; -;
 DR Flybase: FBgn0003444; smo.
 DR GO: GO:0007350; P:blastoderm segmentation; IMP.
 DR GO: GO:0007455; P:eye-antennal disc metamorphosis; IGL.
 DR GO: GO:0007346; P:regulation of mitotic cell cycle; IMP.
 DR InterPro: IPR000539; Fz: Fz.
 DR InterPro: IPR000024; Fz_domain.
 DR InterPro: IPR000832; GPCR_secretin.
 DR Pfam: PF01534; Fz: Fz.
 DR Pfam: PF01392; Fz: Fz.
 DR PRINTS: PRO0489; FRIZZLED.
 DR SMART: SM00063; FRI; 1.
 DR PROSITE: PS50038; Fz; 1.
 DR PROSITE: PS50261; G-PROTEIN_RECEP_F2_4; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein; Signal;
 KW Developmental protein.
 FT SIGNAL 1 31
 FT CHAIN 32 1036
 FT DOMAIN 32 258
 FT TRANSMEM 259 279
 FT DOMAIN 280 287
 FT TRANSMEM 288 308
 FT DOMAIN 309 339
 FT TRANSMEM 340 360
 FT DOMAIN 361 381
 FT TRANSMEM 382 402
 FT DOMAIN 403 421
 FT TRANSMEM 422 442
 FT DOMAIN 443 469
 FT TRANSMEM 470 490
 FT DOMAIN 491 532
 FT TRANSMEM 533 553
 FT DOMAIN 554 1036
 FT DOMAIN 85 206
 FT DOMAIN 816 819
 FT CARBOHYD 55 55
 FT CARBOHYD 95 95
 FT CARBOHYD 184 184
 FT CARBOHYD 195 195

FT CARBOHYD 213 213 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 336 336 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 419 419 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 1036 AA; 116552 MW; 7797FC71A539A87A CRC64;
 Query Match 62.3%; Score 38; DB 1; Length 1036;
 Best Local Similarity 66.7%; Pred No. 36;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 QY 2 RDDRPRYADG 10
 DB 68 RDDRPRYADG 76
 RESULT 16
 POLG_LMVE STANDARD; PRT; 3255 AA.
 ID POLG_LMVE
 AC P89676;
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Genome polypeptide [Contains: N-terminal protein (P1); Helper
 DE component proteinase (EC 3.4.22.45) (HC-Pro); Protein P3; 6 kDa
 DE protein 1 (6k1); Cytoplasmic inclusion protein (CI); 6 kDa protein 2
 DE (6k2); Genome-linked protein (VPG); Nuclear inclusion protein A (NI-A)
 DE (NI-A) (EC 3.4.22.44) (49 kDa proteinase) (49 kDa-Pro); Nuclear
 DE inclusion protein B (NI-B) (NI-B) (RNA-directed RNA polymerase)
 DE (EC 2.7.7.48); Coat protein (CP)].
 OS Lettuce mosaic virus (strain B) (LMV).
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Potyviridae;
 OC Polyvirus.
 OX NCBI_TaxID=117132;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97239892; PubMed=9085548;
 RA Revers F., Yang S.-J., Walter J., Souche S., Lot H., Le Gall O.,
 RA Candresse T., Dunez J.;
 RT "Comparison of the complete nucleotide sequences of two isolates of
 RT lettuce mosaic virus differing in their biological properties.";
 RL Virus Res. 47:167-177(1997).
 CC -I- FUNCTION: HELPER COMPONENT-PROTEINASE IS REQUIRED FOR APHID
 CC TRANSMISSION AND ALSO HAS PROTEOLYTIC ACTIVITY.
 CC -I- FUNCTION: CYTOPLASMIC INCLUSION PROTEIN HAS HELICASE ACTIVITY. IT
 CC MAY BE INVOLVED IN REPLICATION.
 CC -I- FUNCTION: NUCLEAR INCLUSION PROTEIN A HAS PROTEOLYTIC ACTIVITY.
 CC -I- CATALYTIC ACTIVITY: Hydrolyzes glutamyl bonds, and activity is
 CC further restricted by preferences for the amino acids in P6 - P1'
 CC Glu(Ser or Gly) for the enzyme from tobacco etch virus. The
 CC natural substrate is the viral polypeptide, but other proteins and
 CC oligopeptides containing the appropriate consensus sequence are
 CC also cleaved.
 CC -I- CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate +
 CC {RNA} (N).
 CC -I- CATALYTIC ACTIVITY: Hydrolyzes a Gly-I-Gly bond at its own C-
 CC terminus, commonly in the sequence -Tyr-Xaa-Val-Gly-I-Gly, in the
 CC processing of the polioviral polypeptide.
 CC -I- PTM: VPG IS COVALENTLY LINKED TO THE GENOMIC RNA.
 CC -I- PTM: THE VIRAL RNA OF POTYVIRUSES IS EXPRESSED AS A SINGLE
 CC POLYPEPTIDE WHICH UNDERGOES POSTTRANSLATIONAL PROTEOLYTIC
 CC PROCESSING RESULTING IN THE PRODUCTION OF AT LEAST EIGHT
 CC INDIVIDUAL PROTEINS.
 CC -I- SIMILARITY: HC PROTEINASE BELONGS TO PEPTIDASE FAMILY C6.
 CC -I- SIMILARITY: NI-A PROTEINASE BELONGS TO PEPTIDASE FAMILY C4.
 CC -I- SIMILARITY: BELONGS TO THE POTYVIRUSES POLYPEPTIDE FAMILY.
 CC -----
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CC EMBL: X97705; CA666281.1; -
DR MEMOS: C04.001; -
DR MEMOS: C04.001; -
DR InterPro: IPR001410; DEAD.
DR InterPro: IPR001650; Helicase_C.
DR InterPro: IPR001730; Peptidase_C4.
DR InterPro: IPR001456; Peptidase_C6.
DR InterPro: IPR001592; Poly-coat.
DR InterPro: IPR002540; Poly-pl.
DR InterPro: IPR007095; RNA_pol_DS_PS.
DR InterPro: IPR001205; RNA_pol_P3D.
DR InterPro: IPR007094; RNA_pol_PSVir.
DR Pfam: PF00270; DEAD; 1.
DR Pfam: PF00271; Helicase_C; 1.
DR Pfam: PF00863; Peptidase_C4; 1.
DR Pfam: PF00851; Peptidase_C6; 1.
DR Pfam: PF00767; Poly-coat; 1.
DR Pfam: PF01577; Poly-pl; 1.
DR Pfam: PF00680; RNA_dep_RNA_pol; 1.
DR PRINTS: PR00966; NTPOTYPTASE.
DR SMART: SM00487; DEXDC; 1.
DR SMART: SM00490; HELIC; 1.
KW Hydrolase; Transferase; Thiol protease; RNA-directed RNA polymerase;
KW Cap protein; Polypeptide; Covalent protein-RNA linkage; Helicase;
KW ATP-binding.
KW CHAIN 1 N-TERMINAL PROTEIN
KW CHAIN 2 HELPER COMPONENT PROTEINASE.
KW CHAIN 3 PROTEIN P3.
KW CHAIN 4 6 KDa PROTEIN 1.
KW CHAIN 5 CYTOSOLIC INCLUSION PROTEIN.
KW CHAIN 6 6 KDa PROTEIN 2.
KW CHAIN 7 GDNOL-LINKED PROTEIN.
KW CHAIN 8 NUCLEAR INCLUSION PROTEIN A.
KW CHAIN 9 NUCLEAR INCLUSION PROTEIN B.
KW NP_BIND 2978 3255 COAT PROTEIN.
KW NP_BIND 1410 1417 ATP (POTENTIAL).
SQ SEQUENCE 3255 AA; 367618 MW; B3B5852927E01628 CRC64;

Query Match 62.3%; Score 38; DB 1; Length 3255;
Best Local Similarity 66.7%; Pred. No. 1.2e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 CRDDRPYAD 9
DB 2915 CLDEAPYAD 2923

RESULT 17
NGF_CHICK STANDARD; PRT; 243 AA.
AC POS200;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Beta-nerve growth factor precursor (Beta-NGF).
GN NGFB.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBT_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86300646; PubMed=3017695;
RA Ebendahl T., Larhammar D., Persson H.;
RT "Structure and expression of the chicken beta nerve growth factor
RT gene."
RL EMBO J. 5:1483-1487(1986).
RN [2]
RP SEQUENCE OF 118-243 FROM N.A.
RX MEDLINE=86248129; PubMed=3720959;
RA Wion D., Perlet C., Frechin N., Keller A., Behar G., Brachet P.,

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RA Aulfray C.;
RT Molecular cloning of the avian beta-nerve growth factor gene:
RT transcription in brain."
RL FEBS Lett. 203:82-86(1986).
RN [3]
RP SEQUENCE OF 121-243 FROM N.A.
RX MEDLINE=86300647; PubMed=2427334;
RA Meier R., Becker-Andre M., Goltz R., Heumann R., Shaw A., Thoenen H.;
RT "Molecular cloning of bovine and chick nerve growth factor (NGF):
RT delineation of conserved and unconserved domains and their
RT relationship to the biological activity and antigenicity of NGF."
RL EMBO J. 5:1489-1493(1986).
RN [4]
RP SEQUENCE OF 181-222 FROM N.A.
RX MEDLINE=91222573; PubMed=2025430;
RA Halboeck F., Ibanez C.F., Persson H.;
RT "Evolutionary studies of the nerve growth factor family reveal a
RT novel member abundantly expressed in Xenopus ovary."
RL Neuron 6:845-858(1991).
CC -1- FUNCTION: NERVE GROWTH FACTOR IS IMPORTANT FOR THE DEVELOPMENT AND
CC MAINTENANCE OF THE SYMPATHETIC AND SENSORY NERVOUS SYSTEMS. IT
CC STIMULATES DIVISION AND DIFFERENTIATION OF SYMPATHETIC AND
CC EMBRYONIC SENSORY NEURONS.
CC -1- SUBUNIT: HOMODIMER, ASSOCIATED BY NONCOVALENT FORCES.
CC -1- SIMILARITY: BELONGS TO THE NGF-BETA FAMILY.
CC -----
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CC -----
DR EMBL: X04003; CA27633.1; ALT_INT.
DR EMBL: X04067; CA27703.1; -
DR EMBL: M26810; AAA48984.1; -
DR PIR: A26311; A26311.
DR HSSP: P01139; 1BET.
DR InterPro: IPR002072; NGF.
DR Pfam: PF00243; NGF; 1.
DR PRINTS: PR00268; NGF.
DR ProDom: PD002052; NGF; 1.
DR SMART: SM00140; NGF; 1.
DR PROSITE: PS00248; NGF_1; 1.
DR PROSITE: PS0270; NGF_2; 1.
KW Growth factor; Signal.
FT SIGNAL 1 22
FT PROPEP 22 125
FT CHAIN 126 243 BETA-NERVE GROWTH FACTOR.
FT DISULFID 135 204 BY SIMILARITY.
FT DISULFID 182 232 BY SIMILARITY.
FT DISULFID 192 234 BY SIMILARITY.
SQ SEQUENCE 243 AA; 27138 MW; 74C306CB2079DA07 CRC64;

Query Match 60.7%; Score 37; DB 1; Length 243;
Best Local Similarity 60.0%; Pred. No. 12;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 1 CRDDRPYADG 10
DB 182 CRDPEVSSG 191

RESULT 18
PCRB_SACER STANDARD; PRT; 546 AA.
ID PCRB_SACER
AC P53003;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Propionyl-CoA carboxylase beta chain (EC 6.4.1.3) (PCCase) (Propionyl-
DE CoA:carbon dioxide ligase).

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GN PCOB.
OS Saccharopolyspora erythraea (Streptomyces erythraeus).
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Pseudonocardiaceae; Pseudonocardiaceae; Saccharopolyspora.
OX NCBI_TaxID=1836;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NRRL 2338;
RA MEDLINE=96249691; PubMed=8830278;
RX Donadio S., Staver M.J., Katz L.;
RT "Erythromycin production in Saccharopolyspora erythraea does not
RT require a functional propionyl-CoA carboxylase.";
RL Mol. Microbiol. 19:977-984(1996).
CC -1- CATALYTIC ACTIVITY: ATP + propanoyl-CoA + HCO(3)(-) = ADP +
CC phosphate + (S)-methylmalonyl-CoA.
CC -1- PATHWAY: KEY ENZYME IN THE CATABOLIC PATHWAY OF ODD-CHAIN
CC FATTY ACIDS, ISOLEUCINE, THREONINE, METHIONINE, AND VALINE.
CC -1- SUBUNIT: PROBABLY A DODECAMER COMPOSED OF SIX BIOTIN-CONTAINING
CC ALPHA SUBUNITS & SIX BETA SUBUNITS (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE ACCD / PCOB FAMILY.
CC -----
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CC -----
DR EMBL: X92557; CAA63310.1; -.
DR PIR: S71008;
DR InterPro: IPR000438; ACOACC_transf.
DR InterPro: IPR000022; Carboxyl_trans.
DR Pfam: PF01039; Carboxyl_trans. 1.
DR PRINTS: PR01070; ACCCTFRASEB.
DR LIGASE.
KM SEQUENCE 546 AA; 58526 MW; 96A38CA77FC68C5 CRC64;
SQ
Query Match 60.7%; Score 37; DB 1; Length 546;
Best Local Similarity 85.7%; Pred. No. 28;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Oy 4 DRPYADG 10
Db 87 DRPYGDG 93

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RL Submitted (MAR-1997) to the EMBL/Genbank/DBJ databases.
CC -1- FUNCTION: Likely to be an important mediator of ventricular
CC differentiation during cardiac development.
CC -1- SUBCELLULAR LOCATION: Nuclear (Probable).
CC -1- TISSUE SPECIFICITY: Predominantly expressed in cardiac ventricles.
CC -1- SIMILARITY: BELONGS TO THE TALE/IRO HOMEOBOX FAMILY.
CC -----
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CC -----
DR EMBL: AF124733; AAF23887.1; -.
DR EMBL: U90306; AAB50004.1; -.
DR HSSP: PA1778; IDU6.
DR TRANSFAC: T04275; -.
DR GeneW: HGNC:6129; IRX4.
DR MIM: 606199; -.
DR GO: GO:0007507; P:heart development; TAS.
DR InterPro: IPR001356; Homeobox.
DR InterPro: IPR003893; Iroquois_homeo.
DR Pfam: PF00046; homeobox. 1.
DR ProDom: PD000010; Homeobox; 1.
DR SMART: SM00389; HOX; 1.
DR SMART: SM00548; IRO; 1.
DR PROSITE: PS00027; HOMEOBOX_1; 1.
DR PROSITE: PS50071; HOMEOBOX_2; 1.
KM Homeobox: DNA-binding; Nuclear protein.
FT DNA_BIND 143 204 HOMEOBOX (TALE-TYPE).
FT DOMAIN 223 228 POLY-GLU.
FT FT 375 382 POLY-ALA.
FT FT 181 181 I -> T (IN REF. 2).
SQ SEQUENCE 519 AA; 54444 MW; B2FEB278BFC5AD2 CRC64;
Oy 1 CRDD-RPYADG 10
Db 214 CADKRPVADG 224

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RESULT 19
IRX4_HUMAN
ID IRX4_HUMAN STANDARD; PRT; 519 AA.
AC P78413; Q8UHR2;
DT 15-JUL-1998 (Rel. 36, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Iroquois-class homeodomain protein IRX-4 (Iroquois homeobox protein
DE 4).
GN IRX4.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=20092750; PubMed=10625552;
RX Brunau B.G., Bao Z.-Z., Tanaka M., Schott J.J., Izumo S., Cepko C.L.,
RA Seidman J.G., Seidman C.E.;
RT "Cardiac expression of the ventricle-specific homeobox gene Irx4 is
RT modulated by Nkx2-5 and dHAND.";
RL Dev. Biol. 217:266-277(2000).
RN [2]
RP SEQUENCE OF 80-191 FROM N.A.
RA Lewis M.T., Strickland P.A., Ross S., Snyder C.J., Daniel C.W.;
RT "IRX: a new family of human homeobox genes from the breast.";
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RESULT 20
TRMD_BUCAL
ID TRMD_BUCAL STANDARD; PRT; 237 AA.
AC P57476;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE tRNA (Guanine-N(1)-methyltransferase (EC 2.1.1.31) (MG-
DE methyltransferase) (tRNA [GM37] methyltransferase).
GN TRMD OR BU396.
OS Buchnera aphidicola (subsp. Acyrthosiphon pisum) (Acyrthosiphon pisum
OS symbiotic bacterium).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Buchnera.
OX NCBI_TaxID=118099;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Tokyo 1998;
RX MEDLINE=20445173; PubMed=10993077;
RA Shigenobu S., Watanabe H., Hattori M., Sakaki Y., Ishikawa H.;
RT "Genome sequence of the endocellular bacterial symbiont of aphids
RT Buchnera sp. APS.";
RL Nature 407:81-86(2000).
CC -1- FUNCTION: Specifically methylates guanosine-37 in various tRNAs
CC (by similarity).
CC -1- CATALYTIC ACTIVITY: S-adenosyl-L-methionine + tRNA = S-adenosyl-L-
CC homocysteine + tRNA containing N(1)-methylguanine.
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CC -1- SUBCELLULAR LOCATION: Cytoplasmic (Potential)
CC -1- SIMILARITY: BELONGS TO THE RNA METHYLTRANSFERASE TRMD FAMILY.
CC -----
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CC -----
DR EMBL: AF001119; BAB13099.1; -
DR HAMAP: MF_00605; -; 1.
DR InterPro: IPR002649; tRNA_mIG_MT.
DR Pfam: PF01746; tRNA_mIG_MT.1.
DR ProDom: PD004978; tRNA_mIG_MT.1.
DR TIGRFAMs: TIGR00088; tmd; 1.
KW tRNAse; Methyltransferase; tRNA processing; Complete proteome.
SQ SEQUENCE 237 AA; 27335 MW; 86CE3836B35EC4AB CRC64;

Query Match 59.0%; Score 36; DB 1; Length 237;
Best Local Similarity 75.0%; Pred. No. 18;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 DDRPYADG 10
DB 59 DDRPYGCG 66

RESULT 21
TRMD_PASMTU STANDARD: PRT; 245 AA.
AC Q0CCE1;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DE tRNA (Guanine-N(1)-)-methyltransferase (EC 2.1.1.31) (MIG-
DE methyltransferase) (tRNA [GM37] methyltransferase).
GN tRMD OR PM1297.
OS Pasteurella multocida.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
OC Pasteurellaceae; Pasteurella.
OX NCBI_TaxID=747;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PM70;
RA MEDLINE=21145866; PubMed=11248100;
RA May B.T., Zhang Q., Li L.L., Paustian M.L., Whittam T.S., Kapur V.;
RA "Complete genomic sequence of Pasteurella multocida PM70.";
RA Proc. Natl. Acad. Sci. U.S.A. 98:3460-3465(2001).
CC -1- FUNCTION: Specifically methylates guanosine-37 in various tRNAs
CC (By similarity).
CC -1- CATALYTIC ACTIVITY: S-adenosyl-L-methionine + tRNA = S-adenosyl-L-
CC homocysteine + tRNA containing N(1)-methylguanine.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (Potential).
CC -1- SIMILARITY: BELONGS TO THE RNA METHYLTRANSFERASE TRMD FAMILY.
CC -----
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CC -----
DR EMBL: AF006168; AAC0381.1; -
DR HAMAP: MF_00605; -; 1.
DR InterPro: IPR002649; tRNA_mIG_MT.
DR Pfam: PF01746; tRNA_mIG_MT.1.
DR ProDom: PD004978; tRNA_mIG_MT.1.
DR TIGRFAMs: TIGR00088; tmd; 1.
KW tRNAse; Methyltransferase; tRNA processing; Complete proteome.
SQ SEQUENCE 245 AA; 27494 MW; 6A35655295A59354 CRC64;
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Query Match 59.0%; Score 36; DB 1; Length 245;
Best Local Similarity 75.0%; Pred. No. 19;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 DDRPYADG 10
DB 50 DDRPYGCG 57

RESULT 22
TRMD_HAEIN STANDARD: PRT; 246 AA.
AC P43912;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE tRNA (Guanine-N(1)-)-methyltransferase (EC 2.1.1.31) (MIG-
DE methyltransferase) (tRNA [GM37] methyltransferase).
GN tRMD OR H10202.
OS Haemophilus influenzae.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
OC Pasteurellaceae; Haemophilus.
OX NCBI_TaxID=727;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Rd / KM20 / ATCC 51907;
RA MEDLINE=95350630; PubMed=7542800;
RA Krievagmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,
RA Krievagmann A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,
RA McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,
RA Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,
RA Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,
RA Uiterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,
RA Fine L.D., Fritchman J.L., Fuhrman J.L., Geoghegan N.S.M.,
RA Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
RA Venter J.C.;
RT "Whole-genome random sequencing and assembly of Haemophilus influenzae
RT Rd.";
RL Science 269:496-512(1995).
CC -1- FUNCTION: Specifically methylates guanosine-37 in various tRNAs
CC (By similarity).
CC -1- CATALYTIC ACTIVITY: S-adenosyl-L-methionine + tRNA = S-adenosyl-L-
CC homocysteine + tRNA containing N(1)-methylguanine.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (Potential).
CC -1- SIMILARITY: BELONGS TO THE RNA METHYLTRANSFERASE TRMD FAMILY.
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CC -----
DR EMBL: U32705; AAC21871.1; -
DR PIR: C64054; C64054.
DR TIGR: H10202; C64054.
DR HAMAP: MF_00605; -; 1.
DR InterPro: IPR002649; tRNA_mIG_MT.
DR Pfam: PF01746; tRNA_mIG_MT.1.
DR ProDom: PD004978; tRNA_mIG_MT.1.
DR TIGRFAMs: TIGR00088; tmd; 1.
KW tRNAse; Methyltransferase; tRNA processing; Complete proteome.
SQ SEQUENCE 246 AA; 27542 MW; DEEF238159B1003D CRC64;

Query Match 59.0%; Score 36; DB 1; Length 246;
Best Local Similarity 75.0%; Pred. No. 19;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 DDRPYADG 10
DB 50 DDRPYGCG 57
```

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RESULT 23
TRMD_YERPE STANDARD; PRT; 246 AA.
ID TRMD_YERPE
AC 082B09: 08CWM8;
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last sequence update)
DE tRNA (Guanine-N(1)-)-methyltransferase (EC 2.1.1.31) (MIG-
DE methyltransferase) (tRNA [GM37] methyltransferase).
GN TRMD OR YPO3293 OR Y0896.
OS Yersinia pestis.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Yersinia.
ON NCBI_TaxID=632;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CO-92 / Biovar Orientalis;
RX MEDLINE=21470413; PubMed=11586360;
RA Parkhill J., Wren B.W., Thomson N.R., Titball R.W., Holden M.T.G.,
RA Prentice M.B., Sebahitha M., James K.D., Churcher C., Mungall K.L.,
RA Baker S., Basham D., Bentley S.D., Brooks K., Cerdano-Tarraga A.M.,
RA Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G.,
RA Felwell T., Hamlin N., Holroyd S., Jagels K., Karpishev A.V.,
RA Leather S., Moule S., Oyston P.C.F., Quail M., Rutherford K.,
RA Simmonds M., Skelton J., Stevens K., Whitehead S., Barrall B.G.;
RT "Genome sequence of Yersinia pestis, the causative agent of plague."
RL Nature 413:523-527(2001).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=KIM5 / Biovar Medisevalis;
RX MEDLINE=22137863; PubMed=12142430;
RA Deng W., Burland V., Plunkett G., III, Boutin A., Mayhew G.F., Liss P.,
RA Perna N.T., Rose D.J., Mau B., Zhou S., Schwartz D.C.,
RA Reheston J.D., Lindler L.E., Brubaker R.R., Plano G.V.,
RA Straley S.C., McDonough K.A., Nilles M.L., Watson J.S., Blattner F.R.,
RA Perry R.D.;
RT "Genome sequence of Yersinia pestis KIM."
RL J. Bacteriol. 184:4601-4611(2002).
CC -1- FUNCTION: Specifically methylates guanosine-37 in various tRNAs
CC (by similarity).
CC -1- CATALYTIC ACTIVITY: S-adenosyl-L-methionine + tRNA = S-adenosyl-L-
CC homocysteine + tRNA containing N(1)-methylguanine.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (Potential).
CC -1- SIMILARITY: BELONGS TO THE RNA METHYLTRANSFERASE TRMD FAMILY.
CC
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CC -----
DR EMBL: AJ414156; CAC92525.1; -
DR EMBL: AE013692; AAM84480.1; ALT_INIT.
DR PIR: A10399; A10399.
DR HAMAP: MF_00605; -; 1.
DR InterPro: IPR002649; tRNA_m1G_MT.
DR Pfam: PF01746; tRNA_m1G_MT.1.
DR ProDom: PD004978; tRNA_m1G_MT.1.
DR TrEMBL: TIGR00088; trmd; 1.
KW Transferase; Methyltransferase; tRNA processing; Complete proteome.
SQ SEQUENCE 246 AA; 27618 MW; DB800072F976ABCE CRC64;

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RESULT 24
TRMD_VIBVU STANDARD; PRT; 249 AA.
ID TRMD_VIBVU
AC 08CWM5;
DT 15-SEP-2003 (Rel. 42, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last sequence update)
DE tRNA (Guanine-N(1)-)-methyltransferase (EC 2.1.1.31) (MIG-
DE methyltransferase) (tRNA [GM37] methyltransferase).
GN TRMD OR V11617.
OS Vibrio vulnificus.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Vibrrio.
ON NCBI_TaxID=672;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CMCP6;
RX Rhee J.H., Kim S.Y., Chung S.S., Kim J.J., Moon Y.H., Jeong H.,
RA Choy H.E.;
RT "Complete genome sequence of Vibrio vulnificus CMCP6."
RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Specifically methylates guanosine-37 in various tRNAs
CC (by similarity).
CC -1- CATALYTIC ACTIVITY: S-adenosyl-L-methionine + tRNA = S-adenosyl-L-
CC homocysteine + tRNA containing N(1)-methylguanine.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (Potential).
CC -1- SIMILARITY: BELONGS TO THE RNA METHYLTRANSFERASE TRMD FAMILY.
CC
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: AE016802; AAO10036.1; -
DR HAMAP: MF_00605; -; 1.
DR InterPro: IPR002649; tRNA_m1G_MT.
DR Pfam: PF01746; tRNA_m1G_MT.1.
DR ProDom: PD004978; tRNA_m1G_MT.1.
DR TrEMBL: TIGR00088; trmd; 1.
KW Transferase; Methyltransferase; tRNA processing; Complete proteome.
SQ SEQUENCE 249 AA; 28157 MW; B1CF66BCE5D3451 CRC64;

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Query Match 59.0%; Score 36; DB 1; Length 246;
Best Local Similarity 75.0%; Pred. No. 19;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Query Match 59.0%; Score 36; DB 1; Length 249;
Best Local Similarity 75.0%; Pred. No. 19;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Van Ham R.C.H.J., Kamerbeek J., Palacios C., Rausell C., Abascal F.,
RA Basolia U., Fernandez J.M., Jimenez L., Postigo M., Silva F.J.,
RA Tamames J., Vignera E., Latorre A., Valencia A., Moran F., Moya A.;
RA "Reductive genome evolution in Buchnera aphidicola.";
RA Proc. Natl. Acad. Sci. U.S.A. 100:581-586(2003).
CC
CC -1- FUNCTION: Specifically methylates guanosine-37 in various tRNAs
CC (By similarity).
CC -1- CATALYTIC ACTIVITY: S-adenosyl-L-methionine + tRNA = S-adenosyl-L-
CC homocysteine + tRNA containing N(1)-methylguanine.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (Potential).
CC -1- SIMILARITY: BELONGS TO THE RNA METHYLTRANSFERASE TRMD FAMILY.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL: AB014017; AAC27078.1; -.
CC
CC DR HAMAP, MF_00605; -.
CC DR Pfdom, PF004376; tRNA_m1G_MT; 1.
CC KW Methyltransferase; tRNA processing; Complete proteome.
CC
CC SEQUENCE 230 AA; 28637 MW; 1FE321EEF2A6D9DD CRC64;
CC
CC Query Match 59.0%; Score 36; DB 1; Length 250;
CC Best Local Similarity 75.0%; Pred. No. 19;
CC Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
CC
CC Oy 3 DDDPYAGG 10
CC |11111|
CC Db 50 DDDPYGCG 57
CC
CC RESULT 26
CC TRMD_ECOLI STANDARD; PRG: 255 AA.
CC ID P07020;
CC AC 01-APR-1988 (Rel. 07, Last sequence update)
CC DT 01-APR-1988 (Rel. 07, Last sequence update)
CC DT 28-FEB-2003 (Rel. 41, Last annotation update)
CC DE tRNA (Guanine-N(1)-methyltransferase (EC 2.1.1.31) (MIG-
CC methyltransferase) (tRNA [Gm37] methyltransferase).
CC CH NMD OR B2607 OR C3128 OR Z5901 OR EC35470 OR SF2667.
CC OS Escherichia coli O6.
CC OS Escherichia coli O6.
CC OS Escherichia coli O157:H7, and
CC OS Shigella flexneri.
CC OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
CC OC Enterobacteriaceae; Escherichia.
CC OX NCBI_TaxID=562, 217992, 83334, 623;
CC [1]
CC RP SEQUENCE FROM N.A.
CC RC SPECIES-E.COLI;
CC RX MEDLINE=84057772; PubMed=6357787;
CC RA Byström A.S., Hjalmarsson K.J., Wikström P.M., Björk G.R.;
CC "The nucleotide sequence of an Escherichia coli operon containing
CC genes for the tRNA(m1G)methyltransferase, the ribosomal proteins S16
CC and L19 and a 21-k polypeptide.";
CC RT EMBO J. 2:899-905(1983).
CC RL
CC RN
CC RP SEQUENCE FROM N.A.
CC RC SPECIES-E.COLI; STRAIN=K12 / MG1655;
CC RX MEDLINE=97426617; PubMed=9278503;
CC RA Blatner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
CC Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
CC Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
CC Mau B., Shao Y.;
CC "The complete genome sequence of Escherichia coli K-12.";
CC RT Science 277:1453-1474(1997).
CC RL
CC RP SEQUENCE FROM N.A.
CC
CC SPECIES-E.coli; STRAIN=K12;
CC MEDLINE=97349980; PubMed=9205837;
CC Yamamoto Y., Alba H., Baba T., Hayashi K., Inada T., Isono K.,
CC Itoh T., Kimura S., Kitagawa M., Makino K., Miki T., Mitsushashi N.,
CC Mizubuchi K., Mori H., Nakade S., Nakamura Y., Nashimoto H.,
CC Oshima T., Oyama S., Saito N., Sampei G., Satoh Y., Sivasubaram S.,
CC Tagami H., Takahashi H., Takeda J., Takemoto K., Uehara K., Wada C.,
CC Yamagata S., Horikuchi T.;
CC "Construction of a contiguous 874-kb sequence of the Escherichia coli
CC K-12 genome corresponding to 50.0-68.8 min on the linkage map and
CC analysis of its sequence features.";
CC RT DNA Res. 4:91-113(1997).
CC RL
CC RN
CC RP SEQUENCE FROM N.A.
CC RC SPECIES-E.coli; STRAIN=06-H1 / CFT073 / ATCC 700928;
CC RX MEDLINE=22388234; PubMed=12471157;
CC Wachi R.A., Burland V., Plunkett G. III, Redford P., Roesch P.,
CC Maslow G., Buckles E.L., Lion S.-R., Boutin A., Hackett J., Stroud D.,
CC Mobley H.L.T., Domeneberg M.S., Blatner F.R.;
CC Extensive mosaic structure revealed by the complete genome sequence
CC of uropathogenic Escherichia coli.";
CC Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024(2002).
CC RL
CC RN
CC RP SEQUENCE FROM N.A.
CC RC SPECIES-E.coli; STRAIN=0157:H7 / EDL933 / ATCC 700927;
CC MEDLINE=21074935; PubMed=11206551;
CC Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
CC Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
CC Postel G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
CC Apodaca J., Anantharaman T.S., Lim A., Dimalanta E.T., Potamousis K.,
CC Welch R.A., Blatner F.R.;
CC "Genome sequence of enterohaemorrhagic Escherichia coli O157:H7.";
CC Nature 409:529-533(2001).
CC RL
CC RN
CC RP SEQUENCE FROM N.A.
CC RC SPECIES-E.coli; STRAIN=0157:H7 / RIMD 0509952;
CC MEDLINE=21156231; PubMed=11258796;
CC Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,
CC Han C.-G., Ohtsubo F., Nakayama K., Murata T., Tanaka M., Tobe T.,
CC Tida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T.,
CC Kuhara S., Shiba H., Hattori M., Shingawa H.;
CC "Complete genome sequence of enterohaemorrhagic Escherichia coli
CC O157:H7 and genomic comparison with a laboratory strain K-12.";
CC DNA Res. 8:11-22(2001).
CC RL
CC RN
CC RP SEQUENCE FROM N.A.
CC RC SPECIES-S.flexneri; STRAIN=301 / Serotype 2a;
CC MEDLINE=22272406; PubMed=12384590;
CC Jin Q., Yan Z., Xu J., Wang Y., Shen Y., Lu W., Wang J., Liu H.,
CC Yang J., Yang F., Zhang X., Zhang J., Yang G., Wu H., Qu D., Dong J.,
CC Sun L., Xue Y., Zhao A., Gao Y., Zhu J., Kan B., Ding K., Chen S.,
CC Cheng H., Yao Z., He B., Chen R., Ma D., Qiang B., Wen Y., Hou Y.,
CC Yu J.;
CC "Genome sequence of Shigella flexneri 2a: insights into pathogenicity
CC through comparison with genomes of Escherichia coli K12 and O157.";
CC Nucleic Acids Res. 30:4432-4441(2002).
CC RL
CC RN
CC RP CHARACTERIZATION, AND SEQUENCE OF 1-10.
CC RC SPECIES-E.coli;
CC RX MEDLINE=83108856; PubMed=6337136;
CC Hjalmarsson K.J., Byström A.S., Björk G.R.;
CC "Purification and characterization of transfer RNA (guanine-
CC 1)methyltransferase from Escherichia coli.";
CC RT J. Biol. Chem. 258:1343-1351(1983).
CC CC -1- FUNCTION: Specifically methylates guanosine-37 in various tRNAs.
CC -1- CATALYTIC ACTIVITY: S-adenosyl-L-methionine + tRNA = S-adenosyl-L-
CC homocysteine + tRNA containing N(1)-methylguanine.
CC -1- SUBUNIT: Monomer.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (Potential).
CC -1- MISCELLANEOUS: THE SPECIFIC ACTIVITY OF THIS ENZYME INCREASES ONLY
CC SLIGHTLY WITH INCREASED GROWTH RATE.
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CC -1- MISCELLANEOUS: THIS ENZYME IS PRESENT AT CA. 80 MOLECULES/GENOME.
CC -1- SIMILARITY: BELONGS TO THE RNA METHYLTRANSFERASE TRMD FAMILY.
CC -----
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CC -----
DR EMBL: X01818; CA25959.1; -
DR EMBL: AE000346; AAC75656.1; -
DR EMBL: D90888; BA16492.1; -
DR EMBL: AE016764; AAN81578.1; -
DR EMBL: AE005490; AAG57718.1; -
DR EMBL: AP002562; BAB36893.1; -
DR EMBL: AE015282; AAN44162.1; -
DR PIR: A30380; XRECG1.
DR PIR: B85907; B85907.
DR PIR: F91062; F91062.
DR EcoGene: EGI1023; trmd.
DR HAMAP: MF_00605; -; 1.
DR InterPro: IPR002649; tRNA_m1G_MT.
DR Pfam: PF01746; tRNA_m1G_MT; 1.
DR ProDom: PD004978; tRNA_m1G_MT; 1.
DR TIGRPFAMs: TIGR00088; trmd; 1.
DR Transferrase; Methyltransferase; tRNA processing; Complete proteome.
SQ SEQUENCE 255 AA; 28422 MW; B101087229B4CDBD CRC64;

Query Match 59.0%; Score 36; DB 1; Length 255;
Best Local Similarity 75.0%; Pred. No. 20;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 DDRPYADG 10
Db 50 DDRPYGGG 57

RESULT 27
TRMD_SALTY
ID TRMD_SALTY STANDARD; PRT; 255 AA.
AC 082415;
DT 28-FEB-2003 (Rel. 41, Last Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE tRNA (Guanine-N(1)-)-methyltransferase (EC 2.1.1.31) (MIG-
DE methyltransferase) (tRNA [GM37] methyltransferase).
GN TRMD OR STM2861 OR T2629.
OS Salmonella typhi.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Salmonella.
OX NCBI_TaxID=601;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CT18;
RA MEDLINE=21534947; Pubmed=11677608;
RA Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J.,
RA Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebahia M.,
RA Baker S., Basham D., Brooks K., Chillingworth T., Connerton P.,
RA Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J.,
RA Felwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jorgels K.,
RA Krogh A., Larsen T.S., Leather S., Moule S., O'Gea P., Parry C.,
RA Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K.,
RA Whitehead S., Barrall B.G.;
RA "Complete genome sequence of a multiple drug resistant Salmonella
RA enterica serovar Typhi CT18."
RL Nature 413:848-852(2001).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=TY2 / ATCC 700931;
RX MEDLINE=22531367; Pubmed=12644504;
RA Deng W., Liou S.-R., Plunkett G. III, Mayhew G.F., Rose D.J.,

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RA Burland V., Kodoyianni V., Schwartz D.C., Blattner F.R.;
RA "Comparative genomics of Salmonella enterica serovar Typhi strains Ty2
RA and CT18."
RL J. Bacteriol. 185:2330-2337(2003).
CC -1- FUNCTION: Specifically methylates guanosine-37 in various tRNAs
CC (by similarity).
CC -1- CATALYTIC ACTIVITY: S-adenosyl-L-methionine + tRNA = S-adenosyl-L-
CC homocysteine + tRNA containing N(1)-methylguanine.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (potential).
CC -1- SIMILARITY: BELONGS TO THE RNA METHYLTRANSFERASE TRMD FAMILY.
CC -----
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CC -----
DR EMBL: AL62726; CAD05853.1; -
DR EMBL: AE016843; AAO70200.1; -
DR HAMAP: MF_00605; -; 1.
DR InterPro: IPR002649; tRNA_m1G_MT.
DR Pfam: PF01746; tRNA_m1G_MT; 1.
DR ProDom: PD004978; tRNA_m1G_MT; 1.
DR TIGRPFAMs: TIGR00088; trmd; 1.
DR Transferrase; Methyltransferase; tRNA processing; Complete proteome.
SQ SEQUENCE 255 AA; 28318 MW; B96812A32091495F CRC64;

Query Match 59.0%; Score 36; DB 1; Length 255;
Best Local Similarity 75.0%; Pred. No. 20;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 DDRPYADG 10
Db 50 DDRPYGGG 57

RESULT 28
TRMD_SALTY
ID TRMD_SALTY STANDARD; PRT; 255 AA.
AC P36245;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE tRNA (Guanine-N(1)-)-methyltransferase (EC 2.1.1.31) (MIG-
DE methyltransferase) (tRNA [GM37] methyltransferase).
GN TRMD OR STM2674.
OS Salmonella typhimurium.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Salmonella.
OX NCBI_TaxID=602;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=LT2;
RA Persson B.C.;
RA Submitted (SEP-1993) to the EMBL/Genbank/DBJ databases.
RL [2]
RP SEQUENCE FROM N.A.
RC STRAIN=LT2 / SCS1412 / ATCC 700720;
RX MEDLINE=21534948; Pubmed=11677609;
RA McClelland M., Sanderson K.E., Speith J., Clifton S.W., Latreille P.,
RA Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D.,
RA Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,
RA Ryan E., Sun H., Flores L., Miller W., Stoneking T., Nhan M.,
RA Waterston R., Wilson R.K.;
RA "Complete genome sequence of Salmonella enterica serovar Typhimurium
RA LT2."
RL Nature 413:852-856(2001).
CC -1- FUNCTION: Specifically methylates guanosine-37 in various tRNAs
CC (by similarity).
CC -1- CATALYTIC ACTIVITY: S-adenosyl-L-methionine + tRNA = S-adenosyl-L-
CC homocysteine + tRNA containing N(1)-methylguanine.

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CC -1- SUBCELLULAR LOCATION: Cytoplasmic (Potential).
CC -1- SIMILARITY: BELONGS TO THE RNA METHYLTRANSFERASE TRMD FAMILY.
CC -----
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CC -----
DR EMBL: X74933; CAAS2887.1; -.
DR EMBL: AE008821; AAL21563.1; -.
DR PIR: S37175; S37175.
DR StryGene: SG10395; trmd.
DR HAMAP: MF_00605; -. 1.
DR InterPro: IPR002649; tRNA_mig_MT.
DR Pfam: PF01746; tRNA_mig_MT; 1.
DR TrifRAMS: TRIGR00088; trmd; 1.
DR TrifRAMS: Methyltransferase; tRNA processing; Complete proteome.
SQ SEQUENCE 255 AA; 28348 MW; A5691ED3CE1495F CRC64;

Query Match
Best Local Similarity 59.0%; Score 36; DB 1; Length 255;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 DDPRYADG 10
Db 50 DDPRYGGG 57

RESULT 29
TRMD_SERMA STANDARD; PRT; 255 AA.
AC P36244;
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 01-JUN-1994 (Rel. 41, Last annotation update)
DE 28-FEB-2003 (Rel. 41, Last annotation update)
DE tRNA (Guanine-N(1))-methyltransferase (EC 2.1.1.31) (MIG-
DE methyltransferase) (tRNA [GM37] methyltransferase).
GN TRMD.
OS Serratia marcescens.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Serratia.
OX NCBI_TaxID=615;
RN [1]
RP SEQUENCE FROM N.A.
RX SPRAIN-SM6;
RX MEDLINE-94320777; PubMed-8045416;
RA Jin S., Benedix M.O.;
RT "Sequences of the Serratia marcescens rplS and trmd genes.";
RL Gene 143:147-148(1994).
CC -1- FUNCTION: Specifically methylates guanosine-37 in various tRNAs
CC (By similarity).
CC -1- CATALYTIC ACTIVITY: S-adenosyl-L-methionine + tRNA = S-adenosyl-L-
CC homocysteine + tRNA containing N(1)-methylguanine.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (Potential).
CC -1- SIMILARITY: BELONGS TO THE RNA METHYLTRANSFERASE TRMD FAMILY.
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CC -----
DR EMBL: L23334; AAS50783.1; -.
DR HAMAP: MF_00605; 1.
DR InterPro: IPR002649; tRNA_mig_MT.
DR Pfam: PF01746; tRNA_mig_MT; 1.
DR TrifRAMS: TRIGR00088; tRNA_mig_MT; 1.
DR TrifRAMS: Methyltransferase; tRNA processing; Complete proteome.
SQ SEQUENCE 262 AA; 30500 MW; 653A65B1663A04CA CRC64;

```

```

DR TrifRAMS: TRIGR00088; trmd; 1.
DR TrifRAMS: Methyltransferase; tRNA processing.
SQ SEQUENCE 255 AA; 28465 MW; 48A71576D9B3A50B CRC64;

Query Match
Best Local Similarity 59.0%; Score 36; DB 1; Length 255;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 DDPRYADG 10
Db 50 DDPRYGGG 57

RESULT 30
TRMD_BUCAP STANDARD; PRT; 262 AA.
AC O8K9F4;
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE tRNA (Guanine-N(1))-methyltransferase (EC 2.1.1.31) (MIG-
DE methyltransferase) (tRNA [GM37] methyltransferase).
GN TRMD OR B0SG383;
OS Buchnera aphidicola (subsp. Schizaphis graminum).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Buchnera.
OX NCBI_TaxID=98794;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-22084549; PubMed-12089438;
RA Tames I., Klasson L., Canbaeck B., Naeslund A.K., Eriksson A.-S.,
RA Wernegreen J.J., Sandstrom J.P., Moran N.A., Andersson S.G.E.;
RT "50 million years of genomic stasis in endosymbiotic bacteria.";
RL Science 296:2376-2379(2002).
CC -1- FUNCTION: Specifically methylates guanosine-37 in various tRNAs
CC (By similarity).
CC -1- CATALYTIC ACTIVITY: S-adenosyl-L-methionine + tRNA = S-adenosyl-L-
CC homocysteine + tRNA containing N(1)-methylguanine.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (Potential).
CC -1- SIMILARITY: BELONGS TO THE RNA METHYLTRANSFERASE TRMD FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@sib-sib.ch).
CC -----
DR EMBL: AE014114; AAM67935.1; -.
DR InterPro: IPR002649; tRNA_mig_MT.
DR Pfam: PF01746; tRNA_mig_MT; 1.
DR TrifRAMS: TRIGR00088; tRNA_mig_MT; 1.
DR TrifRAMS: Methyltransferase; tRNA processing; Complete proteome.
SQ SEQUENCE 262 AA; 30500 MW; 653A65B1663A04CA CRC64;

Query Match
Best Local Similarity 59.0%; Score 36; DB 1; Length 262;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 DDPRYADG 10
Db 67 DDPRYGGG 74

Search completed: August 29, 2003, 18:45:12
Job time : 8.57143 secs

```

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OK protein - protein search, using sw model

Run on: August 29, 2003, 18:40:25 ; Search time 24.5714 Seconds
(without alignments)
105.021 Million cell updates/sec

Title: US-09-830-876-2
Perfect score: 61
Sequence: 1 CRDPRPADG 10

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database :

1: SP archaea: *
2: SP bacteria: *
3: SP fungi: *
4: SP human: *
5: SP invertebrate: *
6: SP mammal: *
7: SP mhc: *
8: SP organelle: *
9: SP phage: *
10: SP plant: *
11: SP rodent: *
12: SP virus: *
13: SP vertebrate: *
14: SP unclassified: *
15: SP virus: *
16: SP bacteriophage: *
17: SP archaea: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	61	100.0	427	10	Q40015
2	61	100.0	427	10	Q03651
3	56	91.8	429	10	Q40016
4	47	77.0	421	10	Q42504
5	47	77.0	437	10	Q04956
6	44	72.1	416	10	Q08LJ06
7	44	72.1	416	10	Q08GUR0
8	44	72.1	437	10	Q04964
9	44	72.1	437	10	Q40018
10	44	72.1	438	10	Q40017
11	42	68.9	434	10	Q081699
12	42	68.9	437	10	Q081700
13	41	67.2	278	10	Q092472
14	41	67.2	420	10	Q092P43
15	41	67.2	423	10	Q42678
16	41	67.2	424	10	Q08LP27

17	41	67.2	1593	5	Q08X82
18	41	67.2	2871	5	Q09V483
19	41	67.2	2871	5	Q08T87
20	40	65.6	248	16	Q08E74
21	40	65.6	266	16	Q08D041
22	40	65.6	105	16	Q02R82
23	39.5	64.8	175	16	Q09J13
24	39	63.9	144	16	Q09J98
25	39	63.9	370	16	Q09A976
26	39	63.9	382	16	Q09878
27	39	63.9	556	5	Q09NG23
28	39	63.9	594	5	Q09Y113
29	39	63.9	642	5	Q08MP6
30	39	63.9	739	5	Q09GS24
31	39	63.9	742	5	Q08IV3
32	39	63.9	872	16	Q08P73
33	39	63.9	1285	16	Q08DA47
34	38	62.3	109	10	Q04D61
35	38	62.3	386	12	Q09WT61
36	38	62.3	386	12	Q09J56
37	38	62.3	449	10	Q09AV79
38	38	62.3	795	10	Q09AF1
39	38	62.3	740	2	Q093GV9
40	37	60.7	42	6	Q02794
41	37	60.7	136	5	Q09NHL9
42	37	60.7	253	2	Q03093
43	37	60.7	254	5	Q09U78
44	37	60.7	325	10	Q093700
45	37	60.7	413	4	Q096864
46	37	60.7	413	4	Q099984
47	37	60.7	463	5	Q09N2M4
48	37	60.7	463	5	Q02947
49	37	60.7	510	2	Q08K41
50	37	60.7	521	16	Q09AP5
51	37	60.7	766	4	P02987
52	37	60.7	857	13	P79708
53	37	60.7	1023	4	Q09UL17
54	37	60.7	1083	2	Q08K78
55	37	60.7	1417	10	Q09AX82
56	37	60.7	1450	10	Q08C089
57	37	60.7	2287	5	Q08I520
58	37	60.7	6521	2	Q08RL72
59	36	59.0	133	9	Q091166
60	36	59.0	173	16	Q098CT9
61	36	59.0	194	5	Q08SVU7
62	36	59.0	248	16	Q08CX44
63	36	59.0	249	16	Q08CWK5
64	36	59.0	258	2	Q052599
65	36	59.0	282	16	Q08CW8
66	36	59.0	349	10	Q041441
67	36	59.0	418	5	Q09CTK1
68	36	59.0	446	17	Q09HHJ9
69	36	59.0	482	16	Q08K78
70	36	59.0	516	16	Q09CD09
71	36	59.0	537	16	Q09ZLC7
72	36	59.0	1123	5	Q018431
73	36	59.0	1181	16	Q08G634
74	36	59.0	4834	4	Q095714
75	35.5	58.2	206	10	Q09ZTE1
76	35.5	58.2	280	10	Q09LXV2
77	35.5	58.2	164	16	Q09WE4
78	35.5	58.2	118	10	Q094287
79	35	57.4	153	5	Q016208
80	35	57.4	196	10	Q09SJA6
81	35	57.4	207	16	Q08XW6
82	35	57.4	225	12	Q08BOV3
83	35	57.4	269	10	Q08HOC9
84	35	57.4	270	10	Q081934
85	35	57.4	295	2	Q054379
86	35	57.4	330	2	Q08CP47
87	35	57.4	338	10	Q0942E4
88	35	57.4	340	11	Q08BR07
89	35	57.4	340	11	Q08BR07

Q08X82	drosophila
Q09V483	drosophila
Q08T87	drosophila
Q08E74	yeast
Q08D041	yeast
Q02R82	yeast
Q09J13	strepomyces
Q09J98	strepomyces
Q09A976	mycobacter
Q09878	mycobacter
Q09NG23	rhizobium
Q09Y113	rhizobium
Q08MP6	giardia
Q09GS24	giardia
Q08IV3	giardia
Q08P73	giardia
Q08DA47	giardia
Q04D61	giardia
Q09WT61	giardia
Q09J56	giardia
Q09AV79	giardia
Q09AF1	giardia
Q093GV9	giardia
Q02794	giardia
Q09NHL9	giardia
Q03093	giardia
Q09U78	giardia
Q093700	giardia
Q096864	giardia
Q099984	giardia
Q09N2M4	giardia
Q02947	giardia
Q08K41	giardia
Q09AP5	giardia
P02987	giardia
P79708	giardia
Q09UL17	giardia
Q08K78	giardia
Q09AX82	giardia
Q08C089	giardia
Q08I520	giardia
Q08RL72	giardia
Q091166	giardia
Q098CT9	giardia
Q08SVU7	giardia
Q08CX44	giardia
Q08CWK5	giardia
Q052599	giardia
Q08CW8	giardia
Q041441	giardia
Q09CTK1	giardia
Q09HHJ9	giardia
Q08K78	giardia
Q09CD09	giardia
Q09ZLC7	giardia
Q018431	giardia
Q08G634	giardia
Q095714	giardia
Q09ZTE1	giardia
Q09LXV2	giardia
Q09WE4	giardia
Q094287	giardia
Q016208	giardia
Q09SJA6	giardia
Q08XW6	giardia
Q08BOV3	giardia
Q08HOC9	giardia
Q081934	giardia
Q054379	giardia
Q08CP47	giardia
Q0942E4	giardia
Q08BR07	giardia

90	35	57.4	353	16	Q8PPM1
91	35	57.4	352	16	Q8P586
92	35	57.4	362	2	O8B000
93	35	57.4	362	2	O45379
94	35	57.4	443	10	O9T0A1
95	35	57.4	469	16	P74685
96	35	57.4	474	5	O8SVU3
97	35	57.4	485	12	O9DM55
98	35	57.4	553	16	O9XA97
99	35	57.4	554	16	O8NMNO
100	35	57.4	576	16	O8XV03

ALIGNMENTS

RESULT 1
Q40015 PRELIMINARY; PRT; 427 AA.

AC Q40015; 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
 DE Barley (H.vulgaris) alpha-amylase 1.
 OS Hordeum vulgare (Barley).
 OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
 OC Triticeae; Hordeum.
 OX NCBI_TaxID=4513;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Knox C.A.P., Sonthayanon B., Chandra G.R., Muthukrishnan S.;
 RT "Structure and organization of two divergent alpha-amylase genes from
 RL Plant Mol. Biol. 9:3-17(1987).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Muthukrishnan S.;
 RL Submitted (JUL-1988) to the EMBL/GenBank/DBJ databases.
 DR EMBL; M17125; AAA32925.1; -.
 DR HSSP; P04063; IAVA.
 DR InterPro: IPR006047; Alpha-amyl_cat.
 DR InterPro: IPR006046; Glyco_hydro_13.
 DR Pfam; PF00128; alpha-amylase; 1.
 DR PRINTS; PR00110; ALPHAAMYLASE.
 SQ SEQUENCE 427 AA; 47402 MW; D21BA12EAE5F3534 CRC64;

Query Match 100.0%; Score 61; DB 10; Length 427;
 Best Local Similarity 100.0%; Pred. No. 0.0048;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRDDRYPADG 10
 DB 148 CRDDRYPADG 157

RESULT 2
Q03651 PRELIMINARY; PRT; 427 AA.

AC Q03651; 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
 DE Alpha-amylase precursor (EC 3.2.1.1).
 GN AMY46.
 OS Hordeum vulgare (Barley).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
 OC Triticeae; Hordeum.
 OX NCBI_TaxID=4513;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Himalaya;

RX MEDLINE=89066691; PubMed3264283;
 RA Khushf B., Rogers J.C.;
 RT "Barley alpha-amylase genes. Quantitative comparison of steady-state
 RT mRNA levels from individual members of the two different families
 RT expressed in aleurone cells."
 RL J. Biol. Chem. 263:18953-18960(1988).
 DR EMBL; J04202; AAA98615.1; -.
 DR HSSP; P04063; IAVA.
 DR InterPro: IPR006047; Alpha-amyl_cat.
 DR InterPro: IPR006589; Alp_amyl_cat_sub.
 DR InterPro: IPR006046; Glyco_hydro_13.
 DR Pfam; PF00128; alpha-amylase; 1.
 DR PRINTS; PR00110; ALPHAAMYLASE.
 DR SMART; SM00642; Amy; 1.
 KW Glycosidase; Hydrolase; Signal.
 FT CHAIN 26 427
 FT SIGNAL 1 25
 FT POTENTIAL.
 FT ALPHA-AMYLASE.
 SQ SEQUENCE 427 AA; 47456 MW; 5A7496B9E6643824 CRC64;

Query Match 100.0%; Score 61; DB 10; Length 427;
 Best Local Similarity 100.0%; Pred. No. 0.0048;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRDDRYPADG 10
 DB 148 CRDDRYPADG 157

RESULT 3
Q40016 PRELIMINARY; PRT; 429 AA.

AC Q40016; 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
 DE Barley (H.vulgaris) alpha-amylase 1.
 OS Hordeum vulgare (Barley).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
 OC Triticeae; Hordeum.
 OX NCBI_TaxID=4513;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Knox C.A.P., Sonthayanon B., Chandra G.R., Muthukrishnan S.;
 RT "Structure and organization of two divergent alpha-amylase genes from
 RL Plant Mol. Biol. 9:3-17(1987).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Muthukrishnan S.;
 RL Submitted (JUL-1988) to the EMBL/GenBank/DBJ databases.
 DR EMBL; M17125; AAA32926.1; -.
 DR HSSP; P04063; IAVA.
 DR InterPro: IPR006047; Alpha-amyl_cat.
 DR InterPro: IPR006589; Alp_amyl_cat_sub.
 DR Pfam; PF00128; alpha-amylase; 1.
 DR SMART; SM00642; Amy; 1.
 SQ SEQUENCE 429 AA; 47970 MW; 4E7B8B741C944095 CRC64;

Query Match 91.8%; Score 56; DB 10; Length 429;
 Best Local Similarity 90.0%; Pred. No. 0.041;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CRDDRYPADG 10
 DB 148 CRDDRYPADG 157

RESULT 4
Q42504 PRELIMINARY; PRT; 421 AA.

AC Q42504; 01-NOV-1996 (TREMBlrel. 01, Created)


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RC STRAIN=cv. Nanicao; TISSUE=leaf;
RA Vieira A. Jr., Nascimento J.R.O., Lajolo F.M.;
RT "Sequencing and molecular characterization of a banana alpha-amylase
   RT gene.";
RL Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: AY171068; M0011776.1; -.
FW SIGNAL: Hydrolyase; Glycosidase.
KM SIGNAL: 1 15 POTENTIAL.
FT CHAIN 16 416 ALPHA-AMYLASE.
SQ SEQUENCE 416 AA; 4658 MW; 7D5ECE630F21915 CRC64;

Query Match 72.1%; Score 44; DB 10; Length 416;
Best Local Similarity 70.0%; Pred. No. 6.5;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 CRDDRPYADG 10
Db 139 CRDDTKYSDG 148

RESULT 8
O04964 PRELIMINARY; PRT; 437 AA.
AC O04964;
DT 01-JUL-1997 (TREMblrel. 04, Created)
DT 01-JUL-1997 (TREMblrel. 04, Last sequence update)
DT 01-MAR-2003 (TREMblrel. 23, Last annotation update)
DE Alpha-amylase (EC 3.2.1.1).
GN AMY.
OS Hordeum vulgare (Barley).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
OC Triticeae; Hordeum.
OX NCBI_TaxID=4513;
RN [1]
RP SEQUENCE FROM N.A.
RA Matthews P.R., Gubler F., Jacobsen J.V.;
RT "A plant-based expression system for matching cDNA clones and
   RT isozymes.";
RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL: Y11276; CA72143.1; -.
DR HSSP: P04063; IAVA.
DR InterPro: IPR006047; Alpha-amyl_cat.
DR InterPro: IPR006589; Alp_amyl_cat_sub.
DR InterPro: IPR006046; Glyco_hydro_13.
DR Pfam: PF00128; alpha-amylase; 1.
DR PRINTS: PR00110; ALPHAMYLASE.
DR SMART: SM00642; Amy; 1.
KM Glycosidase; Hydrolyase.
SQ SEQUENCE 437 AA; 4776 MW; E16324C8CB2480 CRC64;

Query Match 72.1%; Score 44; DB 10; Length 437;
Best Local Similarity 70.0%; Pred. No. 6.8;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 CRDDRPYADG 10
Db 148 CRDDTKYSDG 157

RESULT 9
O04018 PRELIMINARY; PRT; 437 AA.
AC O04018;
DT 01-NOV-1996 (TREMblrel. 01, Created)
DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)
DT 01-MAR-2003 (TREMblrel. 23, Last annotation update)
DE Barley (H.vulgare) alpha-amylase 2.
OS Hordeum vulgare (Barley).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
OC Triticeae; Hordeum.
OX NCBI_TaxID=4513;

```

```

RN [1]
RP SEQUENCE FROM N.A.
RA Knox C.A.P., Sonthayanon B., Chandra G.R., Muthukrishnan S.;
RT "Structure and organization of two divergent alpha-amylase genes from
   RT barley.";
RL Plant Mol. Biol. 9:3-17(1987).
DR EMBL: M17127; AAA32928.1; -.
DR HSSP: P04063; IAVA.
DR InterPro: IPR006047; Alpha-amyl_cat.
DR InterPro: IPR006589; Alp_amyl_cat_sub.
DR InterPro: IPR006046; Glyco_hydro_13.
DR Pfam: PF00128; alpha-amylase; 1.
DR PRINTS: PR00110; ALPHAMYLASE.
DR SMART: SM00642; Amy; 1.
SQ SEQUENCE 437 AA; 4781 MW; 68866B0A1A650656 CRC64;

Query Match 72.1%; Score 44; DB 10; Length 437;
Best Local Similarity 70.0%; Pred. No. 6.8;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 CRDDRPYADG 10
Db 148 CRDDTKYSDG 157

RESULT 10
O04017 PRELIMINARY; PRT; 438 AA.
AC O04017;
DT 01-NOV-1996 (TREMblrel. 01, Created)
DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)
DT 01-MAR-2003 (TREMblrel. 23, Last annotation update)
DE Barley (H.vulgare) alpha-amylase 2.
OS Hordeum vulgare (Barley).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
OC Triticeae; Hordeum.
OX NCBI_TaxID=4513;
RN [1]
RP SEQUENCE FROM N.A.
RA Knox C.A.P., Sonthayanon B., Chandra G.R., Muthukrishnan S.;
RT "Structure and organization of two divergent alpha-amylase genes from
   RT barley.";
RL Plant Mol. Biol. 9:3-17(1987).
DR EMBL: M17128; AAA32927.1; -.
DR HSSP: P04063; IAVA.
DR InterPro: IPR006047; Alpha-amyl_cat.
DR InterPro: IPR006589; Alp_amyl_cat_sub.
DR Pfam: PF00128; alpha-amylase; 1.
DR SMART: SM00642; Amy; 1.
SQ SEQUENCE 438 AA; 47824 MW; 38945AF6DBA2309 CRC64;

Query Match 72.1%; Score 44; DB 10; Length 438;
Best Local Similarity 70.0%; Pred. No. 6.9;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 CRDDRPYADG 10
Db 149 CRDDTKYSDG 158

RESULT 11
O81699 PRELIMINARY; PRT; 434 AA.
AC O81699;
DT 01-NOV-1998 (TREMblrel. 08, Created)
DT 01-NOV-1998 (TREMblrel. 08, Last sequence update)
DT 01-MAR-2003 (TREMblrel. 23, Last annotation update)
DE Alpha amylase precursor (EC 3.2.1.1).
GN ALPHA-AMY2A.
OS Avena sativa.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;

```


OC Avenae; Avena.
 OX NCBI_TaxID=4499;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Willmott R.L.;
 RL Thesis (1994), University of Bristol.
 RM [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-99077315; PubMed-9862499;
 RA Willmott R.L., Rushton P.J., Hookey R., Lazarus C.M.;
 RT "Dnaei1 footprints suggest the involvement of at least three types of
 transcription factors in the regulation of alpha-Amy2/A by
 gibberellin.";
 RL Plant Mol. Biol. 38:817-825(1998).
 DR EMBL: AJ010728; CA09323.1; -;
 DR HSSP: P04063; IAVA.
 DR InterPro: IPR006047; Alpha_amy1_cat.
 DR InterPro: IPR006589; Alp_amy1_cat_sub.
 DR InterPro: IPR006046; Glyco_hydro_13.
 DR Pfam: PF00128; alpha-amy1ase. 1.
 DR PRINTS: PR00110; ALPHAMYLASE.
 DR SMART: SM00642; Amy1. 1.
 KW Glycosidase; Hydrolase; Signal.
 FT SIGNAL 1 23
 FT CHAIN 24 434 ALPHA AMYLASE.
 SO SEQUENCE 434 AA; 47642 MW; 499F8C3E9767C1E1 CRC64;
 Query Match 68.9%; Score 42; DB 10; Length 434;
 Best Local Similarity 70.0%; Pred. No. 16;
 Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 Oy 1 CRDPRYADG 10
 Db 148 CRDPTTSDG 157

RESULT 12
 ID 081700 PRELIMINARY; PRT; 437 AA.
 AC 081700;
 DT 01-NOV-1998 (TREMBlrel. 08, Created)
 DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
 DE Alpha-amy1ase precursor (EC 3.2.1.1).
 GN ALPHA-AMY2D.
 OS Avena fatua.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
 OC Avenae; Avena.
 OX NCBI_TaxID=4499;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Willmott R.L.;
 RL Thesis (1994), University of Bristol.
 RM [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-99077315; PubMed-9862499;
 RA Willmott R.L., Rushton P.J., Hookey R., Lazarus C.M.;
 RT "Dnaei1 footprints suggest the involvement of at least three types of
 transcription factors in the regulation of alpha-Amy2/A by
 gibberellin.";
 RL Plant Mol. Biol. 38:817-825(1998).
 DR EMBL: AJ010728; CA09324.1; -;
 DR HSSP: P04063; IAVA.
 DR InterPro: IPR006047; Alpha_amy1_cat.
 DR InterPro: IPR006589; Alp_amy1_cat_sub.
 DR InterPro: IPR006046; Glyco_hydro_13.
 DR Pfam: PF00128; alpha-amy1ase. 1.
 DR PRINTS: PR00110; ALPHAMYLASE.
 DR SMART: SM00642; Amy1. 1.
 KW Glycosidase; Hydrolase; Signal.
 FT SIGNAL 1 26
 FT CHAIN 27 437 ALPHA-AMY1ASE.

SO SEQUENCE 437 AA; 48103 MW; 88CE3095737585A CRC64;
 Query Match 68.9%; Score 42; DB 10; Length 437;
 Best Local Similarity 70.0%; Pred. No. 16;
 Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 Oy 1 CRDPRYADG 10
 Db 151 CRDPTTSDG 160

RESULT 13
 ID 004272 PRELIMINARY; PRT; 278 AA.
 AC 004272;
 DT 01-JUL-1997 (TREMBlrel. 04, Created)
 DT 01-JUL-1997 (TREMBlrel. 04, Last sequence update)
 DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
 DE Chitinase (Fragment).
 OS Oryza sativa (Rice).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Ehrharioideae; Oryzeae; Oryza.
 OX NCBI_TaxID=4530.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC SPRAIN-CV. TR36; TRISSUP-leaf;
 RA Yun C.H., Lee M.-C., Lee J.S., Yun K.J., Eun M.Y.;
 RT "Isolation and characterization of a rice chitinase cDNA clone from
 rice blast fungus-infected rice leaves.";
 RL Submitted (Apr-1997) to the EMBL/Genbank/DBJ databases.
 DR EMBL: AF001501; AB58239.1; -;
 DR HSSP: F23951; 2BAA.
 DR Gramene: 004272; -;
 DR InterPro: IPR00726; Glyco_hydro_19.
 DR Pfam: PF00182; Glyco_hydro_19; 1.
 DR ProDom: PD000574; Glyco_hydro_19; 1.
 FT NON_TER 1
 FT TER 1
 SO SEQUENCE 278 AA; 30721 MW; 9D545C1867915382 CRC64;
 Query Match 67.2%; Score 41; DB 10; Length 278;
 Best Local Similarity 60.0%; Pred. No. 15;
 Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 Oy 1 CRDPRYADG 10
 Db 269 CRDQKPYGCG 278

RESULT 14
 ID 092P43 PRELIMINARY; PRT; 420 AA.
 AC 092P43;
 DT 01-MAY-1999 (TREMBlrel. 10, Created)
 DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
 DE Alpha-amy1ase (EC 3.2.1.1).
 OS Phaseolus vulgaris (kidney bean) (French bean).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Core eudicots; Rosidae;
 OC Eurosid 1; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Phaseolus;
 OX NCBI_TaxID=3685;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Mori H.;
 RL Submitted (May-1998) to the EMBL/Genbank/DBJ databases.
 RM [2]
 RP SEQUENCE FROM N.A.
 RA Mori H., Kobayashi T., Tonokawa T., Tatematsu A., Matsui H.,
 RA Kimura A., Chiba S.;
 RT "Molecular cloning of an alpha-Amy1ase cDNA from germinating
 cotyledons of kidney bean (Phaseolus vulgaris L. cv. "Toranabe").";
 RL J. Appl. Glycosci. 45:261-267(1997).

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DR EMBL: AB015131; BAA33879.1; -.
DR HSPSP; P04063; IAVA.
DR InterPro: IPR006047; Alpha_amy1_cat.
DR InterPro: IPR006589; Alp_amy1_cat_sub.
DR InterPro: IPR006046; Glyco_hydro_13.
DR Pfam: PF00128; alpha-amy1ase; 1.
DR PRINTS: PR00110; ALPHAMYLASE.
DR SMART: SM00642; Amy; 1.
KW Glycosidase; Hydrolase.
FT CHAIN 24 420
SQ SEQUENCE 420 AA; 46853 MW; 9A3ECA606C7BB60A CRC64;

Query Match 67.2%; Score 41; DB 10; Length 420;
Best Local Similarity 60.0%; Pred. No. 24;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 CRDDPYADG 10
   1 11 111
Db 146 CKDDTYSDG 155

RESULT 15
ID 042678 PRELIMINARY; PRT; 423 AA.
AC 042678;
DT 01-NOV-1996 (TRENBLREL. 01, Created)
DT 01-NOV-1996 (TRENBLREL. 01, Last sequence update)
DT 01-MAR-2003 (TRENBLREL. 23, Last annotation update)
DE Alpha amy1ase precursor (EC 3.2.1.1) (Fragment).
GN CUS AMY2.
OS Cuscuta reflexa (Southern Asian dodder).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots.
OC Asceridae; Jamids; Solanales; Convolvulaceae; Cuscuta.
OX NCBI_TaxID=4129;
RN [1]
RP SEQUENCE FROM N.A.
RA Ramachandiran S., Srinivasa B., Mahadevan S.;
RT "Molecular cloning and nucleotide sequence of detachment induced alpha
RT amy1ase from Cuscuta reflexa."
RL Submitted (FEB-1994) to the EMBL/GenBank/DBJ databases.
DR EMBL: U06754; AAA16513.1; -.
DR HSPSP; P04063; IAVA.
DR InterPro: IPR006047; Alpha_amy1_cat.
DR InterPro: IPR006589; Alp_amy1_cat_sub.
DR InterPro: IPR006046; Glyco_hydro_13.
DR Pfam: PF00128; alpha-amy1ase; 1.
DR PRINTS: PR00110; ALPHAMYLASE.
DR SMART: SM00642; Amy; 1.
KW Glycosidase; Hydrolase; Signal.
FT NON_TER 1 1
FT SIGNAL <1 18
SQ SEQUENCE 423 AA; 46996 MW; 9EF67F8496C2A9F3 CRC64;

Query Match 67.2%; Score 41; DB 10; Length 423;
Best Local Similarity 60.0%; Pred. No. 24;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 CRDDPYADG 10
   1 11 111
Db 143 CKDDTYSDG 152

RESULT 16
ID 08LP27 PRELIMINARY; PRT; 424 AA.
AC 08LP27;
DT 01-OCT-2002 (TRENBLREL. 22, Created)
DT 01-OCT-2002 (TRENBLREL. 22, Last sequence update)
DT 01-MAR-2003 (TRENBLREL. 23, Last annotation update)
DE Alpha-amy1ase.
GN PNAMY1.
OS Pharbitis nil (Violet) (Japanese morning glory).

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OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; Jamids; Solanales; Convolvulaceae; Ipomoea.
OX NCBI_TaxID=35883;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=2211127; Pubmed=12114559;
RA Nakayama A., Park S., Xu Z., Nakajima M., Yamaguchi I.;
RT "Immunohistochemistry of Active Gibberellins and Gibberellin-Inducible
RT alpha-Amy1ase in Developing Seeds of Morning Glory."
RL Plant Physiol. 129:1045-1053(2002).
DR EMBL: AB077387; BAC02435.1; -.
DR InterPro: IPR006047; Alpha_amy1_cat.
DR InterPro: IPR006589; Alp_amy1_cat_sub.
DR InterPro: IPR006046; Glyco_hydro_13.
DR Pfam: PF00128; alpha-amy1ase; 1.
DR PRINTS: PR00110; ALPHAMYLASE.
DR SMART: SM00642; Amy; 1.
SQ SEQUENCE 424 AA; 47109 MW; 4CC1FF3733D59742 CRC64;

Query Match 67.2%; Score 41; DB 10; Length 424;
Best Local Similarity 60.0%; Pred. No. 24;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 CRDDPYADG 10
   1 11 111
Db 146 CKDDTYSDG 155

RESULT 17
ID 08SX82 PRELIMINARY; PRT; 1593 AA.
AC 08SX82;
DT 01-JUN-2002 (TRENBLREL. 21, Created)
DT 01-JUN-2002 (TRENBLREL. 21, Last sequence update)
DT 01-OCT-2002 (TRENBLREL. 22, Last annotation update)
DE LD15472p (Fragment).
GN UNC-13 OR CG2999.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=Berkeley;
RC Stapleton M., Brokstein P., Hong L., Agdayani A., Carlson J.,
RA Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E.,
RA George R., Gonzalez M., Guarin H., Kronmiller B., Li P., Liao G.,
RA Miranda A., Mungall C.J., Nunoo J., Paclob J., Paragas V., Park S.,
RA Patel S., Phouanavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
RA Ceinlier S.;
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: AY094789; AAM11142.1; -.
DR FLYBase: FBgn0025726; unc-13.
FT NON_TER 1593 1593
SQ SEQUENCE 1593 AA; 174720 MW; 03450414C0876F38 CRC64;

Query Match 67.2%; Score 41; DB 5; Length 1593;
Best Local Similarity 100.0%; Pred. No. 99;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 DDRPYAD 9
   1111111
Db 1305 DDRPYAD 1311

RESULT 18
ID 09V483 PRELIMINARY; PRT; 2871 AA.
AC 09V483;
DT 01-MAY-2000 (TRENBLREL. 13, Created)
DT 01-OCT-2002 (TRENBLREL. 22, Last sequence update)

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RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegwam C.,
 RA Jajali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshneft A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Paclet J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.Y., Messarman D.A., Weinstock G.M., Weissbach J.,
 RA Williams S.M., Woodger, Morley K.C., Wu D., Yang S., Yao Q.A., Ye J.,
 RA Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhou W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of *Drosophila melanogaster*.";
 RL Science 287:2185-2195(2000).
 RN [12]
 RP SEQUENCE FROM N.A.
 RA Ceiniker S.E., Adams M.D., Krommiller B., Wan K.H., Holt R.A.,
 RA Evans C.A., Gocayne J.D., Amanatides P.G., Brandon R.C., Rogers Y.,
 RA Banzon J., An H., Baldwin D., Banzon K.Y., Beeson K.Y., Busan D.A.,
 RA Carlson J.W., Center A., Chapple M., Davenport L.B., Dietz S.M.,
 RA Dodson K., Dorsett V., Doup L.E., Doyle C., Dresnek D., Farfan D.,
 RA Ferreira S., Frise E., Galle R.F., Garg N.S., George R.A.,
 RA Gonzalez M., Houck J., Hoskins R.A., Hostin D., Howard T.J.,
 RA Ibegwam C., Jajali M., Kruse D., Li P., Mattei B., Moshneft A.,
 RA McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nimmo J.,
 RA Paclet J., Paragass V., Park S., Patel S., Pfeiffer B.,
 RA Phouaneavong S., Pittman G.S., Puri V., Richards S., Scheeler F.,
 RA Stapleton M., Strong R., Svirskas R., Tector C., Tyler D.,
 RA Williams S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.;
 RT "Sequencing of *Drosophila melanogaster* genome.";
 RL Submitted (MAR-2000) to the EMBL/Genbank/DBJ databases.
 RN [13]
 RP SEQUENCE FROM N.A.
 RA Mistra S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K.,
 RA Hradecky P., Huang Y., Kaminker J.S., Prochuk S.E., Smith C.D.,
 RA Tupy J.L., Bergman C., Berman B., Carlson J.W., Ceiniker S.E.,
 RA Clamp M., Drysdale R., Emmert D., Frise E., de Grey A., Harris N.,
 RA Krommiller B., Marshall B., Milburn B., Richter J., Russo S.,
 RA Searle S.M.J., Smith E., Shu S., Smutniak F., Whitfield E.,
 RA Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E.;
 RT "Annotation of *Drosophila melanogaster* genome.";
 RL Submitted (MAR-2000) to the EMBL/Genbank/DBJ databases.
 RN [14]
 RP SEQUENCE FROM N.A.
 RA Adams M.D., Ceiniker S.E., Gibbs R.A., Rubin G.M., Venter C.J.;
 RL Submitted (MAR-2000) to the EMBL/Genbank/DBJ databases.
 RN [15]
 RP SEQUENCE FROM N.A.
 RA Flybase;
 RL Submitted (SEP-2002) to the EMBL/Genbank/DBJ databases.
 DR EMBL; AE003847; AAN06592.1; -;
 SQ SEQUENCE 2871 AA; 320291 MW; AD88C392C8C089A5 CRC64;
 Query Match 67.2%; Score 41; DB 5; Length 2871;
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

AC 08ZE74;
 DT 01-MAR-2002 (TREMBLrel. 20, Created)
 DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE Two-component regulatory system, response regulator protein.
 GN RST A OR YPO2308.
 OS *Yersinia pestis*.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; *Yersinia*.
 OX NCBI_TaxID=632;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CO-92 / Bivovar Orientalis;
 RX MEDLINE=21470413; PubMed=11586360;
 RA Parkhill J., Wren B.W., Thomson N.R., Titball R.W., Holden M.T.G.,
 RA Prentice M.B., Sebalina M., James K.D., Churcher C., Mungall K.L.,
 RA Baker S., Basham D., Bentley S.D., Brooks K., Cerdano-Tarraga A.M.,
 RA Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G.,
 RA Feltwell T., Hamlin N., Holroyd S., Jagers K., Karlyshev A.V.,
 RA Leather S., Moule S., Oyston P.C.F., Quail M., Rutherford K.,
 RA Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.;
 RT "Genome sequence of *Yersinia pestis*.
 RL Nature 413:523-527(2001).
 DR EMBL; AJ414151; CAC91113.1; -;
 DR InterPro: IPR001789; Response_reg.
 DR InterPro: IPR001867; Trans_reg.C.
 DR Pfam: PF00072; Response_reg.1.
 DR Pfam: PF00486; Trans_reg.C.1.
 DR ProDom: PD000039; Response_reg.1.
 DR ProDom: PD000329; Trans_reg.C.1.
 DR SMART: SM00448; REC; 1.
 DR PROSITE: PS50110; RESPONSE_REGULATORY; 1.
 KW Complete proteome.
 SQ SEQUENCE 248 AA; 28023 MW; C857427A4DA796A5 CRC64;
 Query Match 65.6%; Score 40; DB 16; Length 248;
 Best Local Similarity 70.0%; Pred. No. 20;
 Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

1 CRDPRYADG 10
 ||| ||| |||
 Db 64 CRDLRPHYDG 73

RESULT 21
 ID 08DOH1 PRELIMINARY; PRT; 266 AA.
 AC 08DOH1;
 DT 01-MAR-2003 (TREMBLrel. 23, Created)
 DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
 DE Response transcriptional regulatory protein (RstB sensor).
 GN RST A OR Y2139.
 OS *Yersinia pestis*.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; *Yersinia*.
 OX NCBI_TaxID=632;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=KIM5 / Bivovar Mediaevalis;
 RX MEDLINE=22137863; PubMed=12142430;
 RA Deng W., Burland V., Plunkett G., III, Boutin A., Mayhew G.F., Liss P.,
 RA Perna N.T., Rose D.J., Mau B., Zhou S., Schwartz D.C.,
 RA Felhnerston J.D., Lindler L.E., Brubaker R.R., Plano G.V.,
 RA Straley S.C., McDonough K.A., Nilles M.L., Watson J.S., Blattner F.R.,
 RA Perry R.D.;
 RT "Genome sequence of *Yersinia pestis* KIM.";
 RL J. Bacteriol. 184:4601-4611(2002).
 DR EMBL; AE013817; AAM85701.1; -;
 SQ SEQUENCE 266 AA; 302220 MW; F5614BF5C0508F1 CRC64;
 Query Match 65.6%; Score 40; DB 16; Length 266;
 Best Local Similarity 70.0%; Pred. No. 22;

Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 CRDPRYADG 10
111111
DB 82 CRDPRYADG 91

RESULT 22

OY2RS2 PRELIMINARY; PRT; 405 AA.

AC 092RS2; 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, last sequence update)
DE 01-OCT-2002 (TREMBLrel. 22, last annotation update)
DE Probable glycolate oxidase subunit protein.
GN GICE OR R00778 OR SMC00833.
OS Rhizobium meliloti (Sinorhizobium meliloti).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Rhizobiaceae; Sinorhizobium.
OX NCBI_TaxID=382;

SEQUENCE FROM N.A.

RP STRAIN=1021;
RX MEDLINE=21396507; PubMed=11481430;
RA Capela D., Barloy-Hubler F., Gouzy J., Bothe G., Ampe F., Batut J.,
RA Boissard P., Becker A., Boutry M., Cadieu E., Dreano S., Gloux S.,
RA Godelle T., Goffeau A., Kahn D., Kiss E., Lelaure V., Maury D.,
RA Pohl T., Portetelle D., Puehler A., Purnelle B., Ramsperger U.,
RA Renard C., Thebaud P., Vandenbol M., Weidner S., Galibert F.;
RT "Analysis of the chromosome sequence of the legume symbiont
RT Sinorhizobium meliloti strain 1021.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:9877-9882(2001).
DR EMBL: AL591784; CAC4530.1; -;
DR InterPro: IPR004113; FAD-oxidase.C.
DR InterPro: IPR006094; Oxid.FAD-bind.
DR Pfam: PF01565; FAD-binding_4; 1.
DR Complete proteome.
SQ SEQUENCE 405 AA; 42687 MW; 3060123D124F81EC CRC64;

Query Match 65.6%; Score 40; DB 16; Length 405;
Best Local Similarity 77.8%; Pred. No. 35;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 2 RDDRYADG 10
111111
DB 282 RDDRYADG 290

RESULT 23

OY3J13 PRELIMINARY; PRT; 175 AA.

AC 093J13; 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, last sequence update)
DE 01-MAR-2003 (TREMBLrel. 23, last annotation update)
DE Partial putative replication initiator protein (Fragment).
GN SC03995 OR SCBAC25E3.32.
OS Streptomyces coelicolor.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycinae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1902;

SEQUENCE FROM N.A.

RP STRAIN=A3(2) / M145;
RX MEDLINE=2196410; PubMed=12000953;
RA Bentley S.D., Chater K.F., Cerdano-Tarraga A.-M., Challis G.L.,
RA Thomson N.R., James K.D., Harris D.E., Quail M.A., Kleser H.,
RA Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
RA Cronin A., Fraser A., Goble A., Hildalgo J., Hornsby T., Howarth S.,
RA Huang C.-H., Kleser T., Larke L., Murphy L., Oliver K., O'Neill S.,
RA Rabbinowitch E., Rajandream M.A., Rutherford K., Rutter S.,
RA Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,

RA Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
RA Hopwood D.A.; complete sequence of the model actinomycete Streptomyces

RT "Complete genome sequence of the model actinomycete Streptomyces
RT coelicolor (strain ATCC 27061 / DSM 4184)";
RL Nature 417:141-147(2002).
DR EMBL: AL939118; CAC44719.1; -;
KM Complete proteome.
FT NON_TER
SQ SEQUENCE 175 AA; 19485 MW; 2433FA9B15BD7EE8 CRC64;

Query Match 64.8%; Score 39.5; DB 16; Length 175;
Best Local Similarity 80.0%; Pred. No. 17;
Matches 8; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

OY 1 CRD-DRPYAD 9
1111111
DB 61 CRD-DRPYAD 70

RESULT 24

OY0398 PRELIMINARY; PRT; 144 AA.

AC 050398; 01-JUN-1998 (TREMBLrel. 06, Created)
DT 01-JUN-1998 (TREMBLrel. 06, last sequence update)
DE 01-MAR-2002 (TREMBLrel. 20, last annotation update)
DE Hypothetical protein RV3369.
GN RV3369 OR MTW004.27 OR MT3478.
OS Mycobacterium tuberculosis.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacteriaceae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1773;

SEQUENCE FROM N.A.

RP STRAIN=H37Rv;
RX MEDLINE=96205987; PubMed=9634230;
RA Cole S.T., Brosch R., Parkhill J., Garner T., Churcher C., Harris D.,
RA Gordon S.V., Eigemeier K., Gas S., Barry C.E. III, Tekala F.,
RA Badcock K., Basmam D., Brown D., Chillingworth T., Connor R.,
RA Davies R., DeLong K., Fellwell T., Gentles S., Hamlin M., Holroyd S.,
RA Hornsby T., Jagels K., Kiroh A., McLean J., Moule S., Murphy L.,
RA Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
RA Rutter S., Seeger K., Skelton S., Squares S., Squares R.,
RA Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;
RT "Deciphering the biology of Mycobacterium tuberculosis from the
RT complete genome sequence.";
RL Nature 393:537-544(1998).

SEQUENCE FROM N.A.

RP STRAIN=CDC 1551 / Oshkosh;
RC Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
RA Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,
RA Kolony J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,
RA Delcher A., Utermack T., Weidman J., Kouri H., Gill J., Mikula A.,
RA Bishai W.;
RT "Whole genome comparison of Mycobacterium tuberculosis clinical and
RT laboratory strains.";
RL Submitted (APR-2001) to the EMBL/Genbank/DBJ databases.
DR EMBL: AL009198; CA15754.1; -;
DR EMBL: AE007154; AAK47816.1; -;
DR TIGR: MT3478; -;
DR TIGR: MT3478; -;
DR Hypothetical protein; Complete proteome.
SQ SEQUENCE 144 AA; 15718 MW; 9102BA411B376DF CRC64;

Query Match 63.9%; Score 39; DB 16; Length 144;
Best Local Similarity 85.7%; Pred. No. 17;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 CRDPRY 7
111111
DB 101 CRDPRY 107

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RESULT 25
Q9A9T6 PRELIMINARY; PRT; 370 AA.
AC Q9A9T6;
DT 01-JUN-2001 (TReMBLrel. 17, Created)
DT 01-JUN-2001 (TReMBLrel. 17, Last sequence update)
DE Hypothetical protein CC0876.
GN CC0876.
OS Caulobacter crescentus.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Caulobacteriales;
OC Caulobacteraceae; Caulobacter.
NCBI_TaxID=153892;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 19089 / CB15;
RX MEDLINE=21173698; PubMed=11259647;
RA Nieman W.C., Feldlyum T.V., Laub M.T., Paulsen I.T., Nelson K.E.,
RA Eisen J., Heidelberg J.F., Alley M.R.K., Ohta N., Maddock J.R.,
RA Potocka I., Nelson W.C., Newton A., Stephens C., Phadke N.D., Ely B.,
RA DeBoy R.T., Dodson R.J., Durkin A.S., Gwinn M.L., Haft D.H.,
RA Kolonay J.F., Smit J., Craven M.B., Khouri H., Shetty J., Berry K.,
RA Uterback T., Tran K., Wolf A., Vamathevan J., Esmolaeva M., White O.,
RA Salzberg S.L., Venter J.C., Shapiro L., Fraser C.M.;
RT "Complete genome sequence of Caulobacter crescentus.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001).
DR EMBL; AE005764; MAK2861.1; -.
DR TIGR; CC0876; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 370 AA; 42422 MW; 1D8908EBCBDF357 CRC64;

Query Match 63.9%; Score 39; DB 16; Length 370;
Best Local Similarity 77.8%; Pred. No. 48;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 RDDRPRYADG 10
Db 234 RDDRPRYADG 242

RESULT 26
Q987T8 PRELIMINARY; PRT; 382 AA.
AC Q987T8;
DT 01-OCT-2001 (TReMBLrel. 18, Created)
DT 01-OCT-2001 (TReMBLrel. 18, Last sequence update)
DE 01-OCT-2002 (TReMBLrel. 22, Last annotation update)
DE Glycolate oxidase subunits, GICE.
GN MIF6919.
OS Rhizobium loti (Mesorhizobium loti).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Phyllobacteriaceae; Mesorhizobium.
NCBI_TaxID=381;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MAFF30309;
RX MEDLINE=21082930; PubMed=11214966;
RA Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S.,
RA Watanabe A., Idesawa K., Ishikawa A., Kawashima K., Kimura T.,
RA Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsumoto A.,
RA Mochizuki Y., Nakayama S., Nakazaki N., Shimpoto S., Sugimoto M.,
RA Takeuchi C., Yamada M., Tabata S.;
RT "Complete genome structure of the nitrogen-fixing symbiotic bacterium
RT Mesorhizobium loti.";
RL DNA Res. 7:331-338(2000).
DR EMBL; AP003010; BAB53112.1; -.
DR InterPro; IPR004113; FAD-oxidase_C.
DR InterPro; IPR006094; Oxid_FAD_bind.
DR Pfam; PF02913; FAD-oxidase_C; 1.
DR Pfam; PF01565; FAD_binding_4; 1.
KW Complete proteome.
SQ SEQUENCE 382 AA; 40337 MW; 82C9A44BAD0B3475 CRC64;

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Query Match 63.9%; Score 39; DB 16; Length 382;
Best Local Similarity 77.8%; Pred. No. 50;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 RDDRPRYADG 10
Db 263 RDDRPRYADG 271

RESULT 27
Q9NGZ3 PRELIMINARY; PRT; 556 AA.
AC Q9NGZ3;
DT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
DE Variant-specific surface protein VSP MM/Sac-C/1 (fragment).
OS Giardia lamblia (Giardia intestinalis).
OC Eukaryota; Diplomonadida; Hexamitidae; Giardinae; Giardia.
NCBI_TaxID=5741;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Ad-1;
RA Mansouri M., Ey P.L.;
RT "Analysis of vsp72-like sequences in Giardia intestinalis.";
RL Submitted (FEB-2000) to the EMBL/Genbank/DBJ databases.
DR EMBL; AF236019; AAF69832.1; -.
DR InterPro; IPR006209; EGF-like.
DR InterPro; IPR006212; Furin_repeat.
DR InterPro; IPR005127; Giardia_VSP.
DR InterPro; IPR006210; IEGF.
DR InterPro; IPR002049; Laminin_EGF.
DR Pfam; PF03302; VSP; 1.
DR SMART; SM00181; EGF; 1.
DR SMART; SM00261; FU; 4.
DR PROSITE; PS01186; EGF_2; 1.
DR PROSITE; PS01248; LAMININ_TYPE_EGF; 1.
FT NON_TER 1
SQ SEQUENCE 556 AA; 57575 MW; F9634B8B13863AB6 CRC64;

Query Match 63.9%; Score 39; DB 5; Length 556;
Best Local Similarity 71.4%; Pred. No. 75;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRDPRY 7
Db 62 CRDPRY 68

RESULT 28
Q9Y113 PRELIMINARY; PRT; 594 AA.
AC Q9Y113;
DT 01-NOV-1999 (TReMBLrel. 12, Created)
DT 01-NOV-1999 (TReMBLrel. 12, Last sequence update)
DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
DE CG12152 protein.
GN BCDNA:GH10333 OR CG12152.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BERKELEY;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Mortan J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazek R.G., Champe M., Pfeiffer B.D.,

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 29, 2003, 18:35:10 ; Search time 30.5714 Seconds

(Without alignments)
51.920 Million cell updates/sec

Title: US-09-830-876-3

Perfect score: 56

Sequence: 1 VMWNVKVGCS 10

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	56	100.0	10	21	AAV93373
2	56	100.0	425	21	AAV93374
3	46	82.1	435	22	AAV50255
4	46	82.1	435	22	AAV50255
5	45	80.4	137	21	AAV97247
6	45	80.4	428	22	AAV50251
7	45	80.4	428	22	AAV97245
8	45	80.4	433	15	AAV51130
9	45	80.4	434	14	AAV32987

10	45	80.4	434	18	AAV10469	Rice alpha-amylase
11	45	80.4	434	18	AAV10471	Rice alpha-amylase
12	45	80.4	434	20	AAV01375	O. sativa alpha-am
13	45	80.4	434	20	AAV84383	Rice alpha-amylase
14	45	80.4	434	21	AAV77982	Rice alpha-amylase
15	42	75.0	428	21	AAV12788	Rice alpha-amylase
16	42	75.0	429	16	AAV76520	Rice alpha-amylase
17	39	69.6	157	16	AAV76520	Rice alpha-amylase
18	39	69.6	157	16	AAV76520	Rice alpha-amylase
19	38	67.9	548	23	AAV84321	Listeria monocytog
20	38	67.9	548	23	AAV84321	Listeria monocytog
21	38	67.9	548	23	AAV84321	Listeria monocytog
22	38	67.9	548	23	AAV84321	Listeria monocytog
23	37	66.1	1077	23	AAV65532	Human prostate spe
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79	37	66.1	1077	23	AAV65532	Human prostate spe
80	37	66.1	1077	23	AAV65532	Human prostate spe
81	37	66.1	1077	23	AAV65532	Human prostate spe
82	37	66.1	1077	23	AAV65532	Human prostate spe

83	35	62.5	132	22	AA01253	Mycobacterium tube
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87	35	62.5	132	23	ABR95358	M tuberculosis ant
88	35	62.5	132	23	ABR95366	M tuberculosis ant
89	35	62.5	132	23	AAE17569	Mycobacterium spec
90	35	62.5	132	24	ABU71789	Prostate cancer as
91	35	62.5	132	24	ABU71797	Prostate cancer as
92	35	62.5	180	22	AA081997	Human haematologic
93	35	62.5	264	23	ABP30446	Streptococcus poly
94	35	62.5	290	23	ABP27789	Streptococcus poly
95	35	62.5	303	19	AA076828	Human TR6 partial
96	35	62.5	303	22	AA088349	Partial amino acid
97	35	62.5	318	22	AA090956	C glutamicum prote
98	35	62.5	327	23	ABR80571	Human sbg614126com
99	35	62.5	355	18	AA022435	Mycobacterium tube
100	35	62.5	355	18	AA02367	Mycobacterium tube

ALIGNMENTS

```

RESULT 1
AA093373
ID AA093373 standard; peptide: 10 AA.
AC AA093373;
DT 04-SEP-2000 (first entry)
DE Amino acid sequence of an epitope of the wheat alpha-amylase.
XX Epitope: wheat; alpha-amylase; two-site immunoassay; weather damage;
KW cereal grain.
XX Triticum aestivum.
XX WO200028319-A1.
XX 18-MAY-2000.
XX 11-NOV-1999; 99WO-AU00995.
XX 11-NOV-1998; 98AU-0007058.
XX (QUAL-) QUALITY WHEAT CRC LTD.
XX Skeritt JH;
XX WPI; 2000-376655/32.
XX Two site immunoassay for the qualitative or quantitative detection of
PT alpha-amylase in a test sample, used to detect weather damage in a
PT cereal grain, such as wheat, rye, triticale or barley -
XX Claim 1; Page 29; 52pp; English.
XX The present sequence represents an epitope from the wheat alpha-amylase.
CC Antibodies which recognise the epitope are used in a two-site
CC immunoassay for qualitative or quantitative detection of alpha-amylase
CC in a test sample. The assay is used for detecting weather damage in a
CC cereal grain. Weather damage is caused by the action of hydrolytic
CC enzymes, e.g. amylases, in the grain endosperm. These enzymes accelerate
CC the breakdown of starch granules and protein in the endosperm of
CC germinating grain. Individual growers can identify areas of sprouting
CC prior to harvest, preventing contamination of sound wheat by weather
CC damaged wheat. The damaged grain can be harvested separately from the
CC sound grain and financial losses resulting from down grading the whole
CC crop can be avoided. The two-site immunoassays can be applied at mill
CC or silo (elevator) receipt of grain or can be used on farms with minimal
CC equipment requirements.
XX

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SQ Sequence 10 AA;
Query Match 100.0%; Score 56; DB 21; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0061;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 VNMVNVKVGGS 10
Db 1 VNMVNVKVGGS 10

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RESULT 2
AA093374
ID AA093374 standard; protein: 425 AA.
AC AA093374;
DT 04-SEP-2000 (first entry)
DE Amino acid sequence a wheat alpha-amylase.
XX Epitope: wheat; alpha-amylase; two-site immunoassay; weather damage;
KW cereal grain.
XX Triticum aestivum.
XX WO200028319-A1.
XX 18-MAY-2000.
XX 11-NOV-1999; 99WO-AU00995.
XX 11-NOV-1998; 98AU-0007058.
XX (QUAL-) QUALITY WHEAT CRC LTD.
XX Skeritt JH;
XX WPI; 2000-376655/32.
XX Two site immunoassay for the qualitative or quantitative detection of
PT alpha-amylase in a test sample, used to detect weather damage in a
PT cereal grain, such as wheat, rye, triticale or barley -
XX Disclosure; Fig 3; 52pp; English.
XX The present sequence represents a wheat alpha-amylase. Antibodies
CC which recognise epitopes from this protein are used in a two-site
CC immunoassay for qualitative or quantitative detection of alpha-amylase
CC in a test sample. The assay is used for detecting weather damage in a
CC cereal grain. Weather damage is caused by the action of hydrolytic
CC enzymes, e.g. amylases, in the grain endosperm. These enzymes accelerate
CC the breakdown of starch granules and protein in the endosperm of
CC germinating grain. Individual growers can identify areas of sprouting
CC prior to harvest, preventing contamination of sound wheat by weather
CC damaged wheat. The damaged grain can be harvested separately from the
CC sound grain and financial losses resulting from down grading the whole
CC crop can be avoided. The two-site immunoassays can be applied at mill
CC or silo (elevator) receipt of grain or can be used on farms with minimal
CC equipment requirements.
XX
SQ Sequence 425 AA;
Query Match 100.0%; Score 56; DB 21; Length 425;
Best Local Similarity 100.0%; Pred. No. 0.29;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 VNMVNVKVGGS 10
Db 251 VNMVNVKVGGS 260

```

RESULT 3

AAM50253
ID AAM50253 standard; Protein: 435 AA.
XX
AC AAM50253;
XX
DT 21-JAN-2002 (first entry)
XX
DE Rice alpha-amylase (alpha-Amy3-C gene product).
XX
KW Alpha-amylase; promoter; rice; transgenic plant; angiosperm;
XX monocot; cereal; brewing.
XX
OS Oryza sativa.
XX
FH Key Location/Qualifiers
FT Peptide 1..25
FT /label= Signal_peptide
FT Protein 26..428
FT /label= Mature_protein
XX
PM US6288302-B1.
XX
PD 11-SEP-2001.
XX
PF 04-MAY-1998; 98US-0072917.
XX
PR 04-NOV-1992; 92US-0973324.
PR 01-AUG-1995; 95US-0509962.
PR 08-OCT-1997; 97US-0947201.
PR 22-NOV-1994; 94US-0343380.
XX
PA (NASC-) NAT SCI COUNCIL ROC.
XX
PI Yu S, Liu L, Chan M;
XX
DR WPI: 2001-647191/74.
DR N-PSDB; AAT70540.
XX
PT Producing a transgenic monocot plant comprising a transgene under
PI control of an alpha amylase promoter and signal peptide sequences,
PI provides transgenic plants particularly cereals for the brewing
XX industry
XX
PS Disclosure: Column 79-82; 44pp; English.
XX
CC The present sequence is that of alpha-amylase encoded by DNA clone
CC alpha-Amy3-C (see AAT70540). Expression of alpha-Amy3-C increases
CC 5-fold following sugar starvation. The invention relates to
CC the use of an alpha-amylase gene promoter and signal sequence in
CC the production of recombinant proteins in transgenic plants and
CC transgenic plant seeds. In a claimed method, a transgenic monocot
CC is obtained by: transforming an immature embryo of the plant via
CC Agrobacterium-mediated transformation with DNA comprising a plant
CC alpha-amylase promoter (e.g. the rice alpha-Amy3-C promoter) that
CC is induced under sugar-depleted or sugar-free conditions, a signal
CC peptide sequence, and an exogenous sequence encoding a gene product;
CC regenerating the transformed plant; and growing the transgenic
CC plant, which expresses the gene product under sugar-depleted or
CC sugar-free conditions. The gene product may also be obtained by
CC culturing an angiosperm host cell. The transgenic monocot plants
CC are especially useful in brewing and to produce glucose from starch.
XX
SQ Sequence 435 AA;
XX
Query Match 82.1%; Score 46; DB 22; Length 435;
Best Local Similarity 88.9%; Pred. No. 14;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

RESULT 4
ID AAB97247 standard; Protein: 435 AA.
XX
AC AAB97247;
XX
DT 31-JUL-2001 (first entry)
XX
DE Alpha-amylase related protein #3.
XX
KW Alpha-amylase; promoter; expression vector; rice.
XX
OS Unidentified.
XX
FH TW402638-A.
XX
PD 21-AUG-2000.
XX
PF 13-FEB-1992; 97TW-0101436.
XX
PR 13-FEB-1992; 97TW-0101436.
XX
PA (NASC-) NAT SCI COUNCIL.
XX
PI Yu S, Liou L;
XX
DR WPI: 2001-167365/17.
DR N-PSDB; AAB20285.
XX
PT Gene expression system comprising the promoter region of alpha-amylase
PI gene, produces large quantities of alpha-amylase in culture medium of
XX sugar starved rice
XX
PS Disclosure; Fig 12; 104pp; Chinese.
XX
CC This invention relates to a gene expression system comprising the
CC alpha-amylase gene promoter DNA encoding the signal peptide of
CC alpha-amylase and the promoter along with the glucuronidase reporter gene
CC and hygromycin resistance gene are used in the construction of a GUS gene
CC expression vector, which when transformed into rice suspension-cultured
CC cells, can be used to investigate the expression of the vector under the
CC control of the promoter. The gene expression system can be used to
CC conduct gene regulation and protein expression and secretion using the
CC characteristics of the alpha-amylase gene promoter and the DNA sequence
CC encoding the signal peptide. The present sequence represents an
CC alpha-amylase related protein used in the course of the present
XX invention.
XX
SQ Sequence 435 AA;
XX
Query Match 82.1%; Score 46; DB 22; Length 435;
Best Local Similarity 88.9%; Pred. No. 14;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
QY 1 VNMVNRVGG 9
DB 253 VNMVNAVGG 261
XX
RESULT 5
ID AAB16272 standard; Protein: 157 AA.
XX
AC AAB16272;
XX
DT 31-OCT-2000 (first entry)
XX
DE Pinus radiata amylase protein sequence SEQ ID NO:34.
XX
KW Eucalyptus grandis; pinus radiata; Monterey pine; modification;
KW plant cell wall; polysaccharide; polysaccharide biosynthetic pathway;
XX transgenic plant.
XX

OS Pinus radiata.
XX
XX WO200022092-A2.
XX
XX 20-APR-2000.
XX
XX 08-OCT-1999; 99WO-NZ00169.
XX
XX 13-OCT-1998; 98US-017086Z.
PR 11-AUG-1999; 99US-0148426.
XX
XX (GENE-) GENESIS RES & DEV CORP LTD.
PA (FLET-) FLETCHER CHALLENGE FORESTS LTD.
XX
XX Bloksberg LN;
PI
XX
XX WPI: 2000-339328/29.
DR N-PSDB; AAA67077.
XX
XX New genes encoding proteins involved in a plant polysaccharide
PT biosynthetic pathway, useful for modulating or altering the
PT polysaccharide content, composition or structure of the plant
XX
XX Claim 17; Page 51; 301pp; English.
XX
XX The present invention describes isolated polynucleotides (PN) comprising
CC a sequence selected from one of 835 nucleotide sequences given in
CC AAA67073 to AAA67907, their (reverse) complements, sequences producing
CC an expectation (E) value of 0.01 or less compared to the 835 sequences,
CC sequences at least 50% identical to them, 200, 100, 40 or 20-mers of the
CC 835 sequences or sequences that are degenerately equivalent or allelic
CC to the 835 sequences. The polynucleotides are used to modify the
CC activity of a polypeptide involved in a polysaccharide biosynthetic
CC pathway in the plant. They are especially used to modulate or alter the
CC polysaccharide content, composition or structure of the plant. AAB16268
CC to AAB16340 are proteins encoded by some of the polynucleotide sequence
CC given in the present invention.
XX
XX Sequence 157 AA;
SQ
Query Match 80.4%; Score 45; DB 21; Length 157;
Best Local Similarity 70.0%; Pred. No. 7;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 1 VNMVNRKVGGS 10
Db 10 VNMVNRKVGGS 19
RESULT 6
AAM50251
ID AAM50251 standard; Protein; 428 AA.
AC AAM50251;
XX
XX 21-JAN-2002 (first entry)
DT
XX
XX Rice alpha-amylase (alpha-Amy7-C gene product).
DE
XX
XX Alpha-amylase; promoter; rice; transgenic plant; angiosperm;
KW monocot; cereal; brewing.
XX
XX Oryza sativa.
OS
XX
XX Key Location/Qualifiers
FH 1..25
FT /label= Signal_peptide
FT 26..428
FT Protein /label= Mature_protein
XX
XX US6288302-B1.
XX
XX 11-SEP-2001.
PD

XX
XX 04-MAY-1998; 98US-0072917.
XX
XX
XX 04-NOV-1992; 92US-0973324.
PR 01-AUG-1995; 95US-0509862.
PR 08-OCT-1997; 97US-0947201.
PR 22-NOV-1994; 94US-0343380.
XX
XX (NASC-) NAT SCI COUNCIL ROC.
PA
XX
XX Yu S, Liu L, Chan M;
PI
XX
XX WPI: 2001-647191/74.
DR N-PSDB; AAI70537.
XX
XX
XX Producing a transgenic monocot plant comprising a transgene under
PT control of an alpha amylase promoter and signal peptide sequences,
PT provides transgenic plants particularly cereals for the brewing
PT industry
XX
XX Example 1; Column 61-64; 44pp; English.
XX
XX The present sequence is that of rice (Oryza sativa) cv. M202
CC alpha-amylase, encoded by isolated genomic DNA clone alpha-Amy7-C
CC (see AAI70537). Expression of alpha-Amy7-C in cultured suspension
CC cells of rice was induced 6-fold at day 12 after sugar depletion,
CC and continued to increase up to day 14. The invention relates to
CC the use of an alpha-amylase gene promoter and signal sequence in
CC the production of recombinant proteins in transgenic plants and
CC transgenic plant seeds. In a claimed method, a transgenic monocot
CC is obtained by: transforming an immature embryo of the plant via
CC Agrobacterium-mediated transformation with DNA comprising a plant
CC alpha-amylase promoter (e.g. the rice alpha-Amy7-C promoter) that
CC is induced under sugar-depleted or sugar-free conditions, a signal
CC peptide sequence, and an exogenous sequence encoding a gene product;
CC regenerating the transformed plant; and growing the transgenic
CC plant, which expresses the gene product under sugar-depleted or
CC sugar-free conditions. The gene product may also be obtained by
CC cultivating an angiosperm host cell. The transgenic monocot plants
CC are especially useful in brewing and to produce glucose from starch.
XX
XX Sequence 428 AA;
SQ
Query Match 80.4%; Score 45; DB 22; Length 428;
Best Local Similarity 70.0%; Pred. No. 20;
Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
QY 1 VNMVNRKVGGS 10
Db 253 VNMVNRKVGGA 262
RESULT 7
AAB97245
ID AAB97245 standard; Protein; 428 AA.
AC AAB97245;
XX
XX 31-JUL-2001 (first entry)
DT
XX
XX Alpha-amylase related protein #1.
DE
XX
XX Alpha-amylase; promoter; expression vector; rice.
KW
XX
XX Unidentified.
OS
XX
XX TW402638-A.
PN
XX
XX 21-AUG-2000.
PD
XX
XX 13-FEB-1992; 97TW-0101436.
XX
XX 13-FEB-1992; 97TW-0101436.
PR

XX (NASC-) NAT SCI COUNCIL.
 XX Yu S, Liou L;
 XX WPI: 2001-167365/17.
 DR N-PSDB; AAH20283.
 XX
 PT Gene expression system comprising the promoter region of alpha-amylase
 PT gene, produces large quantities of alpha-amylase in culture medium of
 PT sugar starved rice -
 XX
 PS Disclosure: Fig 8; 104pp; Chinese.
 XX
 CC This invention relates to a gene expression system comprising the
 CC alpha-amylase gene promoter, DNA encoding the signal peptide of
 CC alpha-amylase and the promoter along with the glucuronidase reporter gene
 CC and hygromycin resistance gene are used in the construction of a cOS gene
 CC expression vector, which when transformed into rice suspension-cultured
 CC cells, can be used to investigate the expression of the vector under the
 CC control of the promoter. The gene expression system can be used to
 CC conduct gene regulation and protein expression and secretion using the
 CC characteristics of the alpha-amylase gene promoter and the DNA sequence
 CC encoding the signal peptide. The present sequence represents an
 CC alpha-amylase related protein used in the course of the present
 CC invention.
 CC
 CC Sequence 428 AA;
 SQ
 XX
 Query Match 80.4%; Score 45; DB 22; Length 428;
 Best Local Similarity 70.0%; Pred. No. 20;
 Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
 OY 1 VNMVKNVCGS 10
 DB 253 VNMVDRVGA 262
 ||||:||||
 RESULT 8
 ID AAR55130 standard; Protein; 433 AA.
 XX
 AC AAR55130;
 XX
 DT 25-MAR-2003 (updated)
 DT 12-JUN-1995 (first entry)
 XX
 DE Rice alpha-amylase coding.
 XX
 KM Virus: recombination; plant virus; alpha trichosanthin; phenotype;
 KM alpha amylase; alpha haemoglobin; brome mosaic virus; gemini virus;
 KM rice necrosis virus tobamovirus; gene expression; chinese cucumber.
 XX
 OS Oryza sativa.
 XX
 PN US5316931-A.
 XX
 PD 31-MAY-1994.
 XX
 PF 31-JUL-1992; 92US-09233692.
 XX
 PR 26-FEB-1988; 88US-0160766.
 PR 26-FEB-1988; 88US-0160771.
 PR 15-JUL-1988; 88US-0219279.
 PR 17-FEB-1989; 89US-0310881.
 PR 05-MAY-1989; 89US-0347637.
 PR 08-JUN-1989; 89US-0363138.
 PR 22-OCT-1990; 90US-0600244.
 PR 16-JAN-1991; 91US-0641617.
 PR 26-JUL-1991; 91US-0737899.
 PR 01-AUG-1991; 91US-0739143.
 XX
 PA (BIOS-) BIOSOURCE GENETICS CORP.

XX Dawson WO, Donson J, Garger SJ, Grantham GL, Grille LK;
 PI Turpen AM, Turpen RH;
 XX WPI: 1994-176269/21.
 DR N-PSDB; AAO65574.
 XX
 PT New recombinant plant viral nucleic acid - capable of systemic
 PT infection and stable expression of non-native nucleic acid in
 PT plant host
 XX
 PS Example 4; Columns 53-56; 44pp; English.
 XX
 CC The rice alpha-amylase gene may be inserted into a recombinant plant
 CC virus which can then be used to infect plants for the production of
 CC non-native products (in this case alpha-amylase). Other genes which
 CC may be inserted into the virus are those which control a phenotypic
 CC trait, such as male sterility, or sequences encoding anti-sense RNA
 CC which can be useful to prevent the expression of undesired phenotypic
 CC traits. The recombinant virus is derived from a plus sense, single
 CC stranded virus selected from tobamovirus, brome mosaic virus, rice
 CC necrosis virus or a gemini virus.
 CC (Updated on 25-MAR-2003 to correct PF field.)
 CC
 CC Sequence 433 AA;
 SQ
 XX
 Query Match 80.4%; Score 45; DB 15; Length 433;
 Best Local Similarity 70.0%; Pred. No. 20;
 Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
 OY 1 VNMVKNVCGS 10
 DB 258 VNMVDRVGA 267
 ||||:||||
 RESULT 9
 ID AAR32987 standard; Protein; 434 AA.
 XX
 AC AAR32987;
 XX
 DT 25-MAR-2003 (updated)
 DT 17-JUN-1993 (first entry)
 XX
 DE Rice alpha-amylase.
 XX
 KM Recombinant products; commercial production; fermentation;
 KM diosynthes; natural products; recombinant proteins;
 KM product expression; protein expression; expressed proteins.
 XX
 OS Oryza sativa.
 XX
 PN WO9303161-A1.
 XX
 PD 18-FEB-1993.
 XX
 PF 31-JUL-1992; 92WO-US06359.
 XX
 PR 01-AUG-1991; 91US-0739143.
 XX
 PA (DAMS/) DAWSON W O.
 PA (DONSON/) DONSON J.
 PA (GARG/) GARGER S J.
 PA (GRANT/) GRANTHAM G L.
 PA (GRILLE/) GRILLE L K.
 PA (TURP/) TURPEN A M.
 PA (TURP/) TURPEN T H.
 XX
 PI Donson J, Dawson WO, Grantham GL, Turpen RH, Garger SJ,
 PI Grille LK.
 XX WPI: 1993-076518/09.
 DR N-PSDB; AAO37680.

```

XX Recombinant plant viral nucleic acids - used to express a prod.,
PT e.g. antibody or IL-1 in a plant
XX
XX Example 4; Page 96; 30pp; English.
PS
XX This sequence is rice alpha amylase. The coding sequence was inserted
CC into a recombinant plant viral nucleic acid which was then used to
CC express a recombinant product (in this case rice alpha-amylase) in a
CC plant. The plant viral sequence may be from tobacco mosaic, cucumber
CC green mottle, cowpea mosaic, bromo mosaic, broad bean mottle, rice
CC necrosis, geminiviruses, tomato golden mosaic, Cassava latent and
CC maize streak viruses.
CC (Updated on 25-MAR-2003 to correct PN field.)
CC (Updated on 25-MAR-2003 to correct PI field.)
CC
XX Sequence 434 AA;
SO

```

```

Query Match 80.4%; Score 45; DB 14; Length 434;
Best Local Similarity 70.0%; Pred. No. 20;
Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

```

```

Oy 1 VNMVNVKVGGS 10
    ||||:||||
Db 259 VNMVDRVGA 268

```

RESULT 10

```
AAW10469
ID AAW10469 standard; Protein: 434 AA.
XX
XX AAW10469;
AC

```

```
DT 26-APR-1997 (first entry)
XX
XX

```

```
DE Rice alpha-amylase.
XX

```

```
KM Recombinant viral nucleic acid; RNA virus; vector.
KM Tobacco mosaic virus; TMV; rice; alpha-amylase; transgenic plant.
XX

```

```
OS Oryza sativa.
XX

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```
PN W09640867-A1.
XX

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```
PD 19-DEC-1996.
XX

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PF 06-JUN-1996; 96WO-US09299.
XX

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```
PR 07-JUN-1995; 95US-0483502.
XX

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PA (BIOS-) BIOSOURCE TECHNOLOGIES INC.
XX

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PI Dawson WO, Donson J, Garger SJ, Grantham GL, Grill LK;
PI Turpen AM, Turpen TH;
XX

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DR WPI: 1997-065181/06.
XX

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```
DR N-PSDB; AAT47095.
XX

```

```
PT Recombinant viral nucleic acid producing, e.g. male sterility in
PT plants - comprises nucleic acid whose transcription is controlled by
PT another sequence
XX

```

```
PS Example 4; Page 127-129; 149pp; English.
XX

```

```
CC A DNA sequence (AAT47095) codes for rice alpha-amylase (AAW10469).
CC Novel viral nucleic acids can be constructed in which the alpha-
CC amylase coding sequence is placed under control of the promoter
CC of the tobacco mosaic virus coat protein gene, which has been
CC deleted. The recombinant viral nucleic acid is capable of self-
CC replication, encapsidation and systemic spread in infected tobacco
CC plants, and directs expression of the alpha-amylase in plant
CC tissue.
XX

```

```
SO Sequence 434 AA;

```

```

Query Match 80.4%; Score 45; DB 18; Length 434;
Best Local Similarity 70.0%; Pred. No. 20;
Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

```

```

Oy 1 VNMVNVKVGGS 10
    ||||:||||
Db 259 VNMVDRVGA 268

```

RESULT 11

```
AAW11871
ID AAW11871 standard; Protein: 434 AA.
XX

```

```
AC AAW11871;
XX

```

```
DT 25-MAR-2003 (updated)
DT 21-APR-1997 (first entry)
XX

```

```
DE Rice alpha-amylase.
XX

```

```
KM Recombinant virus; alpha-haemoglobin; human; chinese cucumber;
KM alpha-trichosanthin; rice; alpha amylase; beta-haemoglobin;
KM subgenomic promoter; coat protein.
XX

```

```
OS Oryza sativa.
XX

```

```
PN US5589367-A.
XX

```

```
PD 31-DEC-1996.
XX

```

```
PE 19-JAN-1994; 94US-0184237.
XX

```

```
PR 17-FEB-1989; 89US-0310881.
PR 05-MAY-1989; 89US-0347637.
XX

```

```
PR 08-JUN-1989; 89US-0363138.
PR 31-JUL-1992; 92US-0923692.
XX

```

```
PR 26-FEB-1988; 88US-0160766.
PR 26-FEB-1988; 88US-0160771.
XX

```

```
PR 15-JUL-1988; 88US-0219279.
PR 22-OCT-1990; 90US-0600244.
XX

```

```
PR 16-JAN-1991; 91US-0641617.
PR 26-JUL-1991; 91US-0737899.
XX

```

```
PR 01-AUG-1991; 91US-0739143.
XX

```

```
PA (BIOS-) BIOSOURCE TECHNOLOGIES INC.
XX

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```
PI Dawson WO, Donson J, Garger SJ, Grantham GL, Grill LK;
PI Turpen AM, Turpen TH;
XX

```

```
DR WPI: 1997-076845/07.
XX

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```
DR N-PSDB; AAT61377.
XX

```

```
PT Recombinant viral DNA for altering plant phenotype or protein prodn
PT - contains non-native sub-genomic promoter for expression of
PT heterologous protein and native promoter for expression of coat
PT protein
XX

```

```
PS Example 4; Column 49-52; 42pp; English.
XX

```

```
CC The sequences given in AAW11868-71 represent proteins which were
CC produced by the recombinant viruses of the invention. The
CC viruses are recombinant plant viruses which comprise a native plant
CC virus subgenomic promoter, at least one non-native plant virus
CC subgenomic promoter, and a sequence encoding a plant virus coat
CC protein. These heterologous sequences are preferably under the
CC control of the native promoter sequence. By using a plant virus
CC existing cells can be altered with a new coding sequences without
CC involving germ cell. The recombinant viruses are stable and can
CC cause systemic infection, with stable expression/transcription in
CC plants that are hosts for the non-native part of the vector. The
CC nucleotide sequences encoding these protein preferably integrated

```

in plant viruses having either the O-coat protein or the U1-coat protein gene.
 CC (updated on 25-MAR-2003 to correct PF field.)
 CC (updated on 25-MAR-2003 to correct PR field.)
 XX Sequence 434 AA;
 SO
 Query Match 80.4%; Score 45; DB 18; Length 434;
 Best Local Similarity 70.0%; Pred. No. 20;
 Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
 OY 1 VNMVNRVGGG 10
 DB 259 VNMVDRVGGG 268
 RESULT 12
 ID AAY01375 standard; Protein: 434 AA.
 AC AAY01375;
 XX 20-MAR-2003 (updated)
 DT 04-JUN-1999 (first entry)
 XX
 DE O. sativa alpha-amylase.
 XX
 KW Recombinant; plant virus; coat protein; systemic infection;
 XX transcription; therapeutic; rice; alpha-amylase.
 OS Oryza sativa.
 XX
 PN US5889190-A.
 PD 30-MAR-1999.
 XX
 PE 07-JUN-1995; 95US-0480432.
 XX
 PR 17-FEB-1989; 89US-0310881.
 PR 05-MAY-1989; 89US-0347637.
 PR 08-JUN-1989; 89US-0363136.
 PR 31-JUL-1992; 92US-0923592.
 PR 12-JAN-1992; 92US-0184237.
 PR 26-FEB-1988; 88US-0160766.
 PR 26-FEB-1988; 88US-0160771.
 PR 15-JUL-1988; 88US-0219279.
 PR 22-OCT-1990; 90US-0600244.
 PR 16-JAN-1991; 91US-0641617.
 PR 26-JUL-1991; 91US-0737899.
 PR 01-AUG-1991; 91US-0739143.
 XX
 PA (BIOS-) BIOSOURCE TECHNOLOGIES INC.
 XX
 PI Dawson WO, Donson J, Garger SJ, Grantham GL, Grill LK;
 PI Turpen AM, Turpen TH;
 XX
 DR WPI: 1999-243290/20.
 DR N-PSDB: AAX29144.
 XX
 PT Recombinant plant viral nucleic acid derived from a plus sense,
 PT single stranded RNA plant virus - useful for the transcription of
 PT products in a host
 XX
 PS Example 4: Columns 47-51; 46pp; English.
 XX
 CC The invention relates to a recombinant plant viral nucleic acid derived
 CC from a plus sense, single stranded RNA plant virus. The recombinant plant
 CC viral nucleic acid comprises: (a) a first plant viral subgenomic promoter
 CC that is native to the plus sense, single stranded RNA plant virus and
 CC operably joined to a first nucleic acid expression sequence; and (b) a
 CC second plant viral subgenomic promoter that is non-native and is operably
 CC joined to a second nucleic acid expression sequence; where, (i) (a) and
 CC (b) are incapable of recombination with one another, (ii) either the

first or the second nucleic acid expression sequence is a plant viral
 CC coat protein coding sequence. The recombinant plant viral nucleic acid
 CC allows the transcription of products in a host, such as therapeutic and
 CC other useful polypeptides or proteins e.g. enzymes, complex biomolecules
 CC and ribozymes. It also gives the option of applying the coding sequence
 CC to the desired organism, tissue, organ or cell, is stable for the foreign
 CC coding sequences and is capable of systemic infection in the plant host.
 CC The transformation and regeneration of target organisms become
 CC unnecessary.
 CC (updated on 20-MAR-2003 to correct PR field.)
 XX
 SO Sequence 434 AA;
 Query Match 80.4%; Score 45; DB 20; Length 434;
 Best Local Similarity 70.0%; Pred. No. 20;
 Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
 OY 1 VNMVNRVGGG 10
 DB 259 VNMVDRVGGG 268
 RESULT 13
 ID AAM84383 standard; Protein: 434 AA.
 AC AAM84383;
 XX
 DT 01-APR-1999 (first entry)
 XX
 DE Rice alpha-amylase sequence.
 XX
 KW Rice; alpha-amylase; plant virus; RNA plant virus promoter;
 KW systemic infection; foreign gene expression; AIDS therapeutic drug.
 XX
 OS Oryza sativa.
 XX
 PN US5866785-A.
 PD 02-FEB-1999.
 XX
 PE 07-JUN-1995; 95US-0482920.
 XX
 PR 31-JUL-1992; 92US-0923692.
 PR 26-FEB-1988; 88US-0160766.
 PR 15-JUL-1988; 88US-0160771.
 PR 17-FEB-1989; 89US-0310881.
 PR 05-MAY-1989; 89US-0347637.
 PR 08-JUN-1989; 89US-0363138.
 PR 22-OCT-1990; 90US-0600244.
 PR 16-JAN-1991; 91US-0641617.
 PR 26-JUL-1991; 91US-0737899.
 PR 01-AUG-1991; 91US-0739143.
 PR 19-JAN-1994; 94US-0184237.
 PR 07-JUN-1995; 95US-0482920.
 XX
 PA (BIOS-) BIOSOURCE TECHNOLOGIES INC.
 XX
 PI Dawson WO, Donson J, Garger SJ, Grantham GL, Grill LK;
 PI Turpen AM, Turpen TH;
 XX
 DR WPI: 1999-142035/12.
 DR N-PSDB: AAX03386.
 XX
 PT Recombinant plant viral vector - that is capable of systemic
 PT infection in host plant and stable production of heterologous DNA
 PT useful for producing therapeutic proteins for treating e.g. AIDS
 XX
 PS Example 4: Columns 51-54; 45pp; English.
 XX
 CC The present sequence represents rice alpha-amylase. The nucleic
 CC acid sequence can be expressed in the plant viral constructs of the

CC invention. The specification describes a recombinant plant viral
CC nucleic acid derived from a positive (+)-sense RNA plant virus comprising
CC a native (+)-sense RNA plant virus promoter that is linked to an
CC expression sequence and a heterologous (+)-sense RNA plant virus
CC promoter that is linked to an expression sequence. The promoters are
CC incapable of recombination with each other, and one of the expression
CC sequences encodes a plant viral coat protein while the other is
CC optionally a heterologous coding sequence. The plant viral nucleic acid
CC is capable of systemic infection in a host plant. The viral construct is
CC useful for the introduction and expression of non-viral foreign genes
CC in plants and the production of e.g. potential AIDS therapeutic drugs.
CC
XX
SQ Sequence 434 AA;
Query Match 80.4%; Score 45; DB 20; Length 434;
Best Local Similarity 70.0%; Pred. No. 20;
Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
OY 1 VNWNKRYGGS 10
DB 259 VNWVDRVGGA 268
||||:||||:
RESULT 14
ID AAY87792 standard; Protein: 434 AA.
AC AAY87792;
XX
XX 24-AUG-2000 (first entry)
DT
XX
DE Rice alpha-amylase protein.
XX
XX Animal RNA virus; viral coat protein; plant; male sterility;
KW Interleukin; EPO; erythropoietin; CSF; colony stimulating factor;
KW Factor VIII; hGH; human growth hormone; melanin; insulin; vaccine;
KW stereo specific catalysis; alpha-amylase; rice.
XX
OS Oryza sativa.
XX
XX US6054566-A.
XX
XX 25-APR-2000.
PD
XX
XX 07-JUN-1995; 9505-0484341.
PE
XX
XX 17-FEB-1989; 89US-0310881.
PR 08-JUN-1989; 89US-0363138.
PR 26-FEB-1988; 88US-0160766.
PR 26-FEB-1988; 88US-0160771.
PR 15-JUL-1988; 88US-0219279.
PR 05-MAY-1989; 89US-0347637.
PR 22-OCT-1990; 90US-0600244.
PR 16-JAN-1991; 91US-0641617.
PR 26-JUL-1991; 91US-0737899.
PR 01-AUG-1991; 91US-0739143.
PR 31-JUL-1992; 92US-0923692.
XX
XX (BIOS-) BIOSOURCE TECHNOLOGIES INC.
PA
XX
XX Garger SJ, Grill LK, Turpen TH, Grantham GL, Dawson WO, Turpen AM;
PI Donson J;
XX
XX WPI: 2000-338510/29.
DR N-PSDB; AAA12394.
XX
XX Recombinant non-retroviral nucleic acid for producing proteins such as
PT Interleukins, melanin and vaccines, comprises subgenomic promoters
PT linked to sequences coding for viral coat protein and heterologous
PT proteins -
XX
PS Example 4; Column 65-68; 51pp; English.
XX

CC This invention describes a novel recombinant viral nucleic acid (I)
CC from a non-retroviral (+) sense, single stranded animal RNA virus
CC comprising a nucleic acid sequence coding for a viral coat protein
CC regulated by a native subgenomic promoter and other two heterologous
CC nucleic acid sequences regulated by two other subgenomic promoters.
CC (I) is useful for expressing foreign genes e.g. genes inducing male
CC sterility in plants. (I) is also useful for producing proteins such as
CC Interleukins, EPO (erythropoietin), CSF (colony stimulating factor),
CC Factor VIII, hGH (human growth hormone), melanin, insulin, vaccines
CC etc., and enzymes that are useful for stereo specific catalysis of
CC organic compounds. (I) is stable and transcribed systemically. The dual
CC subgenomic promoter system reduces the frequency of recombination thus
CC reducing regeneration of the wild type virus. This sequence represents
CC a rice alpha-amylase protein which is described in the method of the
CC invention.
CC
XX
SQ Sequence 434 AA;
Query Match 80.4%; Score 45; DB 21; Length 434;
Best Local Similarity 70.0%; Pred. No. 20;
Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
OY 1 VNWNKRYGGS 10
DB 259 VNWVDRVGGA 268
||||:||||:
RESULT 15
ID AAB12798 standard; Protein: 428 AA.
AC AAB12798;
XX
XX 23-NOV-2000 (first entry)
DT
XX
DE Rice alpha-Amy7-C protein SEQ ID NO:2.
XX
XX Rice; alpha-Amy6-C; alpha-Amy7-C; alpha-Amy8-C; alpha-Amy10-C;
KW gene expression; promoter region; alpha-amylase; transgenic plant.
XX
OS Oryza sativa.
XX
XX JP2000157080-A.
XX
XX 13-JUN-2000.
PD
XX
XX 04-NOV-1993; 99JP-0356560.
PE
XX
XX 05-NOV-1992; 92JP-0321274.
PR 04-NOV-1993; 93JP-0297607.
XX
XX (NASC-) NAT SCI COUNCIL.
XX
XX WPI: 2000-468171/41.
DR N-PSDB; AAA72947.
XX
XX A gene expression system containing the promoter region of
PT alpha-amylase gene, useful for mass production of a desired gene
PT product in a plant host cell
XX
XX
XX Example 1; Page 27-30; 39pp; Japanese.
XX
XX The present invention describes a gene expression system containing the
XX promoter region of an alpha-amylase gene. Also described is a method for
XX preparing a transgenic rice plant comprising: (1) infecting Agrobacterium
XX into an unmaturred embryo of a rice plant; (2) simultaneously culturing
XX the embryo with a suspended culture of a dicotyledon during the
XX transforming step; (3) growing the transformed embryo to a callus in a
XX selective medium containing a plant growth hormone; and (4) regenerating
XX the callus to roots and sprouts in a regeneration medium. The method can
XX be used for mass production of a desired gene product in a plant host
XX cell. The present sequence represents the rice alpha-Amy7-C protein,
XX which is used in an example from the present invention.


```

XX Sequence 428 AA;
SQ
Query Match 75.0%; Score 42; DB 21; Length 428;
Best Local Similarity 70.0%; Pred. No. 62;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 VNMVNVXVGS 10
   ||||:||||
Db 253 VNMVNVHVGCA 262

RESULT 16
AA076520 standard; Protein: 429 AA.
XX
AC AA076520;
XX
DE 14-FEB-1996 (first entry)
XX
DE Alpha-amylase-7-C.
XX
KW Alpha-Amy-6-C; amylase; promoter; vector; heterologous;
KW gene expression system.
XX
OS Oryzae sativa.
XX
Key Location/Qualifiers
FH MISC-difference 35
FT MISC-difference 83 /note- "corresp. to GAC codon"
FT MISC-difference 83 /note- "corresp. to CAG codon"
FT MISC-difference 158 /note- "corresp. to GAC codon"
FT MISC-difference 218 /note- "corresp. to GAC codon"
FT MISC-difference 224 /note- "corresp. to TAC codon"
FT MISC-difference 224 /note- "corresp. to CGG codon"
FT MISC-difference 233 /note- "corresp. to CGT codon"
FT MISC-difference 294 /note- "corresp. to CAG codon"
FT MISC-difference 294 /note- "corresp. to CAG codon"
XX
PN JP07143895-A.
XX
PD 06-JUN-1995.
XX
PP 04-NOV-1993; 93JP-0297607.
XX
PR 05-NOV-1992; 92JP-0321274.
XX
PA (MASC-) NAT SCI COUNCIL.
XX
WP1: 1995-236472/31.
XX
DR N-PSDB; AA092806.
XX
PT Gene expression system contg. alpha-amylase gene promoter - for use
PT in plants for expression of heterologous genes
XX
PS Claim 3; Page 27-30; 42pp; Japanese.
XX
CC AA076519-R76521 represent the amylase gene products alpha-amylase-6-C,
CC alpha-amylase-7-C and alpha-amylase-8-C respectively. The promoter
CC regions of these amylase genes are used in a new gene expression system.
CC The system may be used for the expression of heterologous genes in plant
CC cells and for the large scale production of the encoded products of such
CC genes.
CC NB: some amino acids in this sequence appear to have been wrongly
CC entered, see feature table and the corresp. DNA file AA092806.
CC
SQ Sequence 429 AA;
Query Match 75.0%; Score 42; DB 16; Length 429;

Best Local Similarity 70.0%; Pred. No. 62;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 VNMVNVXVGS 10
   ||||:||||
Db 254 VNMVNVHVGCA 263

RESULT 17
AB048004 standard; Protein: 157 AA.
XX
AC AB048004;
XX
DE 05-FEB-2002 (first entry)
XX
DE Listeria monocytogenes protein #708.
XX
KW Antibacterial; gene therapy; vaccine; biosynthesis; biodegradation;
KW vitamin B12; bacterial infection; disease.
XX
OS Listeria monocytogenes.
XX
PN WO20017335-A2.
XX
PD 18-OCT-2001.
XX
PF 11-APR-2001; 2001WO-FR01118.
XX
PR 11-APR-2000; 2000FR-0004629.
XX
PA (INSP) INST PASTEUR.
XX
PI Buchrisser C, Frangeul L, Couve E, Rusanok C, Fsihl H, Dehoux P,
PI Dussurget O, Chetouani F, Nedjari H, Glaser P, Kunst F, Cossart P;
PI Daniels J, Gobel M, Kreft J, Kuhn M, Ng E, Vazquez-Boland JA;
PI Dominguez-Bernal G, Garrido-Garcia P, Tierrez-Martinez A, Amend A;
PI Charaborty T, Dommann E, Hain T, Berche P, Chardit A, Durant L;
PI Perez-Diaz J, Baquero F, Garcia Del Portillo F, Gomez-Lopez N;
PI Madueno E, de Pablos B, Wehland J, Kaerst U, Entian K, Hauf J;
PI Rose M, Voss H;
XX
DR WP1: 2002-010914/01.
XX
PT Genomic sequence for Listeria monocytogenes, useful e.g. for treatment
PT and prevention of Listeria and related bacterial infections, and
PT related polypeptides.
XX
PS Claim 6; SEQ ID No 709; 192pp; French.
XX
CC The present invention relates to the genome sequence of Listeria
CC monocytogenes EGD-e (see AB030411). The genome sequence and fragments of
CC it are useful for selecting probes and primers for detecting genes in L.
CC monocytogenes and related organisms, and for studying genetic
CC polymorphisms and other genomes. The present invention is a protein
CC encoded by the genome sequence of the present invention. Proteins
CC expressed from the genome sequence are useful for raising specific
CC antibodies, identification of L. monocytogenes and related organisms, and
CC for biosynthesis and biodegradation, especially biosynthesis of Vitamin
CC B12. The genome sequence and proteins encoded by it are also useful for
CC selecting compounds that regulate gene expression and cell replication
CC and modulate L. monocytogenes-related diseases. In addition, the genome
CC sequence and proteins encoded by it are useful in pharmaceutical and
CC vaccines compositions for the treatment or prevention of infections by L.
CC monocytogenes and related organisms.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 157 AA;
Query Match 69.6%; Score 39; DB 23; Length 157;
Best Local Similarity 75.0%; Pred. No. 70;

```

Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 MMVNVKVG 9
11:1111
146 MMVNVKVG 153

Db

RESULT 18
ABG49321
ID ABG49321 standard; Protein: 548 AA.
XX
AC ABG49321;
XX
DT 05-FEB-2002 (first entry)
XX
DE Listeria monocytogenes protein #2025.
XX
KW Antibacterial; gene therapy; vaccine; biosynthesis; biodegradation;
KM vitamin B12; bacterial infection; disease.
XX
OS Listeria monocytogenes.
XX
PN WO200177335-A2.
XX
PD 18-OCT-2001.
XX
PF 11-APR-2001; 2001WO-FR01118.
XX
PR 11-APR-2000; 2000FR-0004629.
XX
PA (INSP) INST PASTEUR.
XX
PI Buchrieser C, Frangeul L, Couve E, Rusniok C, Raihi H, Dehoux P,
PI Dussauguet O, Chetoui F, Nedjari H, Glaser P, Kunst F, Cossart P,
PI Daniels J, Goebel W, Kieft J, Kuhn M, Ng E, Vazquez-Boland JA;
PI Dominguez-Bernal G, Garrido-Garcia P, Tierrez-Martinez A, Amend A;
PI Chakraborty T, Domann E, Hain T, Berche P, Charbit A, Durant L,
PI Perez-Diaz J, Baquero F, Garcia Del Portillo F, Gomez-Lopez N;
PI Meduenlo E, De Padlos B, Wehland J, Kaerst U, Entian K, Haut J;
PI Rose M, Voss H;
XX
DR WPI; 2002-010914/01.
XX
PT Genomic sequence for Listeria monocytogenes, useful e.g. for treatment
PT and prevention of Listeria and related bacterial infections, and
PT related polypeptides -
XX
PS Claim 6; SEQ ID No 2026; 192pp; French.
XX
CC The present invention relates to the genome sequence of Listeria
CC monocytogenes EGD-e (see ABA03041). The genome sequence and fragments of
CC it are useful for selecting probes and primers for detecting genes in L.
CC monocytogenes and related organisms, and for studying genetic
CC polymorphisms and other genomes. The present sequence is a protein
CC encoded by the genome sequence of the present invention. Proteins
CC expressed from the genome sequence are useful for relating specific
CC antibodies, identification of L. monocytogenes and related organisms, and
CC for biosynthesis and biodegradation, especially biosynthesis of Vitamin
CC B12. The genome sequence and proteins encoded by it are also useful for
CC selecting compounds that regulate gene expression and cell replication
CC and modulate L. monocytogenes-related diseases. In addition, the genome
CC sequence and proteins encoded by it are useful in pharmaceutical and
CC vaccines compositions for the treatment or prevention of infections by L.
CC monocytogenes and related organisms.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 548 AA;

Query Match 69.6%; Score 39; DB 23; Length 548;
Best Local Similarity 66.7%; Pred. No. 2.5e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 MMVNVKVG 10
111:111:
137 MMVNVKVG 145

Db

RESULT 19
ABG66859
ID ABG66859 standard; Protein: 54 AA.
XX
AC ABG66859;
XX
DT 24-SEP-2002 (first entry)
XX
DE Human prostate specific protein DEX0283_167.
XX
KW Human; prostate specific protein; cytostatic; PSP; prostate cancer;
KM gene therapy; vaccine; non-cancerous prostatic disease.
XX
OS Homo sapiens.
XX
PN WO200242329-A2.
XX
PD 30-MAY-2002.
XX
PF 20-NOV-2001; 2001WO-US45177.
XX
PR 21-NOV-2000; 2000US-252189P.
XX
PA (DIAD-) DIADEXUS INC.
XX
PI Salceda S, Macina RA, Recipon H, Sun Y, Liu C;
XX
DR WPI; 2002-500278/53.
XX
PT New prostate specific polypeptides useful for identifying, diagnosing,
PT monitoring, staging, imaging and treating prostate cancer and
PT non-cancerous disease states in prostate -
XX
PS Claim 11; Page 225-226; 248pp; English.
XX
CC The invention relates to an isolated polypeptide that comprises a
CC sequence with 60 % sequence identity to one of 103 prostate specific
CC polypeptide (PSP) sequences (SI), given in specification, or a sequence
CC encoded by a nucleic acid comprising one of 114 prostate specific nucleic
CC acid (PSNA) sequences (S2), given in specification. Also included are
CC a vector comprising the PSNA, a host cell comprising the vector,
CC preparation of the PSP, a polypeptide encoded by the PSNA; an anti-PSP
CC antibody the antibody or its fragment, a kit for detecting a risk of
CC cancer or presence of cancer in a patient, comprising a unit for
CC determining the presence of the PSP or the PSNA in a sample of a patient
CC and a vaccine comprising the PSP or the PSNA. The PSNA is useful for
CC determining the presence of a prostate specific nucleic acid (PSNA) in a
CC sample. The antibody to the PSP is useful for determining the presence of
CC a prostate specific protein in a sample. The antibody is also useful for
CC treating a patient with prostate cancer, where the administration of the
CC antibody induces an immune response against the prostate cancer cell
CC expressing the nucleic acid molecule or polypeptide. The PSP or the PSNA
CC is useful for diagnosing and monitoring the presence and metastases of
CC prostate cancer in a patient. The PSP is useful as a vaccine component
CC for eliciting a humoral and/or cellular immune response, and for
CC identifying an agonist and antagonist. The PSNA is used in gene therapy,
CC producing transgenic animals and cells, and for producing engineered
CC prostate tissue for treatment and research. The PSNA is useful for
CC detecting prostate cancer by detecting genetic lesions or mutations. The
CC PSP and the PSNA are useful for detecting, diagnosing, monitoring,
CC staging and predicting cancers. The PSP and the PSNA are also useful for
CC identifying prostate tissue, and thus is useful in forensic science,
CC prostate cell differentiation and development and in tissue engineering.
CC The PSP, the PSNA and the antibody are useful for identifying,
CC diagnosing, monitoring, staging, imaging and treating prostate cancer and
CC non-cancerous disease states in prostate tissue. The present
CC sequence is a prostate specific protein (PSP) sequence.

XX Sequence 54 AA: 67.9%; Score 38; DB 23; Length 54;
 Query Match Best Local Similarity 75.0%; Pred. No. 34;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 VMVNRKVG 8
 :|||||
 43 IMVNLVWG 50

Db

RESULT 20
 AAU65532
 ID AAU65532 standard; Protein: 90 AA.
 XX
 AC AAU65532;
 XX
 DT 27-FEB-2002 (first entry)
 XX
 DE Propionibacterium acnes immunogenic protein #26428.
 XX
 KW SAPRO syndrome; synovitis; acne; pustulosis; hypotosis; osteomyelitis;
 KW uveitis; endophthalmitis; bone; joint; central nervous system; ELISA;
 KW inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay;
 KW dermatological; osteopathic; neuroprotectant.
 XX
 OS Propionibacterium acnes.
 XX
 PN W0200181581-A2.
 XX
 PD 01-NOV-2001.
 XX
 PF 20-APR-2001; 2001WO-US12865.
 XX
 PR 21-APR-2000; 2000US-199047P.
 XX
 PR 02-JUN-2000; 2000US-208841P.
 XX
 PR 07-JUL-2000; 2000US-216747P.
 XX
 PA (CORI-) CORIXA CORP.
 XX
 PI Skelky YAW, Persing DH, Mitcham JL, Wang SS, Bhatia A;
 PI L'maisonneuve J, Zhang Y, Jen S, Carter D;
 XX
 DR WPI: 2001-616774/71.
 XX
 DR N-PSDB: AAS59673.
 XX
 PT Propionibacterium acnes polypeptides and nucleic acids useful for
 PT vaccinating against and diagnosing infections, especially useful for
 PT treating acne vulgaris -
 XX
 PS Example 1; SEQ ID NO 26727; 1069pp; English.
 XX
 CC Sequences AAU39105-AAU68017 represent propionibacterium acnes immunogenic
 CC polypeptides. The proteins and their associated DNA sequences are used in
 CC the treatment, prevention and diagnosis of medical conditions caused by
 CC P. acnes. The disorders include SAPRO syndrome (synovitis, acne,
 CC pustulosis, hypotosis and osteomyelitis), uveitis and endophthalmitis.
 CC P. acnes is also involved in infections of bone, joints and the central
 CC nervous system, however it is particularly involved in the inflammatory
 CC lesions associated with acne vulgaris. A method for detecting the
 CC presence or absence of P. acnes in a patient comprises contacting a
 CC sample with a binding agent that binds to the proteins of the invention
 CC and determining the amount of bound protein in the sample. The
 CC polypeptides may be used as antigens in the production of antibodies
 CC specific for P. acnes proteins. These antibodies can be used to
 CC downregulate expression and activity of P. acnes polypeptides and
 CC therefore treat P. acnes infections. The antibodies may also be used as
 CC diagnostic agents for determining P. acnes presence, for example, by
 CC enzyme linked immunosorbent assay (ELISA).
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 90 AA: 67.9%; Score 38; DB 22; Length 90;
 Query Match Best Local Similarity 62.5%; Pred. No. 58;
 Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 MWVNRKVG 9
 :|||||
 31 NWTNLSIG 38

Db

RESULT 21
 ABP74094
 ID ABP74094 standard; Protein: 1077 AA.
 XX
 AC ABP74094;
 XX
 DT 30-JAN-2003 (first entry)
 XX
 DE Candida albicans essential protein SEQ ID NO 7931.
 XX
 KW Fungus; yeast; tetracycline; promoter; GRACE strain; biosynthesis;
 KW signal transduction; DNA replication; cell division; growth;
 KW proliferation; Candida albicans; fungicide; antifungal.
 XX
 OS Candida albicans.
 XX
 PN W0200253728-A2.
 XX
 PD 11-JUL-2002.
 XX
 PF 26-DEC-2001; 2001WO-US49486.
 XX
 PR 29-DEC-2000; 2000US-259128P.
 XX
 PR 20-FEB-2001; 2001US-0792024.
 XX
 PR 22-AUG-2001; 2001US-314050P.
 XX
 PA (ELIT-) ELITRA PHARM INC.
 XX
 PI Roemer T, Jiang B, Boone C, Bussey H, Ohlsen KL;
 PI WPI: 2002-566694/60.
 XX
 DR N-PSDB: AB232644.
 XX
 PT Constructing strains for identifying gene products as effective targets
 PT for therapeutic intervention, by inactivating in the strain one allele
 PT of a gene and placing other allele of the gene under conditional
 PT expression -
 XX
 PS Claim 44; SEQ ID NO 7931; 167pp + Sequence Listing; English.
 XX
 CC The invention relates to constructing (M1) a strain of diploid fungal
 CC cells in which both alleles of a gene are modified, comprising modifying
 CC one allele by insertion or replacement by a cassette having an
 CC expressible selectable marker and modifying other allele by
 CC recombination, of a promoter replacement fragment with a heterologous
 CC promoter, so that expression of the second allele is regulated by the
 CC promoter. (M1) is useful for constructing a strain of diploid fungal
 CC cells in which both alleles of a gene are modified. The diploid fungal
 CC cells having both alleles modified are useful for identifying a gene that
 CC is essential to the survival or growth of a fungus, a gene that
 CC contributes to the virulence and/or pathogenicity of a fungus, a gene
 CC that contributes to the resistance of a diploid fungus to an antifungal
 CC agent, an antifungal agent that inhibits the growth of a diploid fungus
 CC and for identifying a therapeutic agent for treatment of a mammalian
 CC disease. (M1) is useful for identifying a compound which modulates the
 CC activity of a gene product, preferably enzymatic activity, carbon
 CC compound catabolism, biosynthetic, transporter, transcriptional,
 CC translational, signal transduction, DNA replication and cell division
 CC activity. The method is useful for identifying a compound having the
 CC ability to inhibit growth or proliferation of C. albicans cells and for
 CC treating infection by C. albicans. The present sequence is that of an

CC essential *Candida albicans* protein used in the method of the invention.
CC Note: The sequence data for this patent is not represented in the printed
CC specification but is based on sequence information supplied to Derwent by
CC the European Patent Office.

XX Sequence 1077 AA;

Query Match 67.9%; Score 38; DB 23; Length 1077;

Best Local Similarity 60.0%; Pred. No. 7,4e+02;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 VNMVKNYKGS 10
Db 848 IDWVNEVEGS 857

RESULT 22
AAM82469
ID AAM82469 standard; Protein; 35 AA.

XX AAM82469;

AC AAM82469;

DT 07-NOV-2001 (first entry)

XX Human immune/haematopoietic antigen SEQ ID NO:10062.
XX Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
KW cytosolic; gene therapy; vaccine; metastasis.

OS Homo sapiens.

XX WO200157182-A2.

XX 09-AUG-2001.

XX 17-JAN-2001; 2001WO-US01354.

XX 31-JAN-2000; 2000US-019065.

XX 04-FEB-2000; 2000US-018062.

XX 24-FEB-2000; 2000US-018464.

XX 02-MAR-2000; 2000US-018635.

XX 16-MAR-2000; 2000US-018987.

XX 17-MAR-2000; 2000US-019007.

XX 18-APR-2000; 2000US-019813.

XX 19-MAY-2000; 2000US-020515.

XX 07-JUN-2000; 2000US-020946.

XX 30-JUN-2000; 2000US-021513.

XX 07-JUL-2000; 2000US-021664.

XX 07-JUL-2000; 2000US-021688.

XX 11-JUL-2000; 2000US-021748.

XX 11-JUL-2000; 2000US-021748.

XX 14-JUL-2000; 2000US-021829.

XX 26-JUL-2000; 2000US-022096.

XX 26-JUL-2000; 2000US-022096.

XX 14-AUG-2000; 2000US-022451.

XX 14-AUG-2000; 2000US-022451.

XX 14-AUG-2000; 2000US-022521.

XX 14-AUG-2000; 2000US-022526.

PR 01-SEP-2000; 2000US-022928.

PR 01-SEP-2000; 2000US-022934.

PR 01-SEP-2000; 2000US-022934.

PR 01-SEP-2000; 2000US-022934.

PR 05-SEP-2000; 2000US-022950.

PR 05-SEP-2000; 2000US-022951.

PR 06-SEP-2000; 2000US-023037.

PR 06-SEP-2000; 2000US-023038.

PR 08-SEP-2000; 2000US-023124.

PR 08-SEP-2000; 2000US-023124.

PR 08-SEP-2000; 2000US-023124.

PR 08-SEP-2000; 2000US-023124.

PR 08-SEP-2000; 2000US-023124.

PR 08-SEP-2000; 2000US-023124.

PR 08-SEP-2000; 2000US-023124.

PR 08-SEP-2000; 2000US-023124.

PR 08-SEP-2000; 2000US-023124.

PR 08-SEP-2000; 2000US-023124.

PR 08-SEP-2000; 2000US-023124.

PR 08-SEP-2000; 2000US-023124.

PR 08-SEP-2000; 2000US-023124.

PR 08-SEP-2000; 2000US-023124.

PR 08-SEP-2000; 2000US-023124.

PR 08-SEP-2000; 2000US-023124.

PR 08-SEP-2000; 2000US-023124.

PR 08-SEP-2000; 2000US-023124.

PR 08-SEP-2000; 2000US-023124.

PR 08-SEP-2000; 2000US-023124.

PR 08-SEP-2000; 2000US-023124.

PR 08-SEP-2000; 2000US-023124.

PR 08-SEP-2000; 2000US-023124.

PR 08-SEP-2000; 2000US-023124.

PR 08-SEP-2000; 2000US-023124.

PR 08-SEP-2000; 2000US-023124.

PR 08-SEP-2000; 2000US-023124.

PR 08-SEP-2000; 2000US-023124.

PR 08-SEP-2000; 2000US-023124.

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PR 17-NOV-2000; 2000US-0249212.
PR 17-NOV-2000; 2000US-0249213.
PR 17-NOV-2000; 2000US-0249214.
PR 17-NOV-2000; 2000US-0249215.
PR 17-NOV-2000; 2000US-0249216.
PR 17-NOV-2000; 2000US-0249217.
PR 17-NOV-2000; 2000US-0249218.
PR 17-NOV-2000; 2000US-0249244.
PR 17-NOV-2000; 2000US-0249245.
PR 17-NOV-2000; 2000US-0249264.
PR 17-NOV-2000; 2000US-0249265.
PR 17-NOV-2000; 2000US-0249297.
PR 17-NOV-2000; 2000US-0249299.
PR 17-NOV-2000; 2000US-0249300.
PR 01-DEC-2000; 2000US-0250160.
PR 01-DEC-2000; 2000US-0250391.
PR 05-DEC-2000; 2000US-0251030.
PR 05-DEC-2000; 2000US-0251868.
PR 05-DEC-2000; 2000US-0251869.
PR 06-DEC-2000; 2000US-0251879.
PR 06-DEC-2000; 2000US-0251886.
PR 08-DEC-2000; 2000US-0251889.
PR 08-DEC-2000; 2000US-0251989.
PR 08-DEC-2000; 2000US-0251990.
PR 11-DEC-2000; 2000US-0254097.
PR 05-JAN-2001; 2001US-0259678.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Rosen CA, Barash SC, Ruben SM;
XX
XX WPI; 2001-483426/52.
XX
XX N-PSDB; AAK55250.
XX
XX Nucleic acids encoding human immune/hematopoietic antigen polypeptides,
XX useful for preventing, diagnosing and/or treating cancers and
XX metastasis -
XX
XX Claim 11; SEQ ID NO 10062; 3071bp + Sequence Listing; English.
XX
XX AAK54951 to AAK64702 encode the human immune/hematopoietic antigen (I)
XX amino acid sequences given in AAK62170 to AAK61921. (I) have cytostatic
XX activity, and can be used in gene therapy and vaccine production. (I)
XX proteins and polynucleotides may be used in the prevention, diagnosis and
XX treatment of diseases associated with inappropriate (I) expression. For
XX example, they may be used to treat disorders associated with decreased
XX expression by rectifying mutations or deletions in a patient's genome
XX that affect the activity of (I) by expressing inactive proteins or to
XX supplement the patient's own production of (I). Additionally, (I)
XX polynucleotides may be used to produce the secreted (I), by inserting
XX the nucleic acids into a host cell and culturing the cell to express the
XX protein. (I) proteins and polynucleotides may be used to prevent,
XX diagnose and treat immune/hematopoietic-related diseases, especially
XX cancers and cancer metastases of hematopoietic-derived cells. AAK64703
XX to AAK87694 represent human immune/hematopoietic antigen genomic
XX sequences from the present invention. AAK54942 to AAK54950 and AAK62169
XX represent sequences used in the exemplification of the present invention.
XX
XX Sequence 35 AA;
XX
XX Query Match 66.1%; Score 37; DB 22; Length 35;
XX Best Local Similarity 50.0%; Pred. No. 32;
XX Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
XX
XX OY 1 VNMVNRKVGGS 10
XX :||| :|||
XX DB 6 IMWVRROGGA 15
XX
XX
XX RESULT 23
XX AAB56006
XX ID AAB56006 standard; Protein; 232 AA.
XX
XX
XX AC AAB56006;
XX XX
XX 25-FEB-2003 (first entry)
XX
XX Chlamydia psittaci antigen CPA#13 protein SEQ ID NO.31.
XX
XX Chlamydia psittaci; vaccination; vaccine; antigen; immune response;
XX immunisation; antibacterial; infection.
XX
XX Chlamydia psittaci.
XX
XX WO200253588-A2.
XX
XX 11-JUL-2002.
XX
XX 17-DEC-2001; 2001MO-US48715.
XX
XX 15-DEC-2000; 2000US-0738269.
XX
XX (TEXA) UNIV TEXAS SYSTEM.
XX
XX Johnston SA, Stenke-Hale K, Sykes KF, Kallenboeck B;
XX
XX WPI; 2002-537942/57.
XX
XX N-PSDB; ABQ84762.
XX
XX Vaccine for immunization of animal, preferably bovine, against
XX Chlamydia psittaci, comprises at least one polynucleotide having a C.
XX psittaci sequence, or at least one C. psittaci antigen -
XX
XX Claim 5; Page 136; 164p; English.
XX
XX
XX The present invention describes a vaccine (I) for the immunisation of an
XX animal against Chlamydia psittaci comprising at least one polynucleotide
XX (Ia) having a C. psittaci sequence, or at least one C. psittaci antigen
XX (Ib) and (Ib) have antibacterial activity. (I) is
XX useful for the immunisation of a bovine. The present sequence represents
XX a C. psittaci antigen from the present invention.
XX
XX Sequence 232 AA;
XX
XX Query Match 66.1%; Score 37; DB 23; Length 232;
XX Best Local Similarity 75.0%; Pred. No. 2,2e+02;
XX Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
XX
XX OY 3 VNMVNRKVGGS 10
XX :||| :|||
XX DB 180 WVDKAGGS 187
XX
XX
XX RESULT 24
XX AAB98215
XX ID AAB98215 standard; Protein; 232 AA.
XX
XX AAB98215;
XX
XX 03-OCT-2002 (first entry)
XX
XX Chlamydia polypeptide SEQ ID NO 31.
XX
XX Chlamydia; antibacterial; vaccine; immune response; infection.
XX
XX Chlamydia psittaci.
XX
XX WO200247718-A2.
XX
XX 20-JUN-2002.
XX
XX 17-DEC-2001; 2001MO-US48773.
XX
XX 15-DEC-2000; 2000US-255839P.
XX

```

PA (TEXA) UNIV TEXAS SYSTEM.
 XX
 PT Johnston SA;
 XX
 DR WPI: 2002-583472/62.
 XX N-PSDB: ABQ78020.
 PT Vaccine useful for immunizing an animal, comprising at least one
 PT polynucleotide having a Chlamydia sequence or at least one Chlamydia
 XX antigen
 PS Claim 21: Page 144-145; 183pp; English.
 XX
 CC The invention relates to a vaccine (I) comprising at least one
 CC polynucleotide (ABQ78008-ABQ78039) having a Chlamydia sequence or at
 CC least one Chlamydia antigen (ABQ8203-ABQ8234) and a pharmaceutically
 CC acceptable carrier. The antigens are useful for immunising an animal, by
 CC providing at least one Chlamydia antigen or its antigenic fragment to the
 CC animal, in an amount effective to induce an immune response in the animal
 CC e.g. mammals including bovine or human. The method is effective to induce
 CC an immune response against C. psittaci, C. pneumoniae or non-Chlamydia
 CC infection. The method further involves administering to the animal an
 CC antigen or an antigenic fragment from Chlamydia species other than
 CC C. psittaci or C. pneumoniae or an antigenic fragment from a
 CC non-Chlamydia species.
 CC
 SO Sequence 232 AA:
 Query Match 66.1%; Score 37; DB 23; Length 232;
 Best Local Similarity 75.0%; Pred. No. 2.2e+02;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 OY 3 WVNKVGGS 10
 DB 180 WVDKAGGS 187
 RESULT 25
 ABU66271
 ID ABU66271 standard; Protein; 232 AA.
 XX
 AC ABU66271;
 XX
 DT 20-MAY-2003 (first entry)
 XX
 DE C. psittaci protein from genomic DNA sequence CP4 #13.
 XX
 KW Vaccine: chlamydia infection; blindness; mastitis; infertility;
 KW abortion; sexually transmitted disease; atherosclerotic plaque;
 KW community-acquired pneumonia; coronary heart disease; antigen.
 XX
 OS Chlamydia psittaci.
 XX
 PN US2002183272-A1.
 XX
 PD 05-DEC-2002.
 XX
 PF 17-DEC-2001; 2001US-0023437.
 XX
 PR 16-AUG-2000; 2000US-225839P.
 XX
 PA (JOHN/) JOHNSTON S A.
 PA (STEM/) STEME-HALE K.
 PA (SYKE/) SYKES K F.
 PA (KALT/) KALTENBOECK B.
 XX
 PI Johnston SA, Steme-Hale K, Sykes KF, Kaltenboeck B;
 XX
 DR WPI: 2003-328634/31.
 DR N-PSDB: ABX99187.
 XX
 PT New vaccine comprising a polynucleotide with a Chlamydia sequence or a
 PT Chlamydia antigen, for inducing an immune response against Chlamydia

PT psittaci, Chlamydia pneumoniae, other Chlamydia species, or a
 XX non-Chlamydia infection -
 XX
 PS Claim 21: Page 55; 100pp; English.
 XX
 CC The invention relates to a vaccine comprising a pharmaceutical carrier
 CC and at least one polynucleotide having a Chlamydia sequence or at least
 CC one Chlamydia antigen. The polynucleotide sequences are obtained
 CC from cloned expression library of fragmented genomic DNA (expressed in
 CC the vector PCMV-Ub1(+P3). Also included are immunising an animal
 CC comprising providing to the animal at least one Chlamydia antigen or its
 CC antigenic fragment (expressed from the cloned polynucleotides) to induce
 CC an immune response (the proteins are chosen by transforming a vertebrate
 CC animal with constituents of the library and choosing those which elicit
 CC the best immune response, and then expressing those clones in cell
 CC culture and purifying the protein), preparing antibodies against a
 CC Chlamydia antigen (comprising identifying a Chlamydia antigen that
 CC confers immune resistance against chlamydia bacterial infection when
 CC challenged with the Chlamydia species in which the antigen was prepared,
 CC generating an immune response in a vertebrate animal with the identified
 CC antigen, and obtaining antibodies produced in the animal, the antibodies
 CC are used to assay for the presence of chlamydia infection in a vertebrate
 CC animal) and testing for antigens for a first disease state/infectious
 CC agent (comprising determining an antigenic polypeptide or a nucleic acid
 CC encoding an antigenic polypeptide from a second disease state or
 CC infectious agent, obtaining a homologue of the antigenic polypeptide or
 CC a nucleic acid encoding an antigenic polypeptide from a second disease
 CC state or infectious agent for the first disease state/infectious
 CC agent, and testing the homology to see if it is an antigenic
 CC polypeptide or a nucleic acid encoding an antigenic polypeptide for the
 CC first disease state or infectious agent). The vaccine, antigens and
 CC polynucleotides are useful for inducing a protective immune response in
 CC vertebrate animals against C. psittaci, C. pneumoniae, other species of
 CC Chlamydia, or a non-Chlamydia infection. The antigens are also useful for
 CC antibody preparation techniques. Chlamydia species are responsible
 CC for blindness, sexually transmitted disease, community-acquired
 CC pneumonia and act as co-factors in atherosclerotic plaque formation in
 CC coronary heart disease. C. psittaci in particular is a cause of mastitis,
 CC infertility and abortion in cattle. The present sequence is one of the
 CC Chlamydia psittaci antigens encoded by a genomic DNA fragment of the
 CC
 CC
 SO Sequence 232 AA:
 Query Match 66.1%; Score 37; DB 24; Length 232;
 Best Local Similarity 75.0%; Pred. No. 2.2e+02;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 OY 3 WVNKVGGS 10
 DB 180 WVDKAGGS 187
 RESULT 26
 ABB53463
 ID ABB53463 standard; Protein; 527 AA.
 XX
 AC ABB53463;
 XX
 DT 16-MAY-2002 (first entry)
 XX
 DE Lactococcus lactis protein ydgb.
 XX
 KW Biosynthesis; biodegradation; lactic bacterium; yogurt; cheese.
 KW
 OS Lactococcus lactis IL1403.
 XX
 PN FR2807446-A1.
 XX
 PD 12-OCT-2001.
 XX
 PF 11-APR-2000; 2000FR-0004630.
 XX

```

PR 11-APR-2000; 2000FR-0004630.
XX
XX (INRG ) INRA INST NAT RECH AGRONOMIQUE.
XX
XX Bojotline A, Sorokine A, Renault P, Ehrlich SD;
XX
XX WPI: 2002-043418/06.
XX
XX New nucleotide sequence useful in the identification of Lactococcus
XX lactic acid and related species.
XX
XX Claim 6; SEQ ID No 165; 2504pp; French.
XX
XX The present invention is related to a Lactococcus lactis nucleotide
XX sequence (AA050521) and related proteins (AB053300-AB055621). The
XX nucleic acid sequence is useful in the detection and/or amplification of
XX nucleic acid sequence, particularly to identify Lactococcus lactis or
XX related species. The proteins of the invention are useful for the
XX biosynthesis or biodegradation of a composition of interest. The
XX invention helps research in lactic bacteria, particularly useful in the
XX production of yogurt and cheese.
XX Note: The sequence data for this patent is based on equivalent patent
XX WO2001/77334 (published 18-OCT-2001) which is available in electronic
XX format directly from WIPO at ftp.wipo.int/pub/published_pcl_sequences.
XX
SQ Sequence 527 AA;
XX
Query Match 66.1%; Score 37; DB 23; Length 527;
Best Local Similarity 40.0%; Pred. No. 5.2e+02;
Matches 4; Conservative 4; Mismatches 2; Indels 0; Gaps 0;
XX
OY 1 VNMVKNKVGGS 10
DB 127 INMIGNIGCT 136
XX
RESULT 27
AAW88463
ID AAW88463 standard; Protein; 537 AA.
XX
XX AAW88463;
XX
XX 10-MAY-1999 (first entry)
XX
XX Bacillus agaradhaerens xyloglucanase.
XX
XX Xyloglucanase; XEG1; detergent.
XX
XX Bacillus agaradhaerens.
XX
XX WO9902663-A1.
XX
XX 21-JAN-1999.
XX
XX 01-JUL-1998; 98WO-DK00290.
XX
XX 24-OCT-1997; 97DK-0001213.
XX
XX 07-JUL-1997; 97DK-0000822.
XX
XX (NOVO ) NOVO-NORDISK AS.
XX
XX Bjornvad ME, Jorgensen PL, Outtrup H, Schuelein M;
XX
XX WPI: 1999-120866/10.
XX
XX N-PSDB; AAX06950.
XX
XX New enzyme preparation comprising a xyloglucanase with an activity
XX of 50 % at pH 7 - useful for improving the properties of cellulosic
XX fibres, yarn, (non)woven fabric, and ratting hemp, jute, flax and
XX linen fibres
XX
XX Claim 18; Page 74-76; 87pp; English.
XX

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CC This polypeptide comprise alkaline xyloglucanase XEG1 of
CC Bacillus agaradhaerens NCIMB 40482. The enzyme shows optimal
CC activity at 50 deg C and retains 20% of its activity after 20 min
CC at 60 deg. It retains more than 50% of relative activity in the pH
CC range 5.0-10.5. At pH 7.5, the kcat on xyloglucan was 183/sec and
CC the Km was 0.05 g/l. On CM-cellulose, kcat was 61/sec and Km was
CC 2.2 g/l. An isolated polynucleotide (see AAX06950) can be utilized
CC in the recombinant production of the enzyme. The invention provides
CC expression vectors containing xyloglucanase polynucleotides, and
CC host cells containing these vectors. Xyloglucanase preparations are
CC useful for improving the properties of cellulosic fibres, yarn,
CC (non)woven fabric, and for ratting hemp, jute, flax and linen fibres
CC (claimed). They can also be used in a process for machine treatment
CC of fabrics, and in detergent compositions (claimed). The enzyme
CC preparations exhibit high xyloglucanase activity at alkaline pH
CC without essentially attacking cellulose or cellulose derivatives.
XX
SQ Sequence 537 AA;
XX
Query Match 66.1%; Score 37; DB 20; Length 537;
Best Local Similarity 60.0%; Pred. No. 5.3e+02;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
XX
OY 1 VNMVKNKVGGS 10
DB 62 VTMQNMGMGS 71
XX
RESULT 28
AAW00383
ID AAW00383 standard; Protein; 574 AA.
XX
XX AAW00383;
XX
XX 31-JAN-1997 (first entry)
XX
XX Bacillus cellulase BCE 113.
XX
XX Cellulase; BCE 113; detergent; surfactant; laundry;
XX tensile strength; antipilling.
XX
XX Bacillus sp. strain CBS 669.93.
XX
XX Key Location/Qualifiers
XX Peptide 1..26
XX Protein 27..574
XX /label= Sig-peptide
XX /label= Mat.protein
XX /note= "the 63 kDa mature protein is used in
XX detergent compans."
XX
XX MO9634092-A2.
XX
XX 31-OCT-1996.
XX
XX 26-APR-1996; 96WO-EP01755.
XX
XX 12-MAR-1996; 96US-0614115.
XX
XX 28-APR-1995; 95EP-0201115.
XX
XX (GENEV ) GENENCOR INT INC.
XX
XX Kotwitz B, Lenting HBW, Maurer K, Van Beckhoven RFWC;
XX
XX Van Solingen P, Weiss A;
XX
XX WPI: 1996-497624/49.
XX
XX Cellulase with low ratio of tensile strength loss to antipilling
XX properties - used in detergent composition which provides
XX anti-greying, softening, anti-wrinkling and colour protection to
XX fabrics
XX

```

PS Claim 10; Fig 4; 33pp; English.
 XX
 CC A novel cellulase (AAW00383), designated BCE 113, of alkali-tolerant
 CC *Bacillus* sp. strain CBS 669.93 has a tensile strength loss to
 CC antilinting ratio below 1. It can be isolated from CBS 669.93
 CC fermentation broth or expressed at high levels in transformed host
 CC cells utilizing an isolated gene sequence (AAE41849). Cellulase BCE
 CC 113, and similarly isolated cellulase BCE 103 (see also AAW00382),
 CC show good activity at alkaline pH, and can be used in laundry
 CC detergent compsts. to provide anti-greying, softening, anti-
 CC wrinkling and colour protection to fabrics.
 CC
 SQ Sequence 574 AA;
 Query Match 66.1%; Score 37; DB 17; Length 574;
 Best Local Similarity 50.0%; Pred. No. 5.7e+02;
 Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
 OY 1 VNNVKNKVGGS 10
 | | | | | | | | | |
 Db 87 VTWENRIGGA 96
 RESULT 29
 ABG13298
 ID ABG13298 standard; Protein: 705 AA.
 AC ABG13298;
 XX
 DT 18-FEB-2002 (first entry)
 XX
 DE Novel human diagnostic protein #13289.
 XX
 KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
 KW food supplement; medical imaging; diagnostic; genetic disorder.
 XX
 OS Homo sapiens.
 XX
 PN W0200175067-A2.
 PD 11-OCT-2001.
 XX
 PF 30-MAR-2001; 2001WO-US08631.
 XX
 PR 31-MAR-2000; 2000US-0540217.
 PR 23-AUG-2000; 2000US-0649167.
 XX
 PA (HYSE-) HYSEQ INC.
 XX
 PI Drmanac RT, Liu C, Tang YT;
 XX
 DR WPI; 2001-639362/73.
 DR N-PSDB; AAS77485.
 XX
 PT New isolated polynucleotide and encoded polypeptides, useful in
 PT diagnostics, forensics, gene mapping, identification of mutations
 PT responsible for genetic disorders or other traits and to assess
 PT biodiversity -
 XX
 PS Claim 20; SEQ ID NO 43657; 103pp; English.
 XX
 CC The invention relates to isolated polynucleotide (I) and
 CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
 CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
 CC and gene mapping, and in recombinant production of (II). The
 CC polynucleotides are also used in diagnostics as expressed sequence tags
 CC for identifying expressed genes. (I) is useful in gene therapy techniques
 CC to restore normal activity of (II) or to treat disease states involving
 CC (II). (II) is useful for generating antibodies against it, detecting or
 CC quantitating a polypeptide in tissue, as molecular weight markers and as
 CC a food supplement. (II) and its binding partners are useful in medical
 CC imaging of sites expressing (II). (I) and (II) are useful for treating
 CC disorders involving aberrant protein expression or biological activity.

CC The polypeptide and polynucleotide sequences have applications in
 CC diagnostics, forensics, gene mapping, identification of mutations
 CC responsible for genetic disorders or other traits to assess biodiversity
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. ABG00010-ABG30377 represent novel human
 CC diagnostic amino acid sequences of the invention.
 CC Note: The sequence data for this patent did not appear in the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.
 CC
 SQ Sequence 705 AA;
 Query Match 66.1%; Score 37; DB 22; Length 705;
 Best Local Similarity 66.7%; Pred. No. 7e+02; 2; Indels 0; Gaps 0;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 OY 2 NMVYKRTGS 10
 | | | | | | | | | |
 Db 686 NMVYKRTGS 694
 RESULT 30
 ABG07095
 ID ABG07095 standard; Protein: 941 AA.
 AC ABG07095;
 XX
 DT 13-FEB-2002 (first entry)
 XX
 DE Novel human diagnostic protein #7086.
 XX
 KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
 KW food supplement; medical imaging; diagnostic; genetic disorder.
 XX
 OS Homo sapiens.
 XX
 PN W0200175067-A2.
 PD 11-OCT-2001.
 XX
 PF 30-MAR-2001; 2001WO-US08631.
 XX
 PR 31-MAR-2000; 2000US-0540217.
 PR 23-AUG-2000; 2000US-0649167.
 XX
 PA (HYSE-) HYSEQ INC.
 XX
 PI Drmanac RT, Liu C, Tang YT;
 XX
 DR WPI; 2001-639362/73.
 DR N-PSDB; AAS71282.
 XX
 PT New isolated polynucleotide and encoded polypeptides, useful in
 PT diagnostics, forensics, gene mapping, identification of mutations
 PT responsible for genetic disorders or other traits and to assess
 PT biodiversity -
 XX
 PS Claim 20; SEQ ID NO 37454; 103pp; English.
 XX
 CC The invention relates to isolated polynucleotide (I) and
 CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
 CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
 CC and gene mapping, and in recombinant production of (II). The
 CC polynucleotides are also used in diagnostics as expressed sequence tags
 CC for identifying expressed genes. (I) is useful in gene therapy techniques
 CC to restore normal activity of (II) or to treat disease states involving
 CC (II). (II) is useful for generating antibodies against it, detecting or
 CC quantitating a polypeptide in tissue, as molecular weight markers and as
 CC a food supplement. (II) and its binding partners are useful in medical
 CC imaging of sites expressing (II). (I) and (II) are useful for treating
 CC disorders involving aberrant protein expression or biological activity.
 CC The polypeptide and polynucleotide sequences have applications in
 CC diagnostics, forensics, gene mapping, identification of mutations

CC responsible for genetic disorders or other traits to assess biodiversity
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. ABG00010-ABG30377 represent novel human
 CC diagnostic amino acid sequences of the invention.
 CC Note: The sequence data for this patent did not appear in the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.
 XX

SQ Sequence 941 AA;

Query Match 66.1%; Score 37; DB 22; Length 941;

Best Local Similarity 66.7%; Pred. No. 9.5e+02; Mismatches 2; Indels 0; Gaps 0;

OY 2 NMVNVKVGGS 10

DB 805 NMVVKITGS 813

Search completed: August 29, 2003, 18:44:01
 Job time : 32.5714 secs

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ALIGNMENTS

```
RESULT 1
US-09-072-917A-9
; Sequence 9, Application US/09072917A
; Patent No. 6288302
; GENERAL INFORMATION:
; APPLICANT: Yu, Su-May
; APPLICANT: Liu, Li-Fei
; TITLE OF INVENTION: Application of Alpha-Amylase Gene
; TITLE OF INVENTION: Promoter and Signal Sequence in the Production of
; Patent No. 6288302
; TITLE OF INVENTION: Recombinant Proteins in Transgenic Plants and Transgenic
; TITLE OF INVENTION: Plant Seeds
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 233 South Wacker Drive/6300 Sears Tower
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/072.917A
; FILING DATE:
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/509,962
; FILING DATE: 01-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Gass, David A.
; REGISTRATION NUMBER: 38,153
; REFERENCE/DOCKET NUMBER: 28123/34257
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; INFORMATION FOR SEQ. ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 435 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-072-917A-9
Query Match 82.1%; Score 46; DB 3; Length 435;
Best Local Similarity 88.9%; Pred. No. 5.8;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 VNMVNVKVG 9
Db 253 VNMVNAVGG 261
```

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RESULT 2
US-07-973-324A-4
; Sequence 4, Application US/07973324A
; Patent No. 5460952
; GENERAL INFORMATION:
; APPLICANT: Yu, Su-May
; APPLICANT: Liu, Li-Fei
; TITLE OF INVENTION: Gene Expression System Comprising the
; TITLE OF INVENTION: Promoter Region of the Alpha-Amylase Genes
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
```

```
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/973,324A
; FILING DATE: 04-NOV-1992
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Borun, Michael F.
; REGISTRATION NUMBER: 25447
; REFERENCE/DOCKET NUMBER: 31149
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ. ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 428 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-07-973-324A-4
```

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Query Match 80.4%; Score 45; DB 1; Length 428;
Best Local Similarity 70.0%; Pred. No. 8.2;
Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 VNMVNVKVG 10
Db 253 VNMVNAVGG 262
```

```
RESULT 3
US-08-343-380-4
; Sequence 4, Application US/08343380
; Patent No. 5712112
; GENERAL INFORMATION:
; APPLICANT: Yu, Su-May
; APPLICANT: Liu, Li-Fei
; TITLE OF INVENTION: Gene Expression System Comprising the
; TITLE OF INVENTION: Promoter Region of the Alpha-Amylase Genes
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/343,380
; FILING DATE: 22-NOV-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/973,324
; FILING DATE: 04-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Borun, Michael F.
; REGISTRATION NUMBER: 25447
; REFERENCE/DOCKET NUMBER: 31149
```

```
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEFAX: 25-3856
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 428 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-343-380-4

Query Match      80.4%; Score 45; DB 1; Length 428;
Best Local Similarity 70.0%; Pred. No. 8.2;
Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY      1 VNMVKNYKGS 10
DB      253 VNMVDRVGA 262

RESULT 4
US-09-072-435-4
Sequence 4, Application US/09072435
Patent No. 6215051
GENERAL INFORMATION:
APPLICANT: Yu, Su-May
APPLICANT: Liu, Li-Fei
APPLICANT: Chan, Ming-Tsair
TITLE OF INVENTION: GENE EXPRESSION SYSTEM COMPRISING THE
TITLE OF INVENTION: PROMOTER REGION OF THE ALPHA-AMYLASE GENES
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS: 13
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive/6300 Sears Tower
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/072.435
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/639,792
FILING DATE: 29-APR-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/973,324
FILING DATE: 04-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: Gass, David A.
REGISTRATION NUMBER: 38,153
REFERENCE/DOCKET NUMBER: 28123/34274
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 428 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-072-435-4

Query Match      80.4%; Score 45; DB 3; Length 428;
Best Local Similarity 70.0%; Pred. No. 8.2;
Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY      1 VNMVKNYKGS 10
DB      253 VNMVDRVGA 262

TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEFAX: 25-3856
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 428 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-072-435-4

Query Match      80.4%; Score 45; DB 3; Length 428;
Best Local Similarity 70.0%; Pred. No. 8.2;
Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY      1 VNMVKNYKGS 10
DB      253 VNMVDRVGA 262

RESULT 5
US-09-072-917A-4
Sequence 4, Application US/09072917A
Patent No. 6288302
GENERAL INFORMATION:
APPLICANT: Yu, Su-May
APPLICANT: Liu, Li-Fei
APPLICANT: Chan, Ming-Tsair
TITLE OF INVENTION: Application of Alpha-Amylase Gene
TITLE OF INVENTION: Promoter and Signal Sequence in the production of
Patent No. 6288302
TITLE OF INVENTION: Recombinant Proteins in Transgenic Plants and Transgenic
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive/6300 Sears Tower
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/072.917A
FILING DATE:
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/509,962
FILING DATE: 01-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: Gass, David A.
REGISTRATION NUMBER: 38,153
REFERENCE/DOCKET NUMBER: 28123/34257
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 428 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-072-917A-4

Query Match      80.4%; Score 45; DB 3; Length 428;
Best Local Similarity 70.0%; Pred. No. 8.2;
Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY      1 VNMVKNYKGS 10
DB      253 VNMVDRVGA 262

RESULT 6
US-07-923-692C-6
Sequence 6, Application US/07923692C
Patent No. 5316931
GENERAL INFORMATION:
APPLICANT: Donson, Jon
APPLICANT: Dawson, William O.
APPLICANT: Grantlam, George L.
APPLICANT: Turpen, Thomas H.
APPLICANT: Turpen, Ann Myers
APPLICANT: Garger, Stephen J.
```

APPLICANT: Grill, Laurence K.
TITLE OF INVENTION: RECOMBINANT PLANT VIRAL NUCLEIC ACIDS
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Limbach & Limbach
STREET: 2001 Ferry Building
CITY: San Francisco
STATE: CAL
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/923,692C
FILING DATE: 31-JUL-1992
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 600,244
FILING DATE: 22-OCT-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 641,617
FILING DATE: 16-JAN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 310,881
FILING DATE: 17-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 160,766
FILING DATE: 26-FEB-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 160,771
FILING DATE: 26-FEB-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 347,637
FILING DATE: 05-MAY-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 363,138
FILING DATE: 08-JUN-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 219,279
FILING DATE: 15-JUL-1988
ATTORNEY/AGENT INFORMATION:
NAME: Halluin, Albert P.
REGISTRATION NUMBER: 28,957
REFERENCE/DOCKET NUMBER: BIOG-20121
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-433-4150
TELEFAX: 415-433-8716
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 434 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-923-692C-6
Query Match 80.4%; Score 45; DB 1; Length 434;
Best Local Similarity 70.0%; Pred. No. 8.4;
Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

OY 1 VNMVNVGGS 10
||||:||||
Db 259 VNMVDRVGA 268

RESULT 7
US-08-184-237-6
; Sequence 6, Application US/08184237
; Patent No. 5589367
; GENERAL INFORMATION:
; APPLICANT: Donson, Jon

APPLICANT: Dawson, William O.
TITLE OF INVENTION: RECOMBINANT PLANT VIRAL NUCLEIC ACIDS
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Limbach & Limbach
STREET: 2001 Ferry Building
CITY: San Francisco
STATE: CAL
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/184,237
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 923,692
FILING DATE: 31-JUL-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 600,244
FILING DATE: 22-OCT-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 641,617
FILING DATE: 16-JAN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 310,881
FILING DATE: 17-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 160,766
FILING DATE: 26-FEB-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 160,771
FILING DATE: 26-FEB-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 347,637
FILING DATE: 05-MAY-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 219,279
FILING DATE: 15-JUL-1988
ATTORNEY/AGENT INFORMATION:
NAME: Halluin, Albert P.
REGISTRATION NUMBER: 28,957
REFERENCE/DOCKET NUMBER: BIOG-20121 USA
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-433-4150
TELEFAX: 415-433-8716
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 434 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-184-237-6
Query Match 80.4%; Score 45; DB 1; Length 434;
Best Local Similarity 70.0%; Pred. No. 8.4;
Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

OY 1 VNMVNVGGS 10
||||:||||
Db 259 VNMVDRVGA 268

RESULT 8
US-08-482-920-6
Sequence 6, Application US/08482920
Patent No. 5866785
GENERAL INFORMATION:
APPLICANT: Donson, Jon
APPLICANT: Dawson, William O.
APPLICANT: Grantham, George L.
APPLICANT: Turpen, Thomas H.
APPLICANT: Turpen, Ann Myers
APPLICANT: Garger, Stephen J.
APPLICANT: Grill, Laurence K.
TITLE OF INVENTION: RECOMBINANT PLANT VIRAL NUCLEIC ACIDS
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennile & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,920
FILING DATE: 07-JUNE-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 184,237
FILING DATE: 19-JAN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 600,244
FILING DATE: 22-OCT-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 641,617
FILING DATE: 16-JAN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 310,881
FILING DATE: 17-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 160,766
FILING DATE: 26-FEB-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 160,771
FILING DATE: 26-FEB-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 347,637
FILING DATE: 05-MAY-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 363,138
FILING DATE: 08-JUN-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 219,279
FILING DATE: 15-JUL-1988
ATTORNEY/AGENT INFORMATION:
NAME: Halliuid, Albert P.
REGISTRATION NUMBER: 28,957
REFERENCE/DOCKET NUMBER: 8129-112
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-854-3660
TELEFAX: 415-854-3694
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 434 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-482-920-6

Query Match 80.4%; Score 45; DB 2; Length 434;
Best Local Similarity 70.0%; Pred. No. 8.4;

Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
Qy 1 VNMWNYGGS 10
Db 259 VNMWNYGGA 268

RESULT 9
US-08-484-341-6
Sequence 6, Application US/08484341
GENERAL INFORMATION:
APPLICANT: Donson, Jon
APPLICANT: Dawson, William O.
APPLICANT: Grantham, George L.
APPLICANT: Turpen, Thomas H.
APPLICANT: Turpen, Ann Myers
APPLICANT: Garger, Stephen J.
APPLICANT: Grill, Laurence K.
TITLE OF INVENTION: RECOMBINANT PLANT VIRAL NUCLEIC ACIDS
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Limbach & Limbach
STREET: 2001 Ferry Building
CITY: San Francisco
STATE: CAL
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,341
FILING DATE: 07-Jun-1995
CLASSIFICATION: <unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/184,237
FILING DATE: <unknown>
APPLICATION NUMBER: US 600,244
FILING DATE: 22-OCT-1990
APPLICATION NUMBER: US 641,617
FILING DATE: 16-JAN-1991
APPLICATION NUMBER: US 310,881
FILING DATE: 17-FEB-1989
APPLICATION NUMBER: US 160,766
FILING DATE: 26-FEB-1988
APPLICATION NUMBER: US 160,771
FILING DATE: 26-FEB-1988
APPLICATION NUMBER: US 347,637
FILING DATE: 05-MAY-1989
APPLICATION NUMBER: US 363,138
FILING DATE: 08-JUN-1989
APPLICATION NUMBER: US 219,279
FILING DATE: 15-JUL-1988
ATTORNEY/AGENT INFORMATION:
NAME: Halliuid, Albert P.
REGISTRATION NUMBER: 28,957
REFERENCE/DOCKET NUMBER: BIOG-20121 USA
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-433-4150
TELEFAX: 415-433-8718
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 434 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-08-484-341-6

Query Match 80.4%; Score 45; DB 3; Length 434;
Best Local Similarity 70.0%; Pred. No. 8.4;
Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

OY 1 VNMVKNVGS 10
 Db 259 VNMVDRVGA 268

RESULT 10
 US-08-483-502-6
 ; Sequence 6, Application US/08483502
 ; Patent No. 6284492
 ; GENERAL INFORMATION:
 ; APPLICANT: Donson, Jon
 ; APPLICANT: Dawson, William O.
 ; APPLICANT: Grantham, George L.
 ; APPLICANT: Turpen, Thomas H.
 ; APPLICANT: Turpen, Ann Myers
 ; APPLICANT: Garger, Stephen J.
 ; APPLICANT: Grill, Laurence K.
 ; TITLE OF INVENTION: RECOMBINANT PLANT VIRAL NUCLEIC ACIDS
 ; NUMBER OF SEQUENCES: 11
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Venable, Baetjer, Howard & Civiletti
 ; STREET: 1201 New York Avenue N.W., Suite 1000
 ; CITY: Washington
 ; STATE: DC
 ; COUNTRY: USA
 ; ZIP: 20005
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/483,502
 ; FILING DATE:
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 07/739,143
 ; FILING DATE:
 ; APPLICATION NUMBER: US 600,244
 ; FILING DATE: 22-OCT-1990
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 641,617
 ; FILING DATE: 16-JAN-1991
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 310,881
 ; FILING DATE: 17-FEB-1989
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 160,766
 ; FILING DATE: 26-FEB-1988
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 160,771
 ; FILING DATE: 26-FEB-1988
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 347,637
 ; FILING DATE: 05-MAY-1989
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 363,138
 ; FILING DATE: 08-JUN-1989
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 219,279
 ; FILING DATE: 15-JUL-1988
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Ihnen, Jeffrey L.
 ; REGISTRATION NUMBER: 28,957
 ; REFERENCE/DOCKET NUMBER: 18604-090574
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 202-962-4810
 ; TELEFAX: 202-962-8300
 ; INFORMATION FOR SEQ ID NO: 6:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 434 amino acids
 ; TYPE: amino acid

; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-483-502-6

Query Match 80.4%; Score 45; DB 3; Length 434;
 Best Local Similarity 70.0%; Pred. No. 8.4;
 Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

OY 1 VNMVKNVGS 10
 Db 259 VNMVDRVGA 268

RESULT 11
 US-09-726-651A-6
 ; Sequence 6, Application US/09726651A
 ; Patent No. 6448046
 ; GENERAL INFORMATION:
 ; APPLICANT: Donson, Jon
 ; APPLICANT: Dawson, William O.
 ; APPLICANT: Grantham, George L.
 ; APPLICANT: Turpen, Thomas H.
 ; APPLICANT: Turpen, Ann M.
 ; APPLICANT: Garger, Stephen J.
 ; APPLICANT: Grill, Laurence K.
 ; TITLE OF INVENTION: RECOMBINANT ANIMAL VIRUS NUCLEIC ACIDS
 ; FILE REFERENCE: 008010023CNU501
 ; CURRENT APPLICATION NUMBER: US/09/726,651A
 ; CURRENT FILING DATE: 2002-05-02
 ; PRIOR APPLICATION NUMBER: 08/483,502
 ; PRIOR FILING DATE: 1995-06-07
 ; PRIOR APPLICATION NUMBER: 08/184,237
 ; PRIOR FILING DATE: 1994-01-19
 ; PRIOR APPLICATION NUMBER: 07/923,692
 ; PRIOR FILING DATE: 1992-07-31
 ; PRIOR APPLICATION NUMBER: 07/600,244
 ; PRIOR FILING DATE: 1990-10-22
 ; PRIOR APPLICATION NUMBER: 07/641,617
 ; PRIOR FILING DATE: 1991-01-16
 ; PRIOR APPLICATION NUMBER: 07/737,899
 ; PRIOR FILING DATE: 1991-07-26
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 6
 ; LENGTH: 434
 ; TYPE: PRT
 ; ORGANISM: Oryza sativa
 ; FEATURE:
 ; OTHER INFORMATION: CLONE: alpha-amylase
 ; OTHER INFORMATION: protein
 ; US-09-726-651A-6

Query Match 80.4%; Score 45; DB 4; Length 434;
 Best Local Similarity 70.0%; Pred. No. 8.4;
 Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

OY 1 VNMVKNVGS 10
 Db 259 VNMVDRVGA 268

RESULT 12
 US-09-510-322A-8
 ; Sequence 8, Application US/09510322A
 ; Patent No. 6391557
 ; GENERAL INFORMATION:
 ; APPLICANT: Fox Chase Cancer Center
 ; TITLE OF INVENTION: Nucleic Acid Encoding a Mismatch
 ; FILE REFERENCE: 9503dna
 ; CURRENT APPLICATION NUMBER: US/09/510,322A
 ; CURRENT FILING DATE: 2000-02-22
 ; NUMBER OF SEQ ID NOS: 11

SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 8
LENGTH: 267
TYPE: PRT
ORGANISM: Plant
US-09-510-322A-8

Query Match 67.9% Score 38; DB 4; Length 267;
Best Local Similarity 55.6%; Pred. No. 69;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 NMVNRVGS 10
DB 255 NMVNRVGS 263

RESULT 13
US-09-252-991A-24308
Sequence 24308, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
PRIOR FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 24308
LENGTH: 460
TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-24308

Query Match 66.1% Score 37; DB 4; Length 460;
Best Local Similarity 60.0%; Pred. No. 17e+02;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 VMVNRVGS 10
DB 407 VTMLTEVGS 416

RESULT 14
US-09-110-959A-4
Sequence 4, Application US/09110959A
Patent No. 6268197
GENERAL INFORMATION:
APPLICANT: Schuelein, Martin
APPLICANT: Outtrup, Helle
APPLICANT: Bjornsen, Per Lina
TITLE OF INVENTION: Alkaline Xyloglucanase
FILE REFERENCE: 5206.200-US
CURRENT APPLICATION NUMBER: US/09/110,959A
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 0822/97
PRIOR FILING DATE: 1997-07-07
PRIOR APPLICATION NUMBER: 1213/97
PRIOR FILING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: 60/054,039
PRIOR FILING DATE: 1997-07-28
PRIOR APPLICATION NUMBER: 60/063,694
PRIOR FILING DATE: 1997-10-28
NUMBER OF SEQ ID NOS: 14
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 4
LENGTH: 537
TYPE: PRT

ORGANISM: Bacillus agaradhaerens NCIMB 40482
US-09-110-959A-4

Query Match 66.1% Score 37; DB 3; Length 537;
Best Local Similarity 60.0%; Pred. No. 2e+02;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 VMVNRVGS 10
DB 62 VTWONMGGS 71

RESULT 15
US-09-107-532A-4136
Sequence 4136, Application US/09107532A
Patent No. 6583275
GENERAL INFORMATION:
APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
NUMBER OF SEQUENCES: 7310
CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
STREET: 100 Beaver Street
CITY: Waltham
STATE: Massachusetts
COUNTRY: USA
ZIP: 02154
COMPUTER READABLE FORM:
MEDIUM TYPE: CD-ROM ISO9660
COMPUTER: PC
OPERATING SYSTEM: <Unknown>
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-Jun-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Attinello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-012
TELECOMMUNICATION INFORMATION:
TELEPHONE: (781)893-5007
TELEFAX: (781)893-8277
INFORMATION FOR SEQ ID NO: 4136:
SEQUENCE CHARACTERISTICS:
LENGTH: 544 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
ORGANISM: Enterococcus faecium
FEATURE:
NAME/KEY: misc feature
LOCATION: (2) LOCATION 1..544
SEQUENCE DESCRIPTION: SEQ ID NO: 4136:
US-09-107-532A-4136

Query Match 66.1% Score 37; DB 4; Length 544;
Best Local Similarity 66.7%; Pred. No. 2e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 NMVNRVGS 10
DB 132 DMVSKFGS 140

RESULT 16

TELEPHONE: (781)893-5007
TELEFAX: (781)893-8277
INFORMATION FOR SEQ ID NO: 5530:
SEQUENCE CHARACTERISTICS:
LENGTH: 427 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE: Enterococcus faecium
FEATURE:
NAME/KEY: misc-feature
LOCATION: (8) LOCATION 1...427
SEQUENCE DESCRIPTION: SEQ ID NO: 5530:
US-09-107-532A-5530

Query Match 64.3%; Score 36; DB 1; Length 427;
Best Local Similarity 60.0%; Pred. No. 2.3e+02;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 1 VNMVNRKVGGS 10
DB 75 INWVLGVGGR 84

RESULT 19
US-07-973-324A-2
Sequence 2, Application US/07973324A
Patent No. 5460952
GENERAL INFORMATION:
APPLICANT: Yu, Su-May
APPLICANT: Liu, Li-Pei
TITLE OF INVENTION: Gene Expression System Comprising the
TITLE OF INVENTION: Promoter Region of the Alpha-Amylase Genes
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/973,324A
FILING DATE: 04-NOV-1992
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Borun, Michael F.
REGISTRATION NUMBER: 25447
REFERENCE/DOCKET NUMBER: 31149
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 438 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-973-324A-2

Query Match 64.3%; Score 36; DB 1; Length 438;
Best Local Similarity 66.7%; Pred. No. 2.3e+02;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 VNMVNRKVGGS 9

DB 255 VNMNAQAVGG 263

RESULT 20
US-08-343-380-2
Sequence 2, Application US/08343380
Patent No. 5712112
GENERAL INFORMATION:
APPLICANT: Yu, Su-May
APPLICANT: Liu, Li-Pei
TITLE OF INVENTION: Gene Expression System Comprising the
TITLE OF INVENTION: Promoter Region of the Alpha-Amylase Genes
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/343,380
FILING DATE: 22-NOV-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/973,324
FILING DATE: 04-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: Borun, Michael F.
REGISTRATION NUMBER: 25447
REFERENCE/DOCKET NUMBER: 31149
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 438 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-343-380-2

Query Match 64.3%; Score 36; DB 1; Length 438;
Best Local Similarity 66.7%; Pred. No. 2.3e+02;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 VNMVNRKVGGS 9
DB 255 VNMNAQAVGG 263

RESULT 21
US-09-072-435-2
Sequence 2, Application US/09072435
Patent No. 6215051
GENERAL INFORMATION:
APPLICANT: Yu, Su-May
APPLICANT: Chan, Ming-Tsair
TITLE OF INVENTION: GENE EXPRESSION SYSTEM COMPRISING THE
TITLE OF INVENTION: PROMOTER REGION OF THE ALPHA-AMYLASE GENES
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive/6300 Sears Tower
CITY: Chicago

STATE: Illinois
COUNTRY: United States of America
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/072,435
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/639,792
FILING DATE: 29-APR-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/973,324
FILING DATE: 04-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: Gass, David A.
REGISTRATION NUMBER: 38,153
REFERENCE/DOCKET NUMBER: 28123/34274
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 438 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-072-435-2

Query Match
Best Local Similarity 64.3%; Score 36; DB 3; Length 438;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 VNMVNRKVG 9
Db 255 VNMQAQAVG 263

RESULT 22
US-09-072-917A-2
Sequence 2, Application US/09072917A
Patent No. 6288302
GENERAL INFORMATION:
APPLICANT: Yu, Su-May
APPLICANT: Liu, Li-Fei
APPLICANT: Chan, Ming-Tsair
TITLE OF INVENTION: Application of Alpha-Amylase Gene
TITLE OF INVENTION: Promoter and Signal Sequence in the Production of
Patent No. 6288302
TITLE OF INVENTION: Recombinant Proteins in Transgenic Plants and Transgenic
TITLE OF INVENTION: Plant Seeds
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESSES:
ADDRESS: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive/6300 Sears Tower
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/072,917A
FILING DATE:
CLASSIFICATION: 800
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/509,962
FILING DATE: 01-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: Gass, David A.
REGISTRATION NUMBER: 38,153
REFERENCE/DOCKET NUMBER: 28123/34257
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 438 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-072-917A-2

Query Match
Best Local Similarity 64.3%; Score 36; DB 3; Length 438;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 VNMVNRKVG 9
Db 255 VNMQAQAVG 263

RESULT 23
US-09-527-236A-26
Sequence 26, Application US/09527236A
Patent No. 6358508
GENERAL INFORMATION:
APPLICANT: Ni, Jian
APPLICANT: Yu, Guo-Liang
APPLICANT: Fan, Ping
APPLICANT: Gentz, Reiner L.
TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor TR9
FILE REFERENCE: PF375Pl
CURRENT APPLICATION NUMBER: US/09/527,236A
CURRENT FILING DATE: 2000-03-16
PRIOR APPLICATION NUMBER: 60/052,991
PRIOR FILING DATE: 1997-06-11
PRIOR APPLICATION NUMBER: 09/095,094
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/126,019
PRIOR FILING DATE: 1999-03-24
PRIOR APPLICATION NUMBER: 60/134,220
PRIOR FILING DATE: 1999-05-14
NUMBER OF SEQ ID NOS: 27
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 26
LENGTH: 67
TYPE: PRT
ORGANISM: Homo sapiens
US-09-527-236A-26

Query Match
Best Local Similarity 62.5%; Score 35; DB 4; Length 67;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 VNMVNRKVG 8
Db 35 IKMVKNTG 42

RESULT 24
US-08-983-607-47
Sequence 47, Application US/08983607
Patent No. 6140470
GENERAL INFORMATION:
APPLICANT: Alan Garen
APPLICANT: Xiaohong Cai
TITLE OF INVENTION: Human Anti-Tumor Monoclonal Anti-
TITLE OF INVENTION: bodies

```

?      NUMBER OF SEQUENCES: 51
?      CORRESPONDENCE ADDRESS:
?      ADDRESSEE: Department of Molecular Biophysics
?      ADDRESSEE: and Biochemistry, Yale University
?      STREET: 266 Whitney Avenue
?      CITY: New Haven
?      STATE: Connecticut
?      COUNTRY: United States of America
?      ZIP: 06520-8114
?      COMPUTER READABLE FORM:
?      MEDIUM TYPE: 3.5" 1.44 Mb diskette
?      COMPUTER: IBM PC
?      OPERATING SYSTEM: MS DOS
?      SOFTWARE: Word Processing
?      CURRENT APPLICATION DATA:
?      APPLICATION NUMBER: US/08/993,607
?      FILING DATE: April 27, 1998
?      CLASSIFICATION: 435
?      PRIOR APPLICATION DATA:
?      APPLICATION NUMBER: PCT/IB96/01032
?      FILING DATE: June 28, 1996
?      CLASSIFICATION: 435
?      ATTORNEY/AGENT INFORMATION:
?      NAME: Mary M. Krinsky
?      REGISTRATION NUMBER: 32423
?      REFERENCE/DOCKET NUMBER: OCR-679
?      TELECOMMUNICATION INFORMATION:
?      TELEPHONE: 203-773-9544
?      TELEFAX: 203-773-1183
?      INFORMATION FOR SEQ ID NO: 47:
?      SEQUENCE CHARACTERISTICS:
?      LENGTH: 124 residues
?      TYPE: amino acid
?      STRANDEDNESS: single
?      TOPOLOGY: linear
?      MOLECULE TYPE: polypeptide
?      ORIGINAL SOURCE:
?      ORGANISM: Homo sapiens (melanoma patient
?      ORGANISM: Immunized with autologous tumor cells)
?      INDIVIDUAL ISOLATE: peripheral blood lympho-
?      IMMEDIATE SOURCE: cytes
?      LIBRARY: VH antibodies obtained from fuses
?      CLONE: E26
?      FEATURE:
?      NAME/KEY: heavy chain
?      US-08-983-607-47

Query Match      62.5%; Score 35; DB 3; Length 124;
Best Local Similarity 50.0%; Pred. No. 98;
Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Oy      1 VNMVNRKVGGS 10
Db      45 LEWVSAIGGS 54

RESULT 25
US-08-818-112-66
? Sequence 66, Application US/08818112
? Patent No. 6290969
? GENERAL INFORMATION:
? APPLICANT: Reed, Steven G.
? APPLICANT: Skeiky, Yasir A.W.
? APPLICANT: Dillon, Davin C.
? APPLICANT: Campos-Neto, Antonio
? APPLICANT: Houghton, Raymond
? APPLICANT: Vedvick, Thomas S.
? APPLICANT: Twardzik, Daniel R.
? TITLE OF INVENTION: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY
? TITLE OF INVENTION: AND DIAGNOSIS OF TUBERCULOSIS

?      NUMBER OF SEQUENCES: 153
?      CORRESPONDENCE ADDRESS:
?      ADDRESSEE: SEED and BERRY LLP
?      STREET: 6300 Columbia Center, 701 Fifth Avenue
?      CITY: Seattle
?      STATE: Washington
?      COUNTRY: USA
?      ZIP: 98104-7092
?      COMPUTER READABLE FORM:
?      MEDIUM TYPE: Floppy disk
?      COMPUTER: IBM PC compatible
?      OPERATING SYSTEM: PC-DOS/MS-DOS
?      SOFTWARE: Patentin Release #1.0, Version #1.30
?      CURRENT APPLICATION DATA:
?      APPLICATION NUMBER: US/08/818,112
?      FILING DATE: 13-MAR-1997
?      CLASSIFICATION: 424
?      ATTORNEY/AGENT INFORMATION:
?      NAME: Makl, David J.
?      REGISTRATION NUMBER: 31,392
?      REFERENCE/DOCKET NUMBER: 210121.411C6
?      TELECOMMUNICATION INFORMATION:
?      TELEPHONE: (206) 622-4900
?      TELEFAX: (206) 682-6031
?      INFORMATION FOR SEQ ID NO: 66:
?      SEQUENCE CHARACTERISTICS:
?      LENGTH: 132 amino acids
?      TYPE: amino acid
?      STRANDEDNESS: single
?      TOPOLOGY: linear
?      US-08-818-112-66

Query Match      62.5%; Score 35; DB 3; Length 132;
Best Local Similarity 60.0%; Pred. No. 1e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Oy      1 VNMVNRKVGGS 10
Db      110 VNMOTKSGGT 119

RESULT 26
US-08-818-111-67
? Sequence 67, Application US/08818111
? Patent No. 6338852
? GENERAL INFORMATION:
? APPLICANT: Reed, Steven G.
? APPLICANT: Skeiky, Yasir A.W.
? APPLICANT: Dillon, Davin C.
? APPLICANT: Campos-Neto, Antonio
? APPLICANT: Houghton, Raymond
? APPLICANT: Vedvick, Thomas S.
? APPLICANT: Twardzik, Daniel R.
? TITLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS OF
? TITLE OF INVENTION: TUBERCULOSIS
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: SEED and BERRY LLP
? STREET: 6300 Columbia Center, 701 Fifth Avenue
? CITY: Seattle
? STATE: Washington
? COUNTRY: USA
? ZIP: 98104-7092
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: Patentin Release #1.0, Version #1.30
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/08/818,111
? FILING DATE: 13-MAR-1997
? CLASSIFICATION: 424
? ATTORNEY/AGENT INFORMATION:
? NAME: Makl, David J.
```

REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.417C6
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 67:
SEQUENCE CHARACTERISTICS:
LENGTH: 132 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-818-111-67

Query Match 62.5%; Score 35; DB 4; Length 132;
Best Local Similarity 60.0%; Pred. No. 1e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 1 VNMVNVKVGGS 10
DB 110 VNMOTKSGGT 119

RESULT 27
US-09-056-556-66
Sequence 66, Application US/09056556
Patent No. 6350456
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Skelky, Yasir A.W.
APPLICANT: Dillon, Davin C.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE PREVENTION AND
NUMBER OF SEQUENCES: 241
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED AND BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104-7092

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/056,556
FILING DATE: 07-APR-1998
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Makl, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.457
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 66:
SEQUENCE CHARACTERISTICS:
LENGTH: 132 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-056-556-66

Query Match 62.5%; Score 35; DB 4; Length 132;
Best Local Similarity 60.0%; Pred. No. 1e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 1 VNMVNVKVGGS 10
DB 110 VNMOTKSGGT 119

RESULT 28

US-09-072-596-67
Sequence 67, Application US/09072596
Patent No. 6458366
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Skelky, Yasir A.W.
APPLICANT: Dillon, Davin C.
APPLICANT: Campos-Neto, Antonia
APPLICANT: Houghton, Raymond
APPLICANT: Vedvick, Thomas S.
APPLICANT: Twardzik, Daniel R.
APPLICANT: Lodges, Michael J.
APPLICANT: Hendrickson, Ronald C.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS OF
NUMBER OF SEQUENCES: 350
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED AND BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/072,596
FILING DATE: 05-MAY-1998
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Makl, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.417C9
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 67:
SEQUENCE CHARACTERISTICS:
LENGTH: 132 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-072-596-67

Query Match 62.5%; Score 35; DB 4; Length 132;
Best Local Similarity 60.0%; Pred. No. 1e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 1 VNMVNVKVGGS 10
DB 110 VNMOTKSGGT 119

RESULT 29
US-09-333-593A-4
Sequence 4, Application US/09333593A
Patent No. 6313269
GENERAL INFORMATION:
APPLICANT: DEEN, KEITH C.
APPLICANT: YOUNG, PETER R.
APPLICANT: MARSHALL, LISA A.
APPLICANT: ROSHAK, AMY K.
APPLICANT: TAN, KONG B.
APPLICANT: TRUNEH, ALEMSEGED
TITLE OF INVENTION: TUMOR NECROSIS FACTOR RELATED RECEPTOR,
FILE REFERENCE: GH-50008-2
CURRENT APPLICATION NUMBER: US/09/333,593A
CURRENT FILING DATE: 1999-06-15
PRIOR APPLICATION NUMBER: 08/916,625
PRIOR FILING DATE: 1997-08-22

PRIOR APPLICATION NUMBER: 08/853,684
PRIOR FILING DATE: 1997-05-09
PRIOR APPLICATION NUMBER: 60/041,230
PRIOR FILING DATE: 1997-03-14
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO: 4
LENGTH: 303
TYPE: PRT
ORGANISM: HOMO SAPIENS
US-09-333-593A-4

Query Match 62.5%; Score 35; DB 4; Length 303;
Best Local Similarity 62.5%; Pred. No. 2.4e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 VNMVKNYVG 8
: |||| |
Db 250 IKWVKNKG 257

RESULT 30
US-08-818-112-79
Sequence 79, Application US/08818112
Patent No. 6290969
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Skelky, Vasil A.W.
APPLICANT: Dillon, Davin C.
APPLICANT: Campos-Neto, Antonio
APPLICANT: Houghton, Raymond
APPLICANT: Vardick, Thomas S.
APPLICANT: Twardzik, Daniel R.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF TUBERCULOSIS
NUMBER OF SEQUENCES: 153
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/818,112
FILING DATE: 13-MAR-1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: MAKI, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.411C6
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 682-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 79:
SEQUENCE CHARACTERISTICS:
LENGTH: 355 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-818-112-79

Query Match 62.5%; Score 35; DB 3; Length 355;
Best Local Similarity 60.0%; Pred. No. 2.8e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
OY 1 VNMVKNYVGS 10
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Db 333 VNMQTSKGT 342

Search completed: August 29, 2003, 18:44:41
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GenCore version 5.1.6
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OM protein - protein search, using sw model

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(without alignments)
87.043 Million cell updates/sec

Title: US-09-830-876-3
Perfect score: 56
Sequence: 1 VNMVNRVGS 10

Scoring table:
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Gapop 10.0 , Gapext 0.5

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Total number of hits satisfying chosen parameters: 510680

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	45	80.4	434	12	US-10-280-679B-6	Sequence 6, Appl 1
2	38	67.9	54	14	US-10-001-870-157	Sequence 167, Appl 1
3	38	67.9	147	15	US-10-156-761-13047	Sequence 13047, Appl 1
4	37	66.1	153	15	US-10-156-761-7974	Sequence 7974, Appl 1
5	37	66.1	232	14	US-10-023-437-31	Sequence 31, Appl 1
6	37	66.1	574	14	US-09-863-547B-2	Sequence 2, Appl 1
7	37	66.1	969	14	US-10-023-437-31	Sequence 3, Appl 3
8	36	64.3	149	16	US-10-080-170-434	Sequence 434, Appl 3
9	36	64.3	439	12	US-10-828-063-51	Sequence 51, Appl 1
10	36	64.3	496	15	US-10-281-672-212	Sequence 212, Appl 1
11	36	64.3	519	9	US-09-967-477B-2	Sequence 2, Appl 1
12	36	64.3	550	9	US-09-815-242-13987	Sequence 13987, Appl 1
13	36	64.3	925	10	US-09-924-097-14	Sequence 14, Appl 1
14	36	64.3	964	15	US-10-156-761-9313	Sequence 9313, Appl 1
15	35	62.5	67	10	US-09-756-854-26	Sequence 26, Appl 1

16	35	62.5	67	14	US-10-041-574-26	Sequence 26, App1
17	35	62.5	132	9	US-09-759-143-819	Sequence 819, App
18	35	62.5	132	9	US-09-759-143-848	Sequence 848, App
19	35	62.5	132	9	US-09-780-663-819	Sequence 819, App
20	35	62.5	132	9	US-09-780-663-848	Sequence 848, App
21	35	62.5	132	9	US-09-822-827-819	Sequence 819, App
22	35	62.5	132	9	US-09-822-827-848	Sequence 848, App
23	35	62.5	132	10	US-09-895-793-819	Sequence 819, App
24	35	62.5	132	10	US-09-895-793-848	Sequence 848, App
25	35	62.5	132	10	US-09-895-814-819	Sequence 819, App
26	35	62.5	132	10	US-09-895-814-848	Sequence 848, App
27	35	62.5	132	12	US-10-084-843-66	Sequence 66, App1
28	35	62.5	132	12	US-10-193-002-67	Sequence 67, App1
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30	35	62.5	132	12	US-10-144-678A-848	Sequence 848, App
31	35	62.5	132	10	US-10-012-896-819	Sequence 819, App
32	35	62.5	132	14	US-10-012-896-848	Sequence 848, App
33	35	62.5	180	10	US-09-796-692-2361	Sequence 2361, Ap
34	35	62.5	180	15	US-10-040-862-2361	Sequence 2361, Ap
35	35	62.5	303	8	US-08-916-625B-4	Sequence 4, App11
36	35	62.5	318	10	US-09-738-626-4710	Sequence 4710, Ap
37	35	62.5	355	12	US-10-084-843-79	Sequence 79, App1
38	35	62.5	355	12	US-10-193-002-80	Sequence 80, App1
39	35	62.5	367	10	US-09-801-368-318	Sequence 318, App1
40	35	62.5	411	8	US-08-916-625B-2	Sequence 2, App11
41	35	62.5	411	9	US-08-828-739-2	Sequence 2, App11
42	35	62.5	411	9	US-09-757-421-4	Sequence 4, App11
43	35	62.5	411	9	US-09-874-138-2	Sequence 2, App11
44	35	62.5	411	10	US-09-887-879-11	Sequence 11, App1
45	35	62.5	411	10	US-09-811-098-6	Sequence 6, App1
46	35	62.5	411	10	US-09-993-964-11	Sequence 11, App1
47	35	62.5	411	12	US-10-247-383-11	Sequence 11, App1
48	35	62.5	411	12	US-10-288-937-1	Sequence 1, App11
49	35	62.5	411	13	US-10-035-765-3	Sequence 3, App11
50	35	62.5	411	13	US-10-067-615-2	Sequence 2, App11
51	35	62.5	411	14	US-10-067-798-1	Sequence 1, App11
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53	35	62.5	411	14	US-10-076-754-2	Sequence 2, App11
54	35	62.5	411	14	US-10-076-773-2	Sequence 2, App11
55	35	62.5	411	14	US-10-207-655-194	Sequence 194, App
56	35	62.5	411	15	US-10-314-410-6	Sequence 6, App11
57	35	62.5	432	15	US-10-081-816-11	Sequence 11, App1
58	35	62.5	436	15	US-10-081-816-11	Sequence 11, App1
59	35	62.5	439	15	US-10-156-761-1438	Sequence 1438, A
60	35	62.5	440	9	US-09-757-421-2	Sequence 2, App11
61	35	62.5	440	10	US-09-811-088-4	Sequence 4, App11
62	35	62.5	440	15	US-10-314-410-4	Sequence 4, App11
63	35	62.5	445	15	US-10-156-761-14137	Sequence 14137, A
64	35	62.5	457	15	US-10-081-872-316	Sequence 316, App
65	35	62.5	551	9	US-09-815-242-10464	Sequence 10464, App
66	35	62.5	569	11	US-09-805-337A-2	Sequence 2, App11
67	35	62.5	639	9	US-09-925-301-1158	Sequence 1158, Ap
68	34	60.7	199	11	US-09-791-497-5	Sequence 5, App11
69	34	60.7	640	9	US-09-815-242-10786	Sequence 10786, A
70	33	58.9	34	9	US-09-864-761-48592	Sequence 25, App1
71	33	58.9	67	10	US-09-756-854-25	Sequence 25, App1
72	33	58.9	91	15	US-10-041-574-25	Sequence 734, App
73	33	58.9	97	14	US-10-101-464A-734	Sequence 439, App
74	33	58.9	98	9	US-09-905-243-51	Sequence 439, App
75	33	58.9	210	16	US-10-080-170-439	Sequence 439, App
76	33	58.9	211	10	US-09-738-626-4313	Sequence 4313, App
77	33	58.9	310	11	US-10-141-321A-36	Sequence 36, App1
78	33	58.9	316	15	US-10-141-321-202	Sequence 202, App
79	33	58.9	343	11	US-09-800-321A-37	Sequence 37, App1
80	33	58.9	357	11	US-09-800-321A-35	Sequence 35, App1
81	33	58.9	357	15	US-10-156-761-14581	Sequence 14581, App1
82	33	58.9	357	15	US-09-887-879-14	Sequence 14, App1
83	33	58.9	418	10	US-09-992-964-14	Sequence 14, App1
84	33	58.9	418	10	US-10-242-383-14	Sequence 14, App1
85	33	58.9	418	12	US-10-259-165-74	Sequence 74, App1
86	33	58.9	459	12	US-10-039-785-1	Sequence 1, App11
87	33	58.9	468	13	US-10-226-296-2	Sequence 2, App11
88	33	58.9	468	15		

89	33	58.9	468	15	US-10-226-318-2	Sequence 2, Appl1
90	33	58.9	468	15	US-10-175-902-2	Sequence 2, Appl1
91	33	58.9	477	15	US-10-060-036-164	Sequence 164, App
92	33	58.9	490	14	US-10-016-634A-175	Sequence 175, App
93	33	58.9	503	15	US-10-156-761-8095	Sequence 8095, Ap
94	33	58.9	597	9	US-09-815-242-13226	Sequence 13226, A
95	33	58.9	695	9	US-09-945-258-18	Sequence 18, Appl1
96	33	58.9	747	11	US-09-824-574-6	Sequence 6, Appl1
97	33	58.9	965	11	US-09-842-484A-2	Sequence 2, Appl1
98	33	58.9	965	11	US-09-842-484A-4	Sequence 4, Appl1
99	33	58.9	965	15	US-10-184-485-3	Sequence 3, Appl1
100	33	58.9	965	15	US-10-217-613-3	Sequence 3, Appl1

ALIGNMENTS

RESULT 1
US-10-280-679B-6

; Sequence 6, Application US/10280679B
; Publication No. US20030150019A1

; GENERAL INFORMATION:

; APPLICANT: Large Scale Biology Corporation
; TITLE OF INVENTION: Monopartite RNA Virus Transformation Vectors

; FILE REFERENCE: LSBC-0108-US03

; CURRENT APPLICATION NUMBER: US/10/280,679B

; PRIOR FILING DATE: 2000-04-24

; PRIOR APPLICATION NUMBER: 09/557,941

; PRIOR FILING DATE: 2000-10-24

; PRIOR APPLICATION NUMBER: 08/484,341

; PRIOR FILING DATE: 1995-06-07/923,692

; PRIOR APPLICATION NUMBER: 07/923,692

; PRIOR FILING DATE: 1992-07-31

; PRIOR APPLICATION NUMBER: 07/600,244

; PRIOR FILING DATE: 1990-10-22

; PRIOR APPLICATION NUMBER: 07/641,617

; PRIOR FILING DATE: 1991-01-16

; PRIOR APPLICATION NUMBER: 07/737,899

; PRIOR FILING DATE: 1991-07-26

; PRIOR APPLICATION NUMBER: 07/739,143

; PRIOR FILING DATE: 1991-08-01

; PRIOR APPLICATION NUMBER: 07/310,881

; PRIOR FILING DATE: 1989-02-17

; PRIOR APPLICATION NUMBER: 07/160,766

; PRIOR FILING DATE: 1988-02-26

; PRIOR APPLICATION NUMBER: 07/160,771

; PRIOR FILING DATE: 1988-02-26

; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 11

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 6

; LENGTH: 434

; TYPE: PRT

; ORGANISM: Rice alpha-amylase

US-10-280-679B-6

Query Match

Best Local Similarity 80.4%; Score 45; DB 12; Length 434;

Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VNNVNRKVG 10

DB 259 VNNVNRKVG 268

RESULT 2

US-10-001-870-167

; Sequence 167, Application US/10001870

; Publication No. US20020150924A1

; GENERAL INFORMATION:

; APPLICANT: Salceda, Susana

; APPLICANT: Macina, Roberto

; APPLICANT: Recipon, Herve

; APPLICANT: Sun, Yongming

; APPLICANT: Liu, Chenghua

; TITLE OF INVENTION: Compositions and Methods Relating to Prostate Specific Genes a

; FILE REFERENCE: DEX-0283

; CURRENT APPLICATION NUMBER: US/10/001,870

; PRIOR FILING DATE: 2001-11-20

; PRIOR APPLICATION NUMBER: 60/252,189

; PRIOR FILING DATE: 2000-11-21

; NUMBER OF SEQ ID NOS: 217

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 167

; LENGTH: 54

; TYPE: PRT

; ORGANISM: Homo sapien

US-10-001-870-167

Query Match

Best Local Similarity 67.9%; Score 38; DB 14; Length 54;

Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 VNNVNRKVG 8

DB 43 VNNVNRKVG 50

RESULT 3

US-10-156-761-13047

; Sequence 13047, Application US/10156761

; Publication No. US20030119018A1

; GENERAL INFORMATION:

; APPLICANT: OMURA, SATOSHI

; APPLICANT: IKEDA, HARUO

; APPLICANT: ISHIKAWA, JUN

; APPLICANT: HORIKAWA, HIROSHI

; APPLICANT: SHIBA, TADAYOSHI

; APPLICANT: SAKAKI, YOSHIYUKI

; APPLICANT: HATTORI, MASAHIRA

; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES

; FILE REFERENCE: 249-262

; CURRENT APPLICATION NUMBER: US/10/156,761

; PRIOR FILING DATE: 2002-05-29

; PRIOR APPLICATION NUMBER: JP 2001-204089

; PRIOR FILING DATE: 2001-05-30

; PRIOR APPLICATION NUMBER: JP 2001-272697

; PRIOR FILING DATE: 2001-08-02

; NUMBER OF SEQ ID NOS: 15109

; SEQ ID NO 13047

; LENGTH: 147

; TYPE: PRT

; ORGANISM: Streptomyces avermitilis

US-10-156-761-13047

Query Match

Best Local Similarity 67.9%; Score 38; DB 15; Length 147;

Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 VNNVNRKVG 9

DB 47 VNNVNRKVG 53

RESULT 4

US-10-156-761-7974

; Sequence 7974, Application US/10156761

; Publication No. US20030119018A1

; GENERAL INFORMATION:

; APPLICANT: OMURA, SATOSHI

; APPLICANT: IKEDA, HARUO

; APPLICANT: ISHIKAWA, JUN

; APPLICANT: HORIKAWA, HIROSHI

; APPLICANT: SHIBA, TADAYOSHI

; APPLICANT: SAKAKI, YOSHIYUKI

; APPLICANT: HATTORI, MASAHIRA

FILE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR FILING DATE: 2001-05-30
PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR FILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 7974
LENGTH: 153
TYPE: PRT
ORGANISM: Streptomyces avermitilis
US-10-156-761-7974

Query Match 66.1%; Score 37; DB 15; Length 153;
Best Local Similarity 75.0%; Pred. No. 76;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 2 MNVNRVGG 9
DB 50 HWYRVGG 57

RESULT 5
US-10-023-437-31
Sequence 31, Application US/10023437
Publication No. US20020183272A1
GENERAL INFORMATION:
APPLICANT: JOHNSTON, STEPHEN A.
APPLICANT: STEWART-HALE, KATHERINE
APPLICANT: SYKES, KATHRYN F.
APPLICANT: KALTENBOECK, BERNHARD
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR VACCINATION COMPRISING NUCLEIC ACID
FILE OF INVENTION: AND/OR POLYPEPTIDE SEQUENCES OF CHLAMYDIA
FILE REFERENCE: US/02-73605
CURRENT APPLICATION NUMBER: US/10/023,437
CURRENT FILING DATE: 2001-12-17
PRIOR APPLICATION NUMBER: 60/225,839
PRIOR FILING DATE: 2000-12-15
NUMBER OF SEQ ID NOS: 69
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 31
LENGTH: 232
TYPE: PRT
ORGANISM: Chlamydia psittaci
US-10-023-437-31

Query Match 66.1%; Score 37; DB 14; Length 232;
Best Local Similarity 75.0%; Pred. No. 11e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 3 WYNKVGGS 10
DB 180 WYDKAGGS 187

RESULT 6
US-09-863-547B-2
Sequence 2, Application US/09863547B
Patent No. US2002018166A1
GENERAL INFORMATION:
APPLICANT: Henkel KGaA
APPLICANT: Hermann, Lentus B. M.
APPLICANT: Van Beckhoven, Rudolf F. W. C.
APPLICANT: Maurer, Karl-Heinz
APPLICANT: Kottwitz, Beatrix
APPLICANT: Weiss, Albrecht
APPLICANT: Van Solingen, Pieter
TITLE OF INVENTION: Detergents Comprising Cellulases
FILE REFERENCE: H 1920 A
CURRENT APPLICATION NUMBER: US/09/863,547B
CURRENT FILING DATE: 2002-02-13

PRIOR APPLICATION NUMBER: US 08/945,574
PRIOR FILING DATE: 1998-02-27
PRIOR APPLICATION NUMBER: PCT/EP96/01755
PRIOR FILING DATE: 1996-04-26
PRIOR APPLICATION NUMBER: US 08/614,115
PRIOR FILING DATE: 1996-03-12
PRIOR APPLICATION NUMBER: EP 95201115.3
PRIOR FILING DATE: 1995-04-28
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PatentIn version 3.1
SEQ ID NO 2
LENGTH: 574
TYPE: PRT
ORGANISM: Bacillus sp. 669.93
US-09-863-547B-2

Query Match 66.1%; Score 37; DB 10; Length 574;
Best Local Similarity 50.0%; Pred. No. 2.7e+02;
Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
QY 1 WVNKNVGGGS 10
DB 87 WYENRIGGA 96

RESULT 7
US-10-023-437-33
Sequence 33, Application US/10023437
Publication No. US20020183272A1
GENERAL INFORMATION:
APPLICANT: JOHNSTON, STEPHEN A.
APPLICANT: STEWART-HALE, KATHERINE
APPLICANT: SYKES, KATHRYN F.
APPLICANT: KALTENBOECK, BERNHARD
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR VACCINATION COMPRISING NUCLEIC AC
FILE OF INVENTION: AND/OR POLYPEPTIDE SEQUENCES OF CHLAMYDIA
FILE REFERENCE: US/02-73605
CURRENT APPLICATION NUMBER: US/10/023,437
CURRENT FILING DATE: 2001-12-17
PRIOR APPLICATION NUMBER: 60/225,839
PRIOR FILING DATE: 2000-12-15
NUMBER OF SEQ ID NOS: 69
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 33
LENGTH: 969
TYPE: PRT
ORGANISM: Chlamydia psittaci
US-10-023-437-33

Query Match 66.1%; Score 37; DB 14; Length 969;
Best Local Similarity 75.0%; Pred. No. 4.4e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 3 WYNKVGGS 10
DB 374 WYDKAGGS 381

RESULT 8
US-10-080-170-434
Sequence 434, Application US/10080170
Publication No. US20030129601A1
GENERAL INFORMATION:
APPLICANT: COLE, S.T.
TITLE OF INVENTION: COMPARATIVE MYCOBACTERIAL GENOMICS AS A TOOL FOR
IDENTIFYING TARGETS FOR THE DIAGNOSIS, PROPHYLAXIS OR
TREATMENT OF MYCOBACTERIOSES
FILE REFERENCE: 03495,0218
CURRENT APPLICATION NUMBER: US/10/080,170
CURRENT FILING DATE: 2002-06-10
PRIOR APPLICATION NUMBER: 60/270,123
PRIOR FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 652

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; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 434
; LENGTH: 149
; TYPE: PRF
; ORGANISM: Mycobacterium tuberculosis
US-10-080-170-434

Query Match
Best Local Similarity 64.3%; Score 36; DB 16; Length 149;
Best Local Similarity 62.5%; Pred. No. 1.1e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 WVNKVGGS 10
DB 36 WVNAGGT 43

RESULT 9
US-10-228-063-51
; Sequence 51, Application US/10228063
; Publication No. US20030135865A1
; GENERAL INFORMATION:
; APPLICANT: Lahanan, Mike
; TITLE OF INVENTION: Self-processing plants and plant parts
; FILE REFERENCE: 109846.317
; CURRENT APPLICATION NUMBER: US/10/228,063
; CURRENT FILING DATE: 2002-12-12
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 51
; LENGTH: 439
; TYPE: PRF
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic
US-10-228-063-51

Query Match
Best Local Similarity 64.3%; Score 36; DB 12; Length 439;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 VNVNKKVGG 9
DB 257 VNNAGAVGG 265

RESULT 10
US-10-081-872-212
; Sequence 212, Application US/10081872
; Publication No. US20030125534A1
; GENERAL INFORMATION:
; APPLICANT: Callen, Walter
; APPLICANT: Richardson, Toby
; APPLICANT: Frey, Gerhard
; APPLICANT: Short, Jay M.
; APPLICANT: Mathur, Eric J.
; APPLICANT: Gray, Kevin A.
; APPLICANT: Kervuuo, Janne S.
; APPLICANT: Slupka, Malgorzata
; TITLE OF INVENTION: ENZYMES HAVING ALPHA AMYLASE ACTIVITY
; FILE REFERENCE: 09010-108001
; CURRENT APPLICATION NUMBER: US/10/081,872
; CURRENT FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: US 60/270,495
; PRIOR FILING DATE: 2001-02-21
; PRIOR APPLICATION NUMBER: US 60/270,496
; PRIOR FILING DATE: 2001-02-21
; PRIOR APPLICATION NUMBER: US 60/291,122
; PRIOR FILING DATE: 2001-05-14
; NUMBER OF SEQ ID NOS: 321
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 212
; LENGTH: 496
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; TYPE: PRF
; ORGANISM: Environmental
US-10-081-872-212

Query Match
Best Local Similarity 64.3%; Score 36; DB 15; Length 496;
Best Local Similarity 60.0%; Pred. No. 3.4e+02;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 VNVNKKVGG 10
DB 321 VDMVDATGGS 330

RESULT 11
US-09-967-477B-2
; Sequence 2, Application US/09967477B
; Patent No. US20020156254A1
; GENERAL INFORMATION:
; APPLICANT: Xiao Qiu
; APPLICANT: Haiping Hong
; TITLE OF INVENTION: FAD4, FAD5, FAD5-2, AND FAD6, NOVEL
; TITLE OF INVENTION: FATTY ACID DESATURASE FAMILY MEMBERS AND USES THEREOF
; FILE REFERENCE: BM2-001
; CURRENT APPLICATION NUMBER: US/09/967,477B
; CURRENT FILING DATE: 2002-04-16
; PRIOR APPLICATION NUMBER: 60/236,303
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: 60/297,562
; PRIOR FILING DATE: 2001-06-12
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 519
; TYPE: PRF
; ORGANISM: Thraustochytrium sp.
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: 462
; OTHER INFORMATION: Xaa = Gly
US-09-967-477B-2

Query Match
Best Local Similarity 64.3%; Score 36; DB 10; Length 519;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 WVNKVGGS 9
DB 194 WVNKVG 200

RESULT 12
US-09-815-242-13987
; Sequence 13987, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Karl L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; TITLE OF INVENTION: Prokaryotes
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
```

;; PRIOR FILING DATE: 2000-05-26
;; PRIOR APPLICATION NUMBER: 60/242,578
;; PRIOR FILING DATE: 2000-10-23
;; PRIOR APPLICATION NUMBER: 60/253,625
;; PRIOR FILING DATE: 2000-11-27
;; PRIOR APPLICATION NUMBER: 60/257,931
;; PRIOR FILING DATE: 2000-12-22
;; PRIOR APPLICATION NUMBER: 60/269,308
;; PRIOR FILING DATE: 2001-02-16
;; NUMBER OF SEQ ID NOS: 14110
;; SOFTWARE: PASTSEQ for Windows version 4.0
;; SEQ ID NO: 13987
;; LENGTH: 550
;; TYPE: PRT
;; ORGANISM: Salmonella typhi
;; FEATURE:
;; NAME/KEY: VARIANT
;; LOCATION: (1)...(550)
;; OTHER INFORMATION: Xaa = Any Amino Acid
US-09-815-242-13987

Query Match 64.3%; Score 36; DB 9; Length 550;
Best Local Similarity 66.7%; Pred. No. 3.7e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 2 NWNVKVGGS 10
||:||||
DB 139 NWNVKVGGS 147

RESULT 13
US-09-924-097-14
;; Sequence 14, Application US/09924097
;; Patent No. US20020156240A1
;; GENERAL INFORMATION:
;; APPLICANT: TOMONO, Jun
;; APPLICANT: NOMURA, Yoshiko
;; APPLICANT: SAGAWA, Hiroaki
;; APPLICANT: SAKAI, Takeshi
;; APPLICANT: KATO, Ikunoshin
;; TITLE OF INVENTION: ALPHA-AGARASE AND PROCESS FOR PRODUCING THE SAME
;; FILE REFERENCE: TOMONO-1
;; CURRENT APPLICATION NUMBER: US/09/924,097
;; PRIOR FILING DATE: 2001-08-08
;; PRIOR APPLICATION NUMBER: JP00/00966
;; PRIOR FILING DATE: 2000-02-21
;; PRIOR APPLICATION NUMBER: 11-44890
;; PRIOR FILING DATE: 1999-02-23
;; PRIOR APPLICATION NUMBER: 11-198852
;; PRIOR FILING DATE: 1999-07-13
;; NUMBER OF SEQ ID NOS: 30
;; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO: 14
;; LENGTH: 925
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Amino acid sequence of agarase 1-7
US-09-924-097-14

Query Match 64.3%; Score 36; DB 10; Length 925;
Best Local Similarity 75.0%; Pred. No. 6.1e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 2 NWNVKVGGS 9
||||:|
DB 378 NWNVKVGGS 385

RESULT 14
US-10-156-761-9313
;; Sequence 9313, Application US/10156761
;; Publication No. US20030119018A1

;; GENERAL INFORMATION:
;; APPLICANT: OMURA, SATOSHI
;; APPLICANT: IKEDA, HARUO
;; APPLICANT: ISHIKAWA, JUN
;; APPLICANT: HORIKAWA, HIROSHI
;; APPLICANT: SHIBA, TADAYOSHI
;; APPLICANT: SAKAKI, YOSHIYUKI
;; APPLICANT: HATTORI, MASAHIRA
;; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
;; FILE REFERENCE: 248-262
;; CURRENT APPLICATION NUMBER: US/10/156,761
;; PRIOR FILING DATE: 2001-05-30
;; PRIOR APPLICATION NUMBER: JP 2001-204089
;; PRIOR FILING DATE: 2001-08-02
;; NUMBER OF SEQ ID NOS: 15109
;; SEQ ID NO: 9313
;; LENGTH: 964
;; TYPE: PRT
;; ORGANISM: Streptomyces avermitilis
US-10-156-761-9313

Query Match 64.3%; Score 36; DB 15; Length 964;
Best Local Similarity 71.4%; Pred. No. 6.3e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 2 NWNVKVGGS 8
||||:|
DB 684 NWNVKVGGS 690

RESULT 15
US-09-756-854-26
;; Sequence 26, Application US/09756854
;; Patent No. US2002016484A1
;; GENERAL INFORMATION:
;; APPLICANT: NI, Jian
;; Yu, Guo-Liang
;; Fan, Ping
;; Gentz, Reiner
;; TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor TR9
;; NUMBER OF SEQUENCES: 26
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Human Genome Sciences, Inc.
;; STREET: 9410 Key West Avenue
;; CITY: Rockville
;; STATE: MD
;; COUNTRY: US
;; ZIP: 20850
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/756,854
;; FILING DATE: 10-Jan-2001
;; CLASSIFICATION: <unknown>
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 09/095,094
;; FILING DATE: <unknown>
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Hoover, Kenley K.
;; REGISTRATION NUMBER: 40,302
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 301-309-8439
;; TELEFAX: 301-309-8504
;; INFORMATION FOR SEQ ID NO: 26:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 67 amino acids
;; TYPE: amino acid

```

; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 26:
US-09-756-854-26

Query Match      62.5%; Score 35; DB 10; Length 67;
Best Local Similarity 62.5%; Pred. No. 74;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY      1 VNMVNKVG 8
       : |||||
Db      35 IKWVNKTG 42

RESULT 16
US-10-041-574-26
; Sequence 26, Application US/10041574
; Publication NO. US20020168359A1
; GENERAL INFORMATION:
; APPLICANT: Ni, Jian
; APPLICANT: Yu, Guo-Liang
; APPLICANT: Fan, Ping
; APPLICANT: Gentz, Reiner L.
; TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor TR9
; FILE REFERENCE: PF375P1
; CURRENT APPLICATION NUMBER: US/10/041,574
; CURRENT FILING DATE: 2002-01-10
; PRIOR APPLICATION NUMBER: 09/527,236
; PRIOR FILING DATE: 2000-03-16
; PRIOR APPLICATION NUMBER: 60/052,991
; PRIOR FILING DATE: 1997-06-11
; PRIOR APPLICATION NUMBER: 09/095,094
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/126,019
; PRIOR FILING DATE: 1999-03-24
; PRIOR APPLICATION NUMBER: 60/134,220
; PRIOR FILING DATE: 1999-05-14
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 26
; LENGTH: 67
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-041-574-26

Query Match      62.5%; Score 35; DB 14; Length 67;
Best Local Similarity 62.5%; Pred. No. 74;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY      1 VNMVNKVG 8
       : |||||
Db      35 IKWVNKTG 42

RESULT 17
US-09-759-143-819
; Sequence 819, Application US/09759143
; Patent NO. US2002022248A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqi
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
```

```

; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C23
; CURRENT APPLICATION NUMBER: US/09/759,143
; CURRENT FILING DATE: 2001-01-12
; NUMBER OF SEQ ID NOS: 934
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 819
; LENGTH: 132
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-759-143-819

Query Match      62.5%; Score 35; DB 9; Length 132;
Best Local Similarity 60.0%; Pred. No. 1.4e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY      1 VNMVNKVGGS 10
       : ||| |||
Db      110 VNMOTKSGT 119

RESULT 18
US-09-759-143-848
; Sequence 848, Application US/09759143
; Patent NO. US2002022248A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqi
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C23
; CURRENT APPLICATION NUMBER: US/09/759,143
; CURRENT FILING DATE: 2001-01-12
; NUMBER OF SEQ ID NOS: 934
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 848
; LENGTH: 132
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-759-143-848

Query Match      62.5%; Score 35; DB 9; Length 132;
Best Local Similarity 60.0%; Pred. No. 1.4e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY      1 VNMVNKVGGS 10
       : ||| |||
Db      110 VNMOTKSGT 119

RESULT 19
US-09-780-669-819
; Sequence 819, Application US/09780669
```

```
Patent No. US20020051977A1
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yuqi
APPLICANT: Henderson, Robert A.
APPLICANT: Kalos, Michael D.
APPLICANT: Fanger, Gary R.
APPLICANT: Retter, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Day, Craig H.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Derrick
APPLICANT: Li, Samuel
APPLICANT: Wang, Aijun
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Hepler, William
APPLICANT: Hurai, John
APPLICANT: McNeill, Patricia D.
APPLICANT: Houghton, Raymond L.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
FILE REFERENCE: 210121.427C24
CURRENT APPLICATION NUMBER: US/09/780.669
CURRENT FILING DATE: 2001-02-09
NUMBER OF SEQ ID NOS: 943
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 819
LENGTH: 132
TYPE: PRT
ORGANISM: Homo sapiens
US-09-780-669-819

Query Match          62.5%; Score 35; DB 9; Length 132;
Best Local Similarity 60.0%; Pred. No. 1.4e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 VNMVNRKVGGS 10
DB 110 VNMOTKSGGT 119

RESULT 20
US-09-780-669-848
Sequence 848, Application US/09780669
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yuqi
APPLICANT: Henderson, Robert A.
APPLICANT: Kalos, Michael D.
APPLICANT: Fanger, Gary R.
APPLICANT: Retter, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Day, Craig H.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Derrick
APPLICANT: Li, Samuel
APPLICANT: Wang, Aijun
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Hepler, William
APPLICANT: Hurai, John
APPLICANT: McNeill, Patricia D.
APPLICANT: Houghton, Raymond L.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
FILE REFERENCE: 210121.427C24
CURRENT APPLICATION NUMBER: US/09/780.669
```

```
CURRENT FILING DATE: 2001-02-09
NUMBER OF SEQ ID NOS: 943
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 848
LENGTH: 132
TYPE: PRT
ORGANISM: Homo sapiens
US-09-780-669-848

Query Match          62.5%; Score 35; DB 9; Length 132;
Best Local Similarity 60.0%; Pred. No. 1.4e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 VNMVNRKVGGS 10
DB 110 VNMOTKSGGT 119

RESULT 21
US-09-822-827-819
Sequence 819, Application US/09822827
Patent No. US20020081680A1
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
FILE REFERENCE: 210121.534C1
CURRENT APPLICATION NUMBER: US/09/822.827
CURRENT FILING DATE: 2001-03-28
NUMBER OF SEQ ID NOS: 982
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 819
LENGTH: 132
TYPE: PRT
ORGANISM: Homo sapiens
US-09-822-827-819

Query Match          62.5%; Score 35; DB 9; Length 132;
Best Local Similarity 60.0%; Pred. No. 1.4e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 VNMVNRKVGGS 10
DB 110 VNMOTKSGGT 119

RESULT 22
US-09-822-827-848
Sequence 848, Application US/09822827
Patent No. US20020081680A1
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
FILE REFERENCE: 210121.534C1
CURRENT APPLICATION NUMBER: US/09/822.827
CURRENT FILING DATE: 2001-03-28
NUMBER OF SEQ ID NOS: 982
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 848
LENGTH: 132
TYPE: PRT
ORGANISM: Homo sapiens
US-09-822-827-848

Query Match          62.5%; Score 35; DB 9; Length 132;
Best Local Similarity 60.0%; Pred. No. 1.4e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 VNMVNRKVGGS 10
DB 110 VNMOTKSGGT 119
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```
RESULT 23
US-09-895-793-819
; Sequence 819, Application US/09895793
; Publication No. US20020192763A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yugu
; APPLICANT: Kalos, Michael D.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darlick
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Vinals de Bassols, Carlota
; APPLICANT: Foy, Teresa
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.534C2
; CURRENT APPLICATION NUMBER: US/09/895,793
; CURRENT FILING DATE: 2001-06-29
; NUMBER OF SEQ ID NOS: 982
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 819
; LENGTH: 132
; TYPE: PRT
; ORGANISM: Homo saplen
US-09-895-793-819

Query Match
Best Local Similarity 62.5%; Score 35; DB 10; Length 132;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 VNMVNRKVGGS 10
Db 110 VNMOTKSGGT 119

RESULT 24
US-09-895-793-848
; Sequence 848, Application US/09895793
; Publication No. US20020192763A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yugu
; APPLICANT: Kalos, Michael D.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darlick
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
```

```
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Vinals de Bassols, Carlota
; APPLICANT: Foy, Teresa
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.534C2
; CURRENT APPLICATION NUMBER: US/09/895,793
; CURRENT FILING DATE: 2001-06-29
; NUMBER OF SEQ ID NOS: 982
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 848
; LENGTH: 132
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-895-793-848

Query Match
Best Local Similarity 62.5%; Score 35; DB 10; Length 132;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 VNMVNRKVGGS 10
Db 110 VNMOTKSGGT 119

RESULT 25
US-09-895-814-819
; Sequence 819, Application US/09895814
; Publication No. US20020193296A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yugu
; APPLICANT: Kalos, Michael D.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darlick
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Vinals de Bassols, Carlota
; APPLICANT: Foy, Teresa
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C26
; CURRENT APPLICATION NUMBER: US/09/895,814
; CURRENT FILING DATE: 2001-06-29
; NUMBER OF SEQ ID NOS: 990
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 819
; LENGTH: 132
; TYPE: PRT
; ORGANISM: Homo saplen
US-09-895-814-819

Query Match
Best Local Similarity 62.5%; Score 35; DB 10; Length 132;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 VNMVNRKVGGS 10
Db 110 VNMOTKSGGT 119
```


RESULT 26
US-09-895-814-848
Sequence 848, Application US/09895814
Publication No. US20020193296A1
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, David C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yugu
APPLICANT: Kalos, Michael D.
APPLICANT: Retter, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Day, Craig H.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Darick
APPLICANT: Wang, Aljun
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Hepler, William T.
APPLICANT: Henderson, Robert A.
APPLICANT: Hurai, John
APPLICANT: McNeill, Patricia D.
APPLICANT: Houghton, Raymond L.
APPLICANT: Vinals de Bassols, Carlota
APPLICANT: Foy, Teresa
APPLICANT: Fanger, Gary R.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
FILE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427C26
CURRENT APPLICATION NUMBER: US/09/895,814
CURRENT FILING DATE: 2001-06-29
NUMBER OF SEQ ID NOS: 990
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 848
LENGTH: 132
TYPE: PRT
ORGANISM: Homo sapiens
US-09-895-814-848

Query Match 62.5% Score 35; DB 10; Length 132;
Best Local Similarity 60.0%; Pred. No. 1.4e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 VNMVKNVSGS 10
DB 110 VNMVKNVSGT 119

RESULT 27
US-10-084-843-66
Sequence 66, Application US/10084843
Publication No. US20030143243A1
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Dillon, David C.
APPLICANT: Campos-Neto, Antonio
APPLICANT: Houghton, Raymond
APPLICANT: Vedvick, Thomas S.
APPLICANT: Twardzik, Daniel R.
APPLICANT: Lodes, Michael J.
APPLICANT: Hendrickson, Ronald C.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY
AND DIAGNOSIS OF TUBERCULOSIS
NUMBER OF SEQUENCES: 355
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED AND BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington

COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/084,843
FILING DATE: 25-Feb-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/072,967
FILING DATE: 05-May-1998
ATTORNEY/AGENT INFORMATION:
NAME: MAKI, DAVID J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.411C9
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 66:
SEQUENCE CHARACTERISTICS:
LENGTH: 132 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 66:
US-10-084-843-66

Query Match 62.5% Score 35; DB 12; Length 132;
Best Local Similarity 60.0%; Pred. No. 1.4e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 VNMVKNVSGS 10
DB 110 VNMVKNVSGT 119

RESULT 28
US-10-193-002-67
Sequence 67, Application US/10193002
Publication No. US20030135026A1
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Dillon, David C.
APPLICANT: Campos-Neto, Antonio
APPLICANT: Houghton, Raymond
APPLICANT: Vedvick, Thomas S.
APPLICANT: Twardzik, Daniel R.
APPLICANT: Lodes, Michael J.
APPLICANT: Hendrickson, Ronald C.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS OF
TUBERCULOSIS
NUMBER OF SEQUENCES: 350
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED AND BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/193,002
FILING DATE: 10-Jul-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/072,596
FILING DATE: 05-MAY-1998
ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.417C9
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 67:
SEQUENCE CHARACTERISTICS:
LENGTH: 132 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 67:
US-10-193-002-67

Query Match 62.5%; Score 35; DB 12; Length 132;
Best Local Similarity 60.0%; Pred. No. 1.4e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 1 VNMVNVGGS 10
111 111:
DB 110 VNMQTKSGCT 119

RESULT 29
US-10-144-678A-819
Sequence 819, Application US/10144678A
Publication No. US20030157089A1
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yuqiu
APPLICANT: Henderson, Robert A.
APPLICANT: Kalos, Michael D.
APPLICANT: Fanger, Gary R.
APPLICANT: Retter, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Day, Craig H.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Darriek
APPLICANT: Li, Samuel X.
APPLICANT: Wang, Aljun
APPLICANT: Skelky, Yasir A. W.
APPLICANT: Hepler, William T.
APPLICANT: Hurai, John
APPLICANT: McNeill, Patricia D.
APPLICANT: Houghton, Raymond L.
APPLICANT: Vinals y de Bassols, Carlota
APPLICANT: Foy, Teresa M.
APPLICANT: Watanabe, Yoshihiro
APPLICANT: Deng, Ya
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427C28
CURRENT APPLICATION NUMBER: US/10/144,678A
CURRENT FILING DATE: 2002-08-12
NUMBER OF SEQ ID NOS: 1033
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 819
LENGTH: 132
TYPE: PRT
ORGANISM: Homo sapiens
US-10-144-678A-819

Query Match 62.5%; Score 35; DB 12; Length 132;
Best Local Similarity 60.0%; Pred. No. 1.4e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 1 VNMVNVGGS 10
111 111:
DB 110 VNMQTKSGCT 119

RESULT 30
US-10-144-678A-848
Sequence 848, Application US/10144678A
Publication No. US20030157089A1
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yuqiu
APPLICANT: Henderson, Robert A.
APPLICANT: Kalos, Michael D.
APPLICANT: Fanger, Gary R.
APPLICANT: Retter, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Day, Craig H.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Darriek
APPLICANT: Li, Samuel X.
APPLICANT: Wang, Aljun
APPLICANT: Skelky, Yasir A. W.
APPLICANT: Hepler, William T.
APPLICANT: Hurai, John
APPLICANT: McNeill, Patricia D.
APPLICANT: Houghton, Raymond L.
APPLICANT: Vinals y de Bassols, Carlota
APPLICANT: Foy, Teresa M.
APPLICANT: Watanabe, Yoshihiro
APPLICANT: Deng, Ya
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427C28
CURRENT APPLICATION NUMBER: US/10/144,678A
CURRENT FILING DATE: 2002-08-12
NUMBER OF SEQ ID NOS: 1033
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 848
LENGTH: 132
TYPE: PRT
ORGANISM: Homo sapiens
US-10-144-678A-848

Query Match 62.5%; Score 35; DB 12; Length 132;
Best Local Similarity 60.0%; Pred. No. 1.4e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 1 VNMVNVGGS 10
111 111:
DB 110 VNMQTKSGCT 119

Search completed: August 29, 2003, 18:47:49
Job time: 17.7143 secs

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OM protein - protein search, using sw model

Run on: August 29, 2003, 18:44:06 ; Search time 10.2857 Seconds
(without alignments)
93.497 Million cell updates/sec

Title: US-09-830-876-3
Perfect score: 56
Sequence: 1 VMVNVKVGGS 10

Scoring table: BIOSUM62
Gap0 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 100 summaries

Database :

1: PIR.76:*
2: PIR1:*
3: PIR2:*
4: PIR3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	56	100.0	429	1 JE0406	alpha-amy-lase (EC
2	49	87.5	383	1 ALR20C	alpha-amy-lase (EC
3	48	85.7	438	1 ALBH	alpha-amy-lase (EC
4	47	83.9	427	1 ALBHB	alpha-amy-lase (EC
5	47	83.9	437	2 S07040	alpha-amy-lase (EC
6	46	82.1	435	2 S12625	alpha-amy-lase (EC
7	45	80.4	428	2 JC7137	alpha-amy-lase (EC
8	45	80.4	434	2 S10013	alpha-amy-lase (EC
9	45	80.4	428	2 S12775	alpha-amy-lase (EC
10	42	75.0	440	2 S14958	alpha-amy-lase (EC
11	42	75.0	680	2 H64206	fructose-permease
12	41	73.2	689	2 S69535	hypothetical prote
13	40	71.4	340	2 T36856	hypothetical prote
14	40	71.4	340	2 T28614	hypothetical prote
15	40	71.4	340	2 T27214	hypothetical prote
16	40	71.4	340	2 T37451	hypothetical prote
17	40	71.4	340	2 G42327	hypothetical prote
18	40	71.4	340	2 U01810	hypothetical prote
19	40	71.4	340	2 U01810	hypothetical prote
20	40	71.4	340	2 U01810	hypothetical prote
21	40	71.4	340	2 U01810	hypothetical prote
22	39	69.6	157	2 VCLJBT	env polyprotein pr
23	39	69.6	157	2 AG1312	thioredoxin homolo
24	39	69.6	157	2 AG1684	thioredoxin homolo
25	39	69.6	157	2 H72668	hypothetical prote
26	38	67.9	270	2 AFI231	alpha, alpha-phosph
27	38	67.9	270	2 S17828	nuclease S1 - Pent
28	38	67.9	278	2 JE0408	3'-nucleotidase (E
29	38	67.9	421	2 S10514	probable lysR-fam1

30	38	67.9	627	2 AD2161	alkaline phosphata
31	37	66.1	1078	2 S48842	DNA-directed RNA p
32	37	66.1	132	2 G69272	conserved hypothec
33	37	66.1	228	1 A69094	delta 1 pyroline
34	37	66.1	278	2 T49276	hypothetical prote
35	37	66.1	346	2 T49085	hypothetical prote
36	37	66.1	417	2 S00935	DNA-directed RNA p
37	37	66.1	439	2 H83103	probable MFS trans
38	37	66.1	516	2 T15533	hypothetical prote
39	37	66.1	527	2 G86644	hypothetical prote
40	37	66.1	574	2 C83725	endo-beta-1,4-gluc
41	37	66.1	952	2 JC7227	ent-kaurane syntha
42	37	66.1	1070	2 C29959	DNA-directed RNA p
43	37	66.1	1280	2 T34357	hypothetical prote
44	36	64.3	149	2 H70581	hypothetical prote
45	36	64.3	321	1 B64026	probable S-adenosy
46	36	64.3	384	2 A69552	3-ketoacyl-CoA thi
47	36	64.3	403	2 P84422	hypothetical prote
48	36	64.3	430	2 C97160	uracil permease Ur
49	36	64.3	437	2 S14956	alpha-amy-lase (EC
50	36	64.3	438	2 S14957	alpha-amy-lase (EC
51	36	64.3	439	2 T02956	alpha-amy-lase (EC
52	36	64.3	536	2 G86283	hypothetical prote
53	36	64.3	548	2 AE1585	alpha, alpha-phosph
54	36	64.3	550	2 AE1058	alpha, alpha-phosph
55	36	64.3	559	2 H83758	alpha, alpha-phosph
56	36	64.3	561	2 B69725	alpha, alpha-phosph
57	36	64.3	562	2 C82263	trehalase-6-phosph
58	36	64.3	586	2 D86243	hypothetical prote
59	36	64.3	664	2 RB1136	hypothetical prote
60	36	64.3	664	2 AD1494	MADH flavin oxidor
61	36	64.3	969	2 G71482	probable protein t
62	36	64.3	1070	1 RNMB	DNA-directed RNA p
63	36	64.3	2429	1 SJBHA	spectrin alpha cha
64	35	62.5	98	2 A49085	L-plastin - rabbit
65	35	62.5	183	2 E69388	hypothetical prote
66	35	62.5	229	2 T06204	hypothetical prote
67	35	62.5	251	2 E70521	probable phosphor
68	35	62.5	317	2 D84115	2-keto-3-deoxygluc
69	35	62.5	363	2 F98159	hypothetical prote
70	35	62.5	367	2 S50621	hypothetical prote
71	35	62.5	403	2 AC2271	S5081 protein - ye
72	35	62.5	413	1 ALMW3	precocorrin-6y-dep
73	35	62.5	415	2 AE1844	alpha-amy-lase (EC
74	35	62.5	441	2 B90051	hypothetical prote
75	35	62.5	457	2 T39751	hypothetical prote
76	35	62.5	475	2 T06061	major facilitator
77	35	62.5	493	2 T06061	cellulase (EC 3.2.
78	35	62.5	494	2 T06059	cellulase (EC 3.2.
79	35	62.5	495	2 T12401	NADH2 dehydrogenas
80	35	62.5	509	2 T41034	probable WD-domain
81	35	62.5	551	2 S56465	alpha, alpha-phosph
82	35	62.5	551	2 H91280	trehalase 6-P hydr
83	35	62.5	551	2 H86121	trehalase 6-P hydr
84	35	62.5	627	1 A35835	T-plastin - human
85	35	62.5	627	1 A35835	T-plastin - human
86	35	62.5	627	1 A56535	65k macrophage pro
87	35	62.5	627	1 A56535	plastin, intestina
88	35	62.5	630	1 A34789	T-plastin - human
89	35	62.5	630	1 A34789	limbin - chicken
90	35	62.5	809	2 S32899	ferric-pseudocacti
91	35	62.5	891	2 H86790	hypothetical prote
92	35	62.5	968	2 T51517	preproteolin trans
93	35	62.5	1123	2 T51517	telomerase reverse
94	35	62.5	1123	2 T49914	telomerase reverse
95	35	62.5	1963	2 H71879	toxoin-like outer m
96	35	62.5	2399	2 B64635	toxoin-like outer m
97	34	60.7	119	2 B32530	Ig heavy chain V r
98	34	60.7	122	1 A1HUTR	Ig heavy chain V-I
99	34	60.7	126	2 G71269	probable ribosome-
100	34	60.7	142	2 I47198	Ig heavy chain var

ALIGNMENTS

RESULT 1

JE0406

alpha-amylase (EC 3.2.1.1) B precursor (gene Amy56 and others) - barley
N:Alternate names: 1,4-alpha-D-glucan glucanohydrolase

C:Species: Hordeum vulgare (barley)

C>Date: 17-Apr-1993 #sequence_revision 21-Jan-1997 #text_change 18-Jun-1999

C:Accession: JE0406; S06275; B31960; B21826

R:Rahmatullah, R.J.; Huang, J.K.; Clark, K.L.; Reeck, G.R.; Chandra, G.R.; Muthukrishnan

Plant Mol. Biol. 12, 119-121, 1989

A:Title: Nucleotide and predicted amino acid sequences of two different genes for high-P

A:Reference number: JE0405

A:Accession: JE0406

A:Molecule type: DNA

A:Residues: 1-429 <RAH>

A:Cross-references: EMBL:X15227; NID:g18899; PIDD:CAA3299.1; PID:g295805

A:Experimental source: gene Amy56 for alpha-amylase

A:Genetics: A56

R:Rogers, J.C.

submitted to Genbank, September 1988

A:Reference number: A94535

A:Accession: B30759

A:Status: not compared with conceptual translation

A:Molecule type: DNA

A:Residues: 1-104,'G',106-154,'A',156-160,'PD',163,'G',167-196,'V',198-342,'T',344-392,'

A:Cross-references: GB:J04202; NID:g166984; PIDD:AAA9615.1; PID:g166985

A:Experimental source: cv. Himalaya gene Amy46 for alpha-amylase B

A:Genetics: A46

R:Knox, C.A.P.; Sonthayanon, B.; Chandra, G.R.; Muthukrishnan, S.

Plant Mol. Biol. 9, 3-17, 1987

A:Title: Structure and organization of two divergent alpha-amylase genes from barley.

A:Reference number: S06275

A:Accession: S06275

A:Molecule type: DNA

A:Residues: 1-11,'L',14-32,'S',34-57,'I',59-79,'Y',81-139,'R',141-160,'PA',163-164,'R',

A:Cross-references: EMBL:M17125; NID:g166978; PIDD:AAA32926.1; PID:g166979

A:Experimental source: cv. Sundance gene for alpha-amylase 1 precursor (clone p141.117)

A:Genetics: A41

A:Note: the authors translated the codon TCG for residue 33 as Trp

R:Khurshid, B.; Rogers, J.C.

J. Biol. Chem. 263, 18953-18960, 1988

A:Title: Barley alpha-amylase genes. Quantitative comparison of steady-state mRNA levels

A:Reference number: A92700; MUID:8506691; PMID:3264283

A:Accession: B31960

A:Status: not compared with conceptual translation

A:Molecule type: DNA

A:Residues: 1-51 <KHH>

A:Experimental source: strain Himalaya gene Amy46 for alpha-amylase B precursor

R:Huang, J.K.; Swegle, M.; Dandekar, A.M.; Muthukrishnan, S.

J. Mol. Appl. Genet. 2, 579-588, 1984

A:Reference number: A92837; MUID:85159405; PMID:6335720

A:Accession: B21826

A:Molecule type: mRNA

A:Residues: 379-389,'T',391-392,'D',394-429 <HHA>

A:Cross-references: GB:R02636; NID:g166992; PIDD:AAA32932.1; PID:g166993

A:Experimental source: cv. Himalaya aleurone cell mRNA (clone 96 for alpha-amylase B)

A:Genetics: <A56>

A:Gene: Amy56

A:Introns: 29/3; 346/3

C:Genetics: <A46>

A:Gene: Amy46

C:Genetics: <AA1>

A:Gene: Amy1

A:Map position: 6

A:Introns: 29/3; 346/3

C:Function:

A:Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds

A:Pathway: glycogen/starch degradation

C:Superfamily: wheat alpha-amylase; alpha-amylase core homology

C:Keywords: aleurone cell; germination; glycosylase; hydrolase; polysaccharide degradati

F:172-318/Domain: alpha-amylase core homology <AMY>

F:205,230,315/Active site: Asp, Glu, Asp #status predicted

Query Match 100.0%; Score 56; DB 1; Length 429;
Best Local Similarity 100.0%; Pred. No. 0.036;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 VNMVNRVCGS 10
Db 255 VNMVNRVCGS 264

1 VNMVNRVCGS 10
Db 255 VNMVNRVCGS 264

RESULT 2

ALR20C

alpha-amylase (EC 3.2.1.1) precursor (clone O5Amy-C) - rice

C:Species: Oryza sativa (rice)

C>Date: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change 21-Jan-2000

C:Accession: S19142; PS0158

R:Kim, J.K.; Mu, R.

Plant Mol. Biol. 18, 399-402, 1992

A:Title: Nucleotide sequence of a high-pi rice (Oryza sativa) -amylase gene.

A:Reference number: S19142

A:Accession: S19142

A:Molecule type: DNA

A:Residues: 1-383 <KIM>

A:Cross-references: EMBL:X52240; NID:g20170; PIDD:CAA36485.1; PID:g20171

A:Experimental source: cv. IR26

R:Huang, N.; Kolzumi, N.; Reini, S.; Rodriguez, R.L.

Nucleic Acids Res. 18, 7007-7014, 1990

A:Title: Structural organization and differential expression of rice alpha-amylase ge

A:Reference number: J70945; MUID:91088278; PMID:2263460

A:Accession: PS0158

A:Molecule type: DNA

A:Residues: 1-50 <HDA>

A:Cross-references: GB:M59350; GB:M36983; NID:g169766; PIDD:AAA33893.1; PID:g169767

A:Genetics:

C:Introns: 31/3; 75/3; 313/3

C:Function:

A:Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds

A:Pathway: glycogen/starch degradation

C:Superfamily: wheat alpha-amylase; alpha-amylase core homology

C:Keywords: glycosylase; hydrolase; polysaccharide degradation

F:1-31/Domain: signal sequence #status predicted <SID>

F:32-383/Product: alpha-amylase #status predicted <MAT>

F:150-289/Domain: alpha-amylase core homology <AMY>

Query Match 87.5%; Score 49; DB 1; Length 383;

Best Local Similarity 88.9%; Pred. No. 0.56;

Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 VNMVNRVCGS 9
Db 226 VNMVNRVCGS 234

1 VNMVNRVCGS 9
Db 226 VNMVNRVCGS 234

RESULT 3

ALBH

alpha-amylase (EC 3.2.1.1) precursor - barley

C:Species: Hordeum vulgare (barley)

C>Date: 03-Aug-1984 #sequence_revision 03-Aug-1984 #text_change 18-Jun-1999

C:Accession: A00846; S65602

R:Rogers, J.C.; Millman, C.

J. Biol. Chem. 258, 8169-8174, 1983

A:Title: Isolation and sequence analysis of a barley alpha-amylase cDNA clone.

A:Reference number: A00846; MUID:8328423; PMID:6190808

A:Accession: A00846

A:Molecule type: mRNA

A:Residues: 1-438 <ROG>

A:Cross-references: GB:J01236; NID:g166986; PIDD:AAA32929.1; PID:g166987

A:Experimental source: cv. Himalaya

R:Unger, N.; Rodenburg, K.W.; Guo, X.J.; Chai, J.C.; Svensson, B.

FEBS Lett. 363, 299-303, 1995

A:Title: Isozyme hybrids within the protruding third loop domain of the barley alpha-

A:Reference number: S65602; MUID:9555567; PMID:7737421

A:Accession: S65602
A:Molecule type: protein
A:Residues: 25-29 <TUG>
C:Comment: Production of this enzyme in barley is hormonally regulated. Germinating barl
C:Function:
A:Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
A:Pathway: glycogen/starch degradation
C:Superfamily: wheat alpha-amylase; alpha-amylase core homology
C:Keywords: calcium binding; glycosidase; hydrolase; monomer; polysaccharide degradation
F:1-24/Domain: signal sequence #status predicted <SIG>
F:25-418/Product: alpha-amylase #status predicted <AMT>
F:171-316/Domain: alpha-amylase core homology <AMT>
F:204,229,313/Active site: Asp, Glu, Asp #status experimental

Query Match 85.7%; Score 48; DB 1; Length 438;
Best Local Similarity 80.0%; Pred. No. 0.95;
Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 VNMVNRKVG 10
DB 254 VNMVNRKVG 263

RESULT 4
ALBHB
alpha-amylase (EC 3.2.1.1) B precursor 6-4 - barley
N:Alternate names: 1,4-alpha-D-glucan glucanohydrolase; alpha-amylase 2
C:Species: Hordeum vulgare (barley)
C>Date: 30-Jun-1987 #sequence_revision 01-Sep-1995 #text_change 18-Jun-1999
C:Accession: A31960; A00847; J00405; A26267; A24457; A30759
R:Khurshheed, B.; Rogers, J.C.
J. Biol. Chem. 263: 18953-18960, 1988
A:Title: Barley alpha-amylase genes: Quantitative comparison of steady-state mRNA levels
A:Reference number: A82700; MIMD:89066691; PMID:3264283
A:Accession: A31960
A:Molecule type: DNA
A:Residues: 1-427 <KHO>
A:Cross-references: GB:J04202
A:Experimental source: cv. Himalaya; gene Amy6-4
R:Rogers, J.C. 260, 3731-3738, 1985
J. Biol. Chem. 260, 3731-3738, 1985
A:Title: Two barley alpha-amylase gene families are regulated differently in aleurone ce
A:Reference number: A00847; MIMD:85131184; PMID:3871776
A:Accession: A00847
A:Molecule type: mRNA
A:Residues: 1-133, 'D', 135-194, 'HRL', 198-424, 'Q', 426-427 <ROG>
A:Experimental source: seed
R:Rahmatullah, R.J.; Huang, J.K.; Clark, K.L.; Reeck, G.R.; Chandra, G.R.; Muthukrishnan
Plant Mol. Biol. 12, 119-121, 1989
A:Title: Nucleotide and predicted amino acid sequences of two different genes for high-P
A:Reference number: J00405
A:Accession: J00405
A:Molecule type: DNA
A:Residues: 1-133, 'D', 135-424, 'Q', 426-427 <RAH>
A:Cross-references: EMBL:X15226; NID:g18894; PIDN:CA33298.1; PID:g295804
A:Experimental source: gene Amy152
R:Chandler, P.M.; Zwar, J.A.; Jacobsen, J.V.; Higgins, T.J.V.; Inglis, A.S.
Plant Mol. Biol. 3, 407-418, 1984
A:Title: The effects of gibberellic acid and abscisic acid on alpha-amylase mRNA levels
A:Reference number: A26267
A:Accession: A26267
A:Molecule type: mRNA
A:Residues: 1-133, 'V', 135-184, 'A', 186-366, 'GA' <CHA>
A:Experimental source: cv. Himalaya
A:Note: the authors translated the codon GTC for residue 134 as Gly
R:Swenson, B.; Mundy, J.; Gibson, R.M.; Svendsen, I.
Carlsberg Res. Commun. 50, 15-22, 1985
A:Title: Partial amino acid sequences of alpha-amylase isozymes from barley malt.
A:Reference number: A24457
A:Accession: A24457
A:Molecule type: Protein
A:Residues: 25-59, 'X', 61-67, 'HX', 70-85, 'X', 87-92, 'E', 94, 146-165, 228-251, 297-303, 'X', 305-
C:Comment: The mRNA of this isozyme (B) is present at very low levels in unstimulated al

ed by the embryo during germination.
C:Genes:
A:Gene: Amy2-2
A:Map position: 6
A:Inserts: 29/3; 344/3
A:Note: multigene family on chromosome 6 encodes type B alpha-amylases; type A alpha-
C:Function:
A:Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
A:Pathway: glycogen/starch degradation
C:Superfamily: wheat alpha-amylase; alpha-amylase core homology
C:Keywords: aleurone cell; blocked amino end; calcium binding; germination; glycosida
F:1-24/Domain: signal sequence #status predicted <SIG>
F:25-427/Product: alpha-amylase #status predicted <AMT>
F:170-316/Domain: alpha-amylase core homology <AMT>
F:203,228,313/Active site: blocked amino end (Gln) (in mature form) (probably pyrrolidone ca
F:203,228,313/Active site: Asp, Glu, Asp #status predicted

Query Match 83.9%; Score 47; DB 1; Length 427;
Best Local Similarity 88.9%; Pred. No. 1.4;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 VNMVNRKVG 9
DB 253 VNMVNRKVG 261

RESULT 5
S07040
alpha-amylase (EC 3.2.1.1) 2 precursor (clone p155.3) - barley
C:Species: Hordeum vulgare (barley)
C>Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 22-Jun-1999
C:Accession: S07040
R:Knox, C.A.P.; Sonthayanon, B.; Chandra, G.R.; Muthukrishnan, S.
Plant Mol. Biol. 9, 3-17, 1987
A:Title: Structure and organization of two divergent alpha-amylase genes from barley
A:Reference number: S06275
A:Accession: S07040
A:Molecule type: DNA
A:Residues: 1-437 <KHO>
A:Cross-references: EMBL:M17127; NID:g166962; PIDN:AA32928.1; PID:g166983
C:Genes:
A:Gene: amy2
A:Map position: 1
A:Inserts: 29/3; 74/1; 345/3
C:Function:
A:Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
A:Pathway: glycogen/starch degradation
C:Superfamily: wheat alpha-amylase; alpha-amylase core homology
C:Keywords: glycosidase; hydrolase; polysaccharide degradation
F:170-317/Domain: alpha-amylase core homology <AMT>
F:203,228,314/Active site: Asp, Glu, Asp #status predicted

Query Match 83.9%; Score 47; DB 2; Length 437;
Best Local Similarity 88.9%; Pred. No. 1.4;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 VNMVNRKVG 9
DB 253 VNMVNRKVG 261

RESULT 6
S12625
alpha-amylase (EC 3.2.1.1) 3D - rice
C:Species: Oryza sativa (rice)
C>Date: 04-Dec-1992 #sequence_revision 04-Dec-1992 #text_change 22-Jun-1999
C:Accession: S12625; S12776; S15094; J00945
R:Huang, N.; Koizumi, N.; Reini, S.; Rodriguez, R.L.
Nucleic Acids Res. 18, 7007-7014, 1990
A:Title: Structural organization and differential expression of rice alpha-amylase ge
A:Reference number: J00945; MIMD:91088278; PMID:2263460
A:Accession: S12625
A:Molecule type: DNA

A:Residues: 1-435 <HUA>
 A:Cross-references: EMBL:M59351; NID:g169770; PIDN:AAA33895.1; PID:g169771
 R:O'Neill, S.D.; Kumagai, M.H.; Majumdar, A.; Huang, N.; Sutliff, T.D.; Rodriguez, R.L.
 Mol. Gen. Genet. 221, 235-244, 1990
 A:Title: The alpha-amylase genes in *Oryza sativa*: characterization of cDNA clones and mRNA
 A:Reference number: S12775; MUID:90318322; PMID:2370848
 A:Accession: S12776
 A:Molecule type: mRNA
 A:Residues: 1-435 <ONE>
 A:Cross-references: EMBL:M24287
 R:O'Neill, S.D.; Kumagai, M.H.; Majumdar, A.; Huang, N.; Sutliff, T.D.; Rodriguez, R.L.
 Submitted to the EMBL Data Library, April 1989
 A:Description: The alpha-amylase genes in *Oryza sativa*: Characterization of cDNA clones
 A:Reference number: S15054
 A:Accession: S15054
 A:Molecule type: mRNA
 A:Residues: 1-72, 'R', '75-136, 'R', '138-435 <ONZ>
 A:Cross-references: EMBL:M24287; NID:g169754; PIDN:AAA33886.1; PID:g169755
 A:Genetics: 30/3; 342/3
 A:Function:
 A:Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
 A:Pathway: glycogen/starch degradation
 C:Superfamily: wheat alpha-amylase; alpha-amylase core homology
 C:Keywords: glycosidase; hydrolase; polysaccharide degradation
 F:170-314/Domain: alpha-amylase core homology <AMY>
 F:203,228,311/Active site: Asp, Glu, Asp #status predicted

Query Match 82.1%; Score 46; DB 2; Length 435;
 Best Local Similarity 88.9%; Pred. No. 2.1;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 VNMVNVKVG 9
 Db 253 VNMVNVKVG 261

RESULT 7
 JC7137
 alpha-amylase (EC 3.2.1.1) isozyme I - rice
 N:Alternate names: 1,4-gulcan glucanohydrolase I
 C:Species: *Oryza sativa* (rice)
 C>Date: 04-Mar-2000 #sequence_revision 04-Mar-2000 #text_change 11-May-2000
 C:Accession: JC7137; PC7039
 R:Abd, R.; Yoshida, K.; Aoyagi, M.; Kasahara, S.; Ichishima, E.; Nakajima, T.
 Biosci. Biotechnol. Biochem. 63, 1329-1335, 1999
 A:Title: Characterization of chimeric enzymes constructed between two distinct alpha-amylase
 A:Reference number: JC7137; MUID:99430781; PMID:10500994
 A:Accession: JC7137
 A:Molecule type: mRNA
 A:Residues: 1-435 <ABE>
 A:Accession: PC7039
 A:Molecule type: protein
 A:Residues: 245-252 <AB2>
 C:Comment: This enzyme catalyzes the hydrolysis of internal alpha-glucosidic linkages in
 is important in germinating seeds and is present as multiple isoforms.
 C:Genetics:
 A:Gene: amy-1
 C:Superfamily: wheat alpha-amylase; alpha-amylase core homology
 C:Keywords: calcium binding; germination; glycosidase; hydrolase; seed

Query Match 82.1%; Score 46; DB 2; Length 435;
 Best Local Similarity 88.9%; Pred. No. 2.1;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 VNMVNVKVG 9
 Db 253 VNMVNVKVG 261

RESULT 8
 S10013
 alpha-amylase (EC 3.2.1.1) 1 precursor (clone lambda-O8g2) - rice

C:Species: *Oryza sativa* (rice)
 C>Date: 21-Nov-1993 #sequence_revision 17-Nov-1995 #text_change 22-Jun-1999
 C:Accession: S10013
 R:Huang, N.; Sutliff, T.D.; Lits, J.C.; Rodriguez, R.L.
 Plant Mol. Biol. 14, 655-668, 1990
 A:Title: Classification and characterization of the rice alpha-amylase multigene faml
 A:Reference number: S10013; MUID:91346657; PMID:2102847
 A:Accession: S10013
 A:Molecule type: DNA
 A:Residues: 1-428 <HUA>
 A:Cross-references: EMBL:X16509; NID:g20166; PIDN:CAA34516.1; PID:g20167
 A:Experimental source: var. M202
 C:Genetics: 30/3; 75/1; 345/3
 A:Function:
 A:Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
 A:Pathway: glycogen/starch degradation
 C:Superfamily: wheat alpha-amylase; alpha-amylase core homology
 C:Keywords: glycosidase; hydrolase; polysaccharide degradation
 F:170-317/Domain: alpha-amylase core homology <AMY>

Query Match 80.4%; Score 45; DB 2; Length 428;
 Best Local Similarity 70.0%; Pred. No. 3.1;
 Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

OY 1 VNMVNVKVG 10
 Db 253 VNMVNVKVG 262

RESULT 9
 S12775
 alpha-amylase (EC 3.2.1.1) precursor (clone POS103) - rice
 C:Species: *Oryza sativa* (rice)
 C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 22-Jun-1999
 C:Accession: S12775
 R:O'Neill, S.D.; Kumagai, M.H.; Majumdar, A.; Huang, N.; Sutliff, T.D.; Rodriguez, R.
 Mol. Gen. Genet. 221, 235-244, 1990
 A:Title: The alpha-amylase genes in *Oryza sativa*: characterization of cDNA clones and
 A:Reference number: S12775; MUID:90318322; PMID:2370848
 A:Accession: S12775
 A:Molecule type: mRNA
 A:Residues: 1-434 <ONE>
 A:Cross-references: EMBL:M24286; NID:g169752; PIDN:AAA33885.1; PID:g169753
 A:Function:
 A:Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
 A:Pathway: glycogen/starch degradation
 C:Superfamily: wheat alpha-amylase; alpha-amylase core homology
 C:Keywords: glycosidase; hydrolase; polysaccharide degradation
 F:176-323/Domain: alpha-amylase core homology <AMY>
 F:209,234,320/Active site: Asp, Glu, Asp #status predicted

Query Match 80.4%; Score 45; DB 2; Length 434;
 Best Local Similarity 70.0%; Pred. No. 3.2;
 Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

OY 1 VNMVNVKVG 10
 Db 259 VNMVNVKVG 268

RESULT 10
 S14958
 alpha-amylase (EC 3.2.1.1) - rice
 C:Species: *Oryza sativa* (rice)
 C>Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 22-Jun-1999
 C:Accession: S14958
 R:Sutliff, T.D.; Huang, N.; Lits, J.C.; Rodriguez, R.L.
 Plant Mol. Biol. 16, 579-591, 1991
 A:Title: Characterization of an alpha-amylase multigene cluster in rice.
 A:Reference number: S14958; MUID:91329692; PMID:1714518
 A:Accession: S14958
 A>Status: translation not shown

A:Molecule type: DNA
A:Residues: 1440 <SUT>
A:Cross-references: EMBL:X56336; NID:g20334; PIDN:CAA39776.1; PID:g20335
C:Genetics: 33/3; 78/1; 346/3
A:Introns:
C:Function:
A:Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
A:Pathway: glycogen/starch degradation
C:Superfamily: wheat alpha-amylase; alpha-amylase core homology
C:Keywords: glycosidase; hydrolase; polysaccharide degradation
F:174-318/Domain: alpha-amylase core homology <AMY>
F:207,232,315/Active site: Asp, Glu, Asp #status predicted

Query Match 75.0%; Score 42; DB 2; Length 440;
Best Local Similarity 77.8%; Pred. No. 11;
Matches 7; Conservative 1; Mismatches 0; Gaps 0;

OY 1 VMVNRKVG 9
DB 257 VMVNRKVG 265

RESULT 11
H64206
fructose-permease IIIC component frua homolog - Mycoplasma genitalium
C:Species: Mycoplasma genitalium
C:Date: 17-Nov-1995 #sequence_revision 17-Nov-1995 #text_change 21-Jul-2000
C:Accession H64206
R:Fraser, C.M.; Gocayne, J.D.; White, O.; Adams, M.D.; Clayton, R.A.; Fleischmann, R.D.; M.; Fuhmann, J.; Nguyen, D.; Uitterback, T.R.; Saudek, D.M.; Phillips, C.A.; Merrick, J.; Science 270, 397-403, 1995
A:Title: The minimal gene complement of Mycoplasma genitalium.
A:Reference number: A64200; MUID:95026346; PMID:756993
A:Accession: H64206
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-680 <TIGR>
A:Cross-references: GB:U09685; GB:LA3967; NID:93844658; PIDN:ACG1279.1; PID:91045736; T
A:Experimental source: strain G-37
C:Genetics:
A:Genetic code: SGC3
C:Superfamily: phosphotransferase system enzyme II, fructose-specific; phosphotransferas

Query Match 75.0%; Score 42; DB 2; Length 680;
Best Local Similarity 75.0%; Pred. No. 17;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 2 NMVNRKVG 9
DB 346 NMVNRKVG 353

RESULT 12
S69535
hypothetical protein 27 - phage HPI
C:Species: phage HPI
C:Date: 06-Dec-1996 #sequence_revision 13-Mar-1997 #text_change 08-Oct-1999
C:Accession: S69535
R:Esposito, D.; Fitzmaurice, W.P.; Benjamin, R.C.; Goodman, S.D.; Waldman, A.S.; Scoocca, Nucleic Acids Res. 24, 2360-2368, 1996
A:Title: The complete nucleotide sequence of bacteriophage HPI DNA.
A:Reference number: S69503; MUID:96279738; PMID:8710508
A:Accession: S69535
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-689 <ESP>
A:Cross-references: EMBL:U24159; NID:g1046235; PIDN:AAB09214.1; PID:g1046256
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, April 1995

Query Match 73.2%; Score 41; DB 2; Length 689;
Best Local Similarity 75.0%; Pred. No. 26;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 2 NMVNRKVG 9
DB 166 NMVNRKVG 173

RESULT 13
I36856
B18L protein - variola virus
N:Alternate names: B17L protein (COP)
C:Species: variola virus
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 23-Mar-2001
C:Accession: I36856; S46875
R:Blinov, V.M.
submitted to Genbank, November 1992
A:Reference number: A36859
A:Accession: I36856
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-340 <BLI>
A:Cross-references: GB:X69198; NID:9456758; PIDN:CAA49127.1; PID:9457077
A:Experimental source: strain India-1967, ssp. major, isolate Ind3
R:Koltyhalov, A.A.; Blinov, V.M.; Gytarov, V.V.; Pozdnyakov, S.G.; Chizhikov, V.E.; F. submitted to the EMBL Data Library April 1992
A:Description: Nucleotide sequence analysis of the region of Variola virus XhoI F O H
A:Reference number: S46868
A:Accession: S46875
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-340 <KOL>
A:Cross-references: EMBL:X67117; NID:9516428; PIDN:CAA47527.1; PID:9516436
A:Experimental source: strain India-1967, isolate Ind3
C:Superfamily: vaccinia virus probable 39.6k protein

Query Match 71.4%; Score 40; DB 2; Length 340;
Best Local Similarity 77.8%; Pred. No. 19;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 2 NMVNRKVG 10
DB 96 NMVNRKVG 104

RESULT 14
T28614
hypothetical protein B15L - variola major virus
C:Species: variola major virus
C:Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 21-Jul-2000
C:Accession: T28614
R:Massing, R.F.; Esposito, J.J.; Liu, L.I.; Qi, J.; Uitterback, T.R.; Knlyht, J.C.; Au Nature 366, 748-751, 1993
A:Title: Potential virulence determinants in terminal regions of variola smallpox vir
A:Reference number: Z20488; MUID:94088747; PMID:8264798
A:Accession: T28614
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-340 <MAS>
A:Cross-references: EMBL:L22579; NID:9623595; PIDN:AAA60924.1; PID:9439093
A:Experimental source: strain Bangladesh 1975
C:Superfamily: vaccinia virus probable 39.6k protein

Query Match 71.4%; Score 40; DB 2; Length 340;
Best Local Similarity 77.8%; Pred. No. 19;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 2 NMVNRKVG 10
DB 96 NMVNRKVG 104

RESULT 15
B72174
D7L protein - variola minor virus (strain Garcia-1966)

C:Species: variola minor virus
 C:Date: 24-Nov-1999 #sequence_revision 24-Nov-1999 #text_change 21-Jul-2000
 C:Accession: B72174
 R:Shchelkunov, S.N.; Tolmaren, A.V.; Gutorov, V.V.; Safonov, P.F.; Massung, R.F.; Lopat
 submitted to GenBank, March 1998
 A:Description: Analysis of the complete coding sequence of DNA of alastrim variola minor
 A:Reference number: A72150
 A:Accession: B72174
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-340 <SMC>
 A:Cross-references: GB:Y16780; NID:q5830555; PIDN:CAB54788.1; PID:q5830749
 A:Experimental source: strain garcia-1966
 C:Genetics:
 A:Gene: D7L
 C:Superfamily: vaccinia virus probable 39.6K protein

Query Match 71.4%; Score 40; DB 2; Length 340;
 Best Local Similarity 77.8%; Pred. No. 19;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 2 MNVNRKVGGS 10
 |||:||||
 Db 96 NMVSKVGDS 104

RESULT 16
 T37451
 probable 39.6K protein - vaccinia virus (strain Ankara)
 C:Species: vaccinia virus
 A:Variety: strain Ankara
 C:Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 20-Jun-2000
 C:Accession: T37451
 R:Antoine, G.; Scheiflinger, F.; Falkner, F.G.; Dornier, F.
 submitted to the EMBL data library, March 1997
 A:Description: The complete genomic sequence of the Modified Vaccinia Ankara (MVA) strain
 A:Reference number: Z20877
 A:Accession: T37451
 A:Status: preliminary; translated from GB/EMBL/DDBJ
 A:Molecule type: DNA
 A:Residues: 1-340 <ANT>
 A:Cross-references: EMBL:U94848; PIDN:AA96481.1
 A:Experimental source: strain Ankara
 C:Genetics:
 A:Note: MVA185L
 C:Superfamily: vaccinia virus probable 39.6K protein

Query Match 71.4%; Score 40; DB 2; Length 340;
 Best Local Similarity 77.8%; Pred. No. 19;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 2 MNVNRKVGGS 10
 |||:||||
 Db 96 NMVSKVGDS 104

RESULT 17
 B17L protein - vaccinia virus (strain Copenhagen)
 C:Species: vaccinia virus
 A:Note: host Homo sapiens (man)
 C:Date: 09-Nov-1990 #sequence_revision 09-Nov-1990 #text_change 21-Jul-2000
 C:Accession: G42527
 R:Johnson, G.P.
 submitted to GenBank, June 1990
 A:Reference number: A33172
 A:Accession: G42527
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-340 <JOH>
 C:Superfamily: vaccinia virus probable 39.6K protein

Query Match 71.4%; Score 40; DB 2; Length 340;

Best Local Similarity 77.8%; Pred. No. 19;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 2 MNVNRKVGGS 10
 |||:||||
 Db 96 NMVSKVGDS 104

RESULT 18
 JQ1810
 B16L protein - vaccinia virus (strain WR)
 C:Species: vaccinia virus
 C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jul-2000
 C:Accession: JQ1810
 R:Smith, G.L.; Chan, Y.S.; Howard, S.T.
 J. Gen. Virol. 72, 1349-1376, 1991
 A:Title: Nucleotide sequence of 42Kbp of vaccinia virus strain WR from near the right
 A:Reference number: JQ1767; MID:91259063; PMID:2045793
 A:Accession: JQ1810
 A:Molecule type: DNA
 A:Residues: 1-340 <SMI>
 A:Cross-references: DDBJ:D11079; NID:q222717; PIDN:BA01846.1; PID:q222761
 C:Superfamily: vaccinia virus probable 39.6K protein

Query Match 71.4%; Score 40; DB 2; Length 340;
 Best Local Similarity 77.8%; Pred. No. 19;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 2 MNVNRKVGGS 10
 |||:||||
 Db 96 NMVSKVGDS 104

RESULT 19
 JQ1527
 alpha-amylase (EC 3.2.1.1) 2A - rice
 C:Species: Oryza sativa (rice)
 C:Date: 17-Aug-1992 #sequence_revision 17-Aug-1992 #text_change 22-Jun-1999
 C:Accession: JQ1527
 R:Huang, N.; Rehl, S.J.; Rodriguez, R.L.
 Gene 111, 223-228, 1992
 A:Title: Rmy2A: a novel alpha-amylase-encoding gene in rice.
 A:Reference number: JQ1527; MID:92175526; PMID:1541400
 A:Accession: JQ1527
 A:Molecule type: DNA
 A:Residues: 1-443 <HUA>
 A:Cross-references: GB:M74177; NID:q169768; PIDN:AAA33894.1; PID:q169769
 C:Comment: Rice alpha-amylases are encoded by three multigene families, Amy1, Amy2
 C:Genetics:
 A:Gene: Rmy2A
 A:Introns: 27/3; 71/1; 345/3
 C:Function:
 A:Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
 A:Pathway: glycogen/starch degradation
 C:Superfamily: wheat alpha-amylase; alpha-amylase core homology
 C:Keywords: glycosidase; hydrolase; polysaccharide degradation
 F:168-317/Domain: alpha-amylase core homology <AMT>
 F:202,228,314/Active site: Asp, Glu, Asp #status predicted

Query Match 71.4%; Score 40; DB 2; Length 443;
 Best Local Similarity 60.0%; Pred. No. 25;
 Matches 6; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

OY 1 VMVNRKVGGS 10
 |:||||:
 Db 253 VDMVDRVGGT 262

RESULT 20
 S19990
 alpha-amylase (EC 3.2.1.1) - rice
 C:Species: Oryza sativa (rice)
 C:Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 22-Jun-1999

C:Accession: S19990
 R:Goldman, S.; Mawal, Y.; Wu, R.
 submitted to the EMBL Data Library, February 1992
 A:Reference number: S19990
 A:Accession: S19990
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-445 <GO>
 A:Cross-references: EMBL:X64619; NID:g20172; PIDN:CAAM5903.1; PID:g20173
 C:Function:
 A:Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
 A:Pathway: glycogen/starch degradation
 C:Superfamily: wheat alpha-amylase; alpha-amylase core homology
 C:Keywords: glycosidase; hydrolase; polysaccharide degradation
 F:168-317/Domain: alpha-amylase core homology <AMY>
 F:202,228,314/Active site: Asp, Glu, Asp #status predicted

Query Match 71.4%; Score 40; DB 2; Length 445;
 Best Local Similarity 60.0%; Pred. No. 25;
 Matches 6; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

OY 1 MNMNRKVGCS 10
 DB 253 VDMVDRVGGT 262
 ||:|||||

RESULT 21
 VCLJBT
 env polyprotein precursor - bovine immunodeficiency virus (isolate 127)
 N:Alternate names: coat polyprotein
 N:Contains: coat protein gp40; coat protein gp62
 C:Species: bovine immunodeficiency virus
 C:Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 31-Jan-1997
 C:Accession: E34742
 R:Garvey, K.J.; Oberste, M.S.; Elser, J.E.; Braun, M.J.; Gonda, M.A.
 Virology 175, 391-409, 1990
 A:Title: Nucleotide sequence and genome organization of biologically active proviruses C
 A:Reference number: A34742; MUID:90223985; PMID:2183467
 A:Accession: E34742
 A:Molecule type: genomic RNA
 A:Residues: 1-904 <GAR>
 A:Cross-references: GB:M32690
 C:Genetics:
 A:Gene: env
 C:Superfamily: HIV env polyprotein
 C:Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyprot
 F:1-13/Domain: signal sequence #status predicted <SIG>
 F:14-555/Product: coat protein gp62 #status predicted <GPI>
 F:556-904/Product: coat protein gp40 #status predicted <GPI>
 F:556-572/Domain: transmembrane #status predicted <TM1>
 F:729-747/Domain: transmembrane #status predicted <TM2>
 F:827-843/Domain: transmembrane #status predicted <TM3>
 F:131,235,277,296,329,367,376,385,410,427,432,452,491,509,541,597,663,694,877/Binding si

Query Match 71.4%; Score 40; DB 1; Length 904;
 Best Local Similarity 66.7%; Pred. No. 50;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 2 MNMNRKVGCS 10
 DB 788 MNMNRKIGES 796
 ||:|||||

RESULT 22
 thioedoxin homolog lmo1903 [imported] - Listeria monocytogenes (strain EGD-e)
 C:Species: Listeria monocytogenes
 C:Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 27-Nov-2001
 C:Accession: AG1312
 R:Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloec
 D.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurgey, O.; Entlian, K.D.; Fsihl, H.
 Science 294, 849-852, 2001
 A:Authors: Krefelt, J.; Kuhn, M.; Kunst, F.; Kurapkāt, G.; Madueno, E.; Maltournam, A.;

ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehla
 A:Title: Comparative genomics of Listeria species.
 A:Reference number: AB1077; MUID:21537279; PMID:11679669
 A:Accession: AG1312
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-157 <GLA>
 A:Cross-references: GB:NC_003210; PIDN:CAK39981.1; PID:g16411356; GSPDB:GN00177
 A:Experimental source: strain EGD-e
 C:Genetics:
 A:Gene: lmo1903

Query Match 69.6%; Score 39; DB 2; Length 157;
 Best Local Similarity 75.0%; Pred. No. 13;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 2 MNMNRKVG 9
 DB 146 MNMNRKVS 153
 ||:|||||

RESULT 23
 AG1684
 thioedoxin homolog lln2017 [imported] - Listeria innocua (strain Clp11262)
 C:Species: Listeria innocua
 C:Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 27-Nov-2001
 C:Accession: AG1684
 R:Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloec
 D.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurgey, O.; Entlian, K.D.; Fsihl,
 D.; Jones, L.M.; Karst, U.
 Science 294, 849-852, 2001
 A:Authors: Krefelt, J.; Kuhn, M.; Kunst, F.; Kurapkāt, G.; Madueno, E.; Maltournam, A.;
 ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehla
 A:Title: Comparative genomics of Listeria species.
 A:Reference number: AB1077; MUID:21537279; PMID:11679669
 A:Accession: AG1684
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-157 <GLA>
 A:Cross-references: GB:AL592022; PIDN:CAK97247.1; PID:g16414518; GSPDB:GN00178
 A:Experimental source: strain Clp11262
 C:Genetics:
 A:Gene: lln2017

Query Match 69.6%; Score 39; DB 2; Length 157;
 Best Local Similarity 75.0%; Pred. No. 13;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 2 MNMNRKVG 9
 DB 146 MNMNRKVS 153
 ||:|||||

RESULT 24
 H72668
 hypothetical protein APE0774 - Aeropyrum pernix (strain K1)
 C:Species: Aeropyrum pernix
 C:Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jun-2000
 C:Accession: H72668
 R:Kawarabayashi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Halkawa, Y.; Jin-no, K.; Ta
 awa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J
 DNA Res. 6, 83-101, 1999
 A:Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aero
 A:Reference number: A72450; MUID:99310339; PMID:10382966
 A:Accession: H72668
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-397 <RAW>
 A:Cross-references: DDBJ:AP000060; NID:g5104188; PIDN:BAW79752.1; PID:d1043538; PID:g
 A:Experimental source: strain K1
 C:Genetics:
 A:Gene: APE0774
 C:Superfamily: Aeropyrum pernix hypothetical protein APE0774

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Query Match          69.6%; Score 39; DB 2; Length 397;
Best Local Similarity 55.6%; Pred. No. 33;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 1 VNMVKNKVG 9
Db 167 LNMVRRIGG 175

RESULT 25
AF1231
alpha,alpha-phosphotrehalase homolog lmo1254 [imported] - Listeria monocytogenes (strain
C:Species: Listeria monocytogenes
C>Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 14-Dec-2001
C:Accession: AF1231
R:Glaser, P.; Frangenul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloeker
; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihl, H
D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A:Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkai, G.; Madueno, E.; Maitouram, A.; Ma
ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehlant,
A:Title: Comparative genomics of Listeria species.
A:Reference number: AB1077; MUID:21537279; PMID:11679669
A:Accession: AF1231
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-548 <GLA>
A:Cross-references: GB:NC_003210; PIDN:CAC99332.1; PID:g16410670; GSPDB:GN00177
A:Experimental source: strain EGD-e
C:Genetics:
A:Gene: lmo1254
C:Superfamily: alpha-glucosidase; alpha-amylase core homology

Query Match          69.6%; Score 39; DB 2; Length 548;
Best Local Similarity 66.7%; Pred. No. 46;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 2 NMVKNKVG 10
Db 137 NMVSKFGGN 145

RESULT 26
S17828
nuclease S1 - Penicillium citrinum
C:Species: Penicillium citrinum
C>Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jun-2000
C:Accession: S17828
R:Maekawa, K.; Tsunasawa, S.; Dibo, G.; Sakiyama, F.
Eur. J. Biochem. 200, 651-661, 1991
A:Title: Primary structure of nuclease P1 from Penicillium citrinum.
A:Reference number: S17828; MUID:92007841; PMID:1915339
A:Accession: S17828
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-270 <MAE>
C:Superfamily: Penicillium citrinum nuclease S1

Query Match          67.9%; Score 38; DB 2; Length 270;
Best Local Similarity 55.6%; Pred. No. 34;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 2 NMVKNKVG 10
Db 258 NMINEIHGS 266

RESULT 27
JE0408
3-nucleotidase (EC 3.1.3.6) PA3 - Penicillium sp.
N:Alternate names: nuclease PA3
C:Species: Penicillium sp.

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C>Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 20-Jun-2000
C:Accession: JE0408; PS0155
R:Tabata, N.; Kazama, H.; Ohgi, K.; Irie, M.
Agric. Biol. Chem. 55, 461-469, 1991
A:Title: Primary structure of a nuclease (nuclease PA3) from a Penicillium sp.
A:Reference number: JE0408; MUID:91299282; PMID:1369324
A:Accession: JE0408
A:Molecule type: protein
A:Residues: 1-270 <TAB>
C:Superfamily: Penicillium citrinum nuclease S1
C:Keywords: glycoprotein; phosphoric monoester hydrolase; zinc
F;92,118,184,197/Binding site: carbohydrate (asn) (covalent) #status experimental

Query Match          67.9%; Score 38; DB 2; Length 270;
Best Local Similarity 55.6%; Pred. No. 34;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 2 NMVKNKVG 10
Db 258 NMINEIHGS 266

RESULT 28
AI0930
probable LysR-family transcription regulatory protein SRY3708 [imported] - Salmonella
C:Species: Salmonella enterica subsp. enterica serovar Typh
A:Note: this species has also been called Salmonella typhi
C>Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
C:Accession: AI0930
R:Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Church
th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farr
, S.; Mule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A:Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens,
A:Title: Complete genome sequence of a multiple drug resistant Salmonella enterica se
A:Reference number: AB0502; MUID:21534947; PMID:11677608
A:Accession: AI0930
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-278 <PAR>
A:Cross-references: GB:AL513382; PIDN:CAD09467.1; PID:g16504584; GSPDB:GN00176
C:Genetics:
A:Gene: SRY3708

Query Match          67.9%; Score 38; DB 2; Length 278;
Best Local Similarity 66.7%; Pred. No. 35;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 VNMVKNKVG 9
Db 230 VNMANKKG 238

RESULT 29
S10514
alpha-amylase (EC 3.2.1.1) precursor - black gram
C:Species: Vigna mungo (black gram)
C>Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 22-Jun-1999
C:Accession: S10514; S61336; S40201; S61334
R:Yamauchi, D.; Minamikawa, T.
Nucleic Acids Res. 18, 4250, 1990
A:Title: Nucleotide sequence of cDNA for alpha-amylase from cotyledons of germinating
A:Reference number: S10514; MUID:90332425; PMID:2377468
A:Accession: S10514
A:Molecule type: mRNA
A:Residues: 1-421 <YAM>
A:Cross-references: EMBL:X53049; NID:g22059; PIDN:CAA37217.1; PID:g22060
A:Accession: S61336
A:Molecule type: protein
A:Residues: 24-31 <YAM>
R:Takeuchi, H.; Yamauchi, D.; Wada, S.; Minamikawa, T.
submitted to the EMBL Data Library, June 1993
A:Description: Nucleotide sequence of the alpha-amylase gene from Vigna mungo.

```

A:Reference number: S40201
 A:Accession: S40201
 A:Molecule type: DNA
 A:Residues: 1-421 <TAK>
 A:Cross-references: EMBL:X73301; NID:g437944; PIDD:CAA51734.1; PID:g437945
 C:Genetics:
 A:Introns: 28/3; 72/1; 340/3
 C:Function:
 A:Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
 A:Pathway: glycogen/starch degradation
 C:Superfamily: wheat alpha-amylase; alpha-amylase core homology
 C:Keywords: glycosidase; hydrolase; polysaccharide degradation; seed
 F:1-23/domain: signal sequence #status predicted <Sig>
 F:24-421/Product: alpha-amylase #status experimental <MAT>
 F:168-312/domain: alpha-amylase core homology <AMY>
 F:201,226,309/Active site: Asp, Glu, Asp #status predicted

Query Match 67.9%; Score 38; DB 2; Length 421;
 Best Local Similarity 60.0%; Pred. No. 53;
 Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 1 VNMVKNKVGGS 10
 ||||| ||:
 DB 251 VNMVESAGGA 260

RESULT 30
 AD2161
 alkaline phosphatase [imported] - Nostoc sp. (strain PCC 7120)
 C:Species: Nostoc sp. PCC 7120
 A:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
 C:Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002
 C:Accession: AD2161
 R:Kaneko, T.; Nakamura, Y.; Wolk, C. P.; Kurlitz, T.; Sasamoto, S.; Watanabe, A.; Iriyuchi, Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S
 DNA Res. 8, 205-213, 2001
 A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anabaena
 A:Reference number: AB1807; WUID:21595285; PMID:11759840
 A:Accession: AD2161
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-627 <KUR>
 A:Cross-references: GB:BA000019; PIDD:BA874542.1; PID:g17131937; GSPDB:GN00179
 A:Experimental source: strain PCC 7120
 C:Genetics:
 A:Gene: al12843

Query Match 67.9%; Score 38; DB 2; Length 627;
 Best Local Similarity 55.6%; Pred. No. 79;
 Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 1 VNMVKNKVGGS 9
 ::::| | | |
 DB 486 ISMINKNGC 494

Search completed: August 29, 2003, 18:48:31
 Job time : 12.2857 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 29, 2003, 18:39:11 ; Search time 6.57143 Seconds

(without alignments)

71.562 Million cell updates/sec

Title: US-09-830-876-3

Perfect score: 56

Sequence: 1 VNMWNVGGS 10

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database: SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Query Length	DB ID	Description
1	56	100.0	429	1	AMV6_HORVU
2	49	87.5	383	1	AMC1_ORRSA
3	48	85.7	438	1	AMV1_HORVU
4	47	83.9	368	1	AMV3_HORVU
5	47	83.9	427	1	AMV3_HORVU
6	46	82.1	435	1	AMV3_ORRSA
7	45	80.4	428	1	AMV3_ORRSA
8	42	75.0	440	1	AMV3_ORRSA
9	42	75.0	680	1	AMV3_ORRSA
10	41	73.2	273	1	AROE_BUCAP
11	41	73.2	689	1	Y027_BPHH1
12	40	71.4	340	1	VB17_VACCV
13	40	71.4	340	1	VB17_VACCV
14	40	71.4	443	1	VB17_VACCV
15	40	71.4	443	1	AMV2_ORRSA
16	40	71.4	445	1	AMV2_ORRSA
17	40	71.4	875	1	ENV_BIV27
18	40	71.4	904	1	ENV_BIV27
19	38	67.9	270	1	NUP3_PENCI
20	38	67.9	278	1	NUP3_PENCI
21	38	67.9	278	1	NUP3_PENCI
22	38	67.9	278	1	NUP3_PENCI
23	38	67.9	278	1	NUP3_PENCI
24	38	67.9	278	1	NUP3_PENCI
25	37	66.1	417	1	RPOB_SINAF
26	37	66.1	417	1	RPOB_SINAF
27	37	66.1	417	1	RPOB_SINAF
28	36	64.3	321	1	YECF_HABIN
29	36	64.3	437	1	AMV3_ORRSA
30	36	64.3	438	1	AMV3_ORRSA
31	36	64.3	561	1	TREC_BACSU
32	36	64.3	969	1	SECA_CHLTR
33	36	64.3	1070	1	RPOB_LOTVA

34	36	64.3	1070	1	RPOB_TOBAC	P06271 nicotiana t
35	36	64.3	1072	1	RPOB_OENHO	P06271 nicotiana t
36	36	64.3	2618	1	SPCA_HUMAN	P02549 homo sapien
37	35	62.5	264	1	MUR1_STR35	P08377 streptococc
38	35	62.5	264	1	MUR1_STR35	P08377 streptococc
39	35	62.5	367	1	SERC_YEAST	P40073 saccharomyc
40	35	62.5	373	1	SERC_YEAST	P59492 buchnera ap
41	35	62.5	413	1	AMV3_HORVU	P08117 triticum ae
42	35	62.5	440	1	TREB_ECOLI	P17164 bacillus th
43	35	62.5	551	1	TREB_ECOLI	P28904 escherichia
44	35	62.5	569	1	TREB_ECOLI	P28904 escherichia
45	35	62.5	627	1	PLST_MOUSE	P13796 homo sapien
46	35	62.5	627	1	PLST_MOUSE	P13796 homo sapien
47	35	62.5	627	1	PLST_MOUSE	P13796 homo sapien
48	35	62.5	627	1	PLST_MOUSE	P13796 homo sapien
49	35	62.5	627	1	PLST_MOUSE	P13796 homo sapien
50	35	62.5	629	1	PLST_MOUSE	P13796 homo sapien
51	35	62.5	630	1	PLST_MOUSE	P13796 homo sapien
52	35	62.5	769	1	TEF1_FELCA	P19179 gallus gall
53	35	62.5	770	1	TEF1_FELCA	P19179 gallus gall
54	35	62.5	809	1	TEF1_FELCA	P19179 gallus gall
55	35	62.5	891	1	TEF1_FELCA	P19179 gallus gall
56	35	62.5	938	1	TEF1_FELCA	P19179 gallus gall
57	35	62.5	968	1	TEF1_FELCA	P19179 gallus gall
58	34	60.7	122	1	HY3A_HUMAN	P01762 homo sapien
59	34	60.7	126	1	HY3A_HUMAN	P01762 homo sapien
60	34	60.7	199	1	IL11_HUMAN	P20809 homo sapien
61	34	60.7	240	1	IL11_HUMAN	P20809 homo sapien
62	34	60.7	365	1	C713_SOLME	P37119 solanum mel
63	34	60.7	448	1	C713_SOLME	P37119 solanum mel
64	34	60.7	507	1	C713_SOLME	P37119 solanum mel
65	34	60.7	507	1	C713_SOLME	P37119 solanum mel
66	34	60.7	507	1	C713_SOLME	P37119 solanum mel
67	34	60.7	507	1	C713_SOLME	P37119 solanum mel
68	34	60.7	507	1	C713_SOLME	P37119 solanum mel
69	34	60.7	507	1	C713_SOLME	P37119 solanum mel
70	34	60.7	507	1	C713_SOLME	P37119 solanum mel
71	34	60.7	507	1	C713_SOLME	P37119 solanum mel
72	34	60.7	507	1	C713_SOLME	P37119 solanum mel
73	34	60.7	507	1	C713_SOLME	P37119 solanum mel
74	34	60.7	507	1	C713_SOLME	P37119 solanum mel
75	34	60.7	507	1	C713_SOLME	P37119 solanum mel
76	34	60.7	507	1	C713_SOLME	P37119 solanum mel
77	34	60.7	507	1	C713_SOLME	P37119 solanum mel
78	34	60.7	507	1	C713_SOLME	P37119 solanum mel
79	34	60.7	507	1	C713_SOLME	P37119 solanum mel
80	34	60.7	507	1	C713_SOLME	P37119 solanum mel
81	34	60.7	507	1	C713_SOLME	P37119 solanum mel
82	34	60.7	507	1	C713_SOLME	P37119 solanum mel
83	34	60.7	507	1	C713_SOLME	P37119 solanum mel
84	34	60.7	507	1	C713_SOLME	P37119 solanum mel
85	34	60.7	507	1	C713_SOLME	P37119 solanum mel
86	34	60.7	507	1	C713_SOLME	P37119 solanum mel
87	34	60.7	507	1	C713_SOLME	P37119 solanum mel
88	34	60.7	507	1	C713_SOLME	P37119 solanum mel
89	34	60.7	507	1	C713_SOLME	P37119 solanum mel
90	34	60.7	507	1	C713_SOLME	P37119 solanum mel
91	34	60.7	507	1	C713_SOLME	P37119 solanum mel
92	34	60.7	507	1	C713_SOLME	P37119 solanum mel
93	34	60.7	507	1	C713_SOLME	P37119 solanum mel
94	34	60.7	507	1	C713_SOLME	P37119 solanum mel
95	34	60.7	507	1	C713_SOLME	P37119 solanum mel
96	34	60.7	507	1	C713_SOLME	P37119 solanum mel
97	34	60.7	507	1	C713_SOLME	P37119 solanum mel
98	34	60.7	507	1	C713_SOLME	P37119 solanum mel
99	34	60.7	507	1	C713_SOLME	P37119 solanum mel
100	34	60.7	507	1	C713_SOLME	P37119 solanum mel

ALIGNMENTS

AMT6_HORVU STANDARD; PRT; 429 AA.
 ID AMT6_HORVU
 AC P04750;
 DT 13-AUG-1987 (Rel. 05, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE Alpha-amylase type B isozyme precursor (EC 3.2.1.1) (1,4-alpha-D-glucan glucanohydrolase) (Clones GRAM56 and 963).
 GN AMY1.6.
 OS Hordeum vulgare (Barley).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae; OC Triticeae; Hordeum.
 NC NCBL_TaxID=4513;
 RN [1]
 RP SEQUENCE FROM N.A. (CLONE GRAM56).
 RA Rahmatullah R.J., Huang J.-K., Clark K.L., Reek G.R.,
 RT Chandra G.R., Muthukrishnan S.;
 RT "Nucleotide and predicted amino acid sequences of two different genes for high-pi alpha-amylases from barley.";
 RL Plant Mol. Biol. 12:119-121(1989).
 RN [2]
 RP SEQUENCE OF 380-429 FROM N.A. (CLONE 963).
 RX MEDLINE=65159405; PubMed=6335720;
 RA Huang J.-K., Swegle M., Dandekar A.M., Muthukrishnan S.;
 RT "Expression and regulation of alpha-amylase gene family in barley aleurones.";
 RL J. Mol. Appl. Genet. 2:579-588(1984).
 CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic linkages in oligosaccharides and polysaccharides.
 CC -1- COFACTOR: BINDS A CALCIUM ION REQUIRED FOR ITS ACTIVITY.
 CC -1- DEVELOPMENTAL STAGE: PRODUCTION OF ALPHA-AMYLASE IS HORMONALLY REGULATED. GERMINATING EMBRYOS PRODUCE THE HORMONE GIBBERELIC ACID, WHICH WITHIN 10 HOURS STIMULATES THE ALEURONE CELLS COVERING THE ENDOSPERM OF THE SEED TO PRODUCE ALPHA-AMYLASE. THE ENZYME THEN DEGRADES THE STARCH WITHIN THE ENDOSPERM FOR USE BY THE DEVELOPING PLANT EMBRYO.
 CC -1- MISCELLANEOUS: THERE ARE AT LEAST 4 TYPES OF ALPHA-AMYLASE IN BARLEY.
 CC -1- MISCELLANEOUS: TYPE B ISOZYME MRNA IS UNDETECTABLE IN UNSTIMULATED CELLS AND INCREASES A HUNDRED-FOLD AFTER STIMULATION WITH GIBBERELIC ACID.
 CC -1- SIMILARITY: BELONGS TO FAMILY 13 OF GLYCOSYL HYDROLASES, ALSO KNOWN AS THE ALPHA-AMYLASE FAMILY.
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 CC EMBL: X15227; CA3329.1; -
 CC EMBL: K02636; AA32932.1; -
 CC PIR: JE0406; J0406.
 CC HSSP: P04063; IAVA.
 CC InterPro: IPR006589; Alp_amy1_cat_sub.
 CC InterPro: IPR006047; Alpha_amy1_cat.
 CC Pfam: PF00128; alpha-amylase: 1.
 CC SMART: SM00642; Amyy: 1.
 CC Hydrolyase; Glycosidase; Carbohydrate metabolism; Seed; Germination;
 CC Calcium; Multigene family; Signal.
 CC SIGNAL
 CC CHAIN 25 429 ALPHA-AMYLASE TYPE B ISOZYME.
 CC ACT_SITE 205 205 BY SIMILARITY.
 CC ACT_SITE 315 315 BY SIMILARITY.
 CC SEQUENCE 429 AA; 47937 MW; 1C924CA631905262 CRC64;

Query Match 100.0%; Score 56; DB 1; Length 429;
 Best Local Similarity 100.0%; Pred. No. 0.014;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VNMVKNVGG3 10
 DB 255 VNMVKNVGG3 264

RESULT 2
 AMCL_ORYSA STANDARD; PRT; 383 AA.
 ID AMCL_ORYSA
 AC P27940;
 DT 01-AUG-1992 (Rel. 23, Created)
 DT 01-AUG-1992 (Rel. 23, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE Alpha-amylase isozyme C precursor (EC 3.2.1.1) (1,4-alpha-D-glucan glucanohydrolase) (Isozyme 1B).
 GN Oryza sativa (Rice).
 OS Oryza sativa (Rice).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; OC Eriarthoidae; Oryzaceae; Oryza.
 NC NCBL_TaxID=4530;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Indica-IR26; TISSUE=Leaf;
 RX MEDLINE=92119260; PubMed=1731997;
 RA Kim J.-K., Wu R.;
 RT "Nucleotide sequence of a high-pi rice (Oryza sativa) -amylase gene.";
 RL Plant Mol. Biol. 18:399-402(1992).
 RN [2]
 RP SEQUENCE OF 1-50 FROM N.A.
 RC STRAIN=cv. Japonica M202; TISSUE=Etiolated leaf;
 RX MEDLINE=91088278; PubMed=2263460;
 RA Huang N., Koizumi N., Reini S., Rodriguez R.L.;
 RT "Structural organization and differential expression of rice alpha-amylase genes.";
 RL Nucleic Acids Res. 18:7007-7014(1990).
 CC -1- FUNCTION: IMPORTANT FOR BREAKDOWN OF ENDOSPERM STARCH DURING GERMINATION.
 CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic linkages in oligosaccharides and polysaccharides.
 CC -1- COFACTOR: BINDS A CALCIUM ION REQUIRED FOR ITS ACTIVITY.
 CC -1- SUBUNIT: Monomer.
 CC -1- TISSUE SPECIFICITY: IN CALLUS, WEAKLY EXPRESSED.
 CC -1- DEVELOPMENTAL STAGE: EXPRESSED AT A HIGH LEVEL DURING GERMINATION IN THE ALEURONE CELLS UNDER THE CONTROL OF THE PLANT HORMONE GIBBERELIC ACID AND IN THE DEVELOPING GRAINS AT A LOW LEVEL.
 CC -1- SIMILARITY: BELONGS TO FAMILY 13 OF GLYCOSYL HYDROLASES, ALSO KNOWN AS THE ALPHA-AMYLASE FAMILY.
 CC CAUTION: ALL THE CATALYTIC RESIDUES ARE HIDDEN BY WHAT SEEMS TO BE FRAMESHIFT ERRORS FROM THE ORIGINAL NUCLEOTIDE REFERENCE.
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 CC EMBL: X52240; CA36485.1; -
 CC EMBL: M59350; AA33893.1; -
 CC PIR: S19142; ALRZOC.
 CC HSSP: P04063; IAVA.
 CC Gramene: P27940;
 CC Hydrolyase; Glycosidase; Carbohydrate metabolism; Calcium; Signal;
 CC Multigene family.
 CC SIGNAL
 CC CHAIN 1 31 POTENTIAL.
 CC ACT_SITE 32 383 ALPHA-AMYLASE ISOZYME C.
 CC SEQUENCE 383 AA; 43254 MW; 7426B9BE7C411B54 CRC64;

Query Match 87.5%; Score 49; DB 1; Length 383;
 Best Local Similarity 88.9%; Pred. No. 0.22;
 Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 VNMVKNVGG 9
 DB 226 VNMVKNVGG 234

RESULT 3
 ID AMY1_HORVU STANDARD; PRT; 438 AA.
 AC P00693;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Alpha-amylase type A isozyme precursor (EC 3.2.1.1) (1,4-alpha-D-glucan glucoamylase) (AMY1) (low pI alpha-amylase).
 GN AMY1.1.
 OS Hordeum vulgare (Barley).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae; Triticeae; Hordeum.
 CC NCBI_TaxID=4513;
 RX MEDLINE=61338423; PubMed=6190808;
 RA Rogers J.C., Millman C.;
 RT "Isolation and sequence analysis of a barley alpha-amylase cDNA clone."
 RL J. Biol. Chem. 258:8169-8174(1983).
 CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic linkages in oligosaccharides and polysaccharides.
 CC -1- COFACTOR: BINDS A CALCIUM ION REQUIRED FOR ITS ACTIVITY.
 CC -1- SUBCELLULAR LOCATION: Extracellular.
 CC -1- DEVELOPMENTAL STAGE: PRODUCTION OF ALPHA-AMYLASE IS HORMONALLY REGULATED. GERMINATING EMBRYOS PRODUCE THE HORMONE GIBBERELLIC ACID, WHICH WITHIN 10 HOURS STIMULATES THE ALEURONE CELLS COVERING THE ENDOSPERM OF THE SEED TO PRODUCE ALPHA-AMYLASE. THE ENZYME THEN DEGRADES THE STARCH WITHIN THE ENDOSPERM FOR USE BY THE DEVELOPING PLANT EMBRYO.
 CC -1- MISCELLANEOUS: THERE ARE AT LEAST 4 TYPES OF ALPHA-AMYLASE IN BARLEY.
 CC -1- SIMILARITY: BELONGS TO FAMILY 13 OF GLYCOSYL HYDROLASES, ALSO KNOWN AS THE ALPHA-AMYLASE FAMILY.
 CC -----
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 CC -----
 DR EMBL: J01236; AAA32929.1; -.
 DR PTR: A00846; ALBH.
 DR HSSP: P04063; IAVA.
 DR InterPro: IPR006589; Alp_amy1_cat_sub.
 DR InterPro: IPR006047; Alpha_amy1_cat.
 DR Pfam: PF00128; alpha-amylase; 1.
 DR SMART: SM00642; Amy; 1.
 KW Hydrolyase; Glycosidase; Carbohydrate metabolism; Seed; Germination;
 KW Calcium; Multigene family; Signal.
 FT SIGNAL 1 24
 FT CHAIN 25 438 ALPHA-AMYLASE TYPE A ISOZYME.
 FT ACT_SITE 204 204 BY SIMILARITY.
 FT ACT_SITE 229 229 BY SIMILARITY.
 FT ACT_SITE 315 315 BY SIMILARITY.
 SO SEQUENCE 438 AA; 47796 MW; 2393FDC5180F51 CRC64;

Query Match 85.7%; Score 48; DB 1; Length 438;
 Best Local Similarity 80.0%; Pred. No. 0.38;
 Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 1 VNMVKNVGG 10
 |||||:||||

DB 254 VNMVKNVGG 263

RESULT 4
 ID AMY3_HORVU STANDARD; PRT; 368 AA.
 AC P04747;
 DT 13-AUG-1987 (Rel. 05, Created)
 DT 13-AUG-1987 (Rel. 05, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Alpha-amylase type B isozyme precursor (EC 3.2.1.1) (1,4-alpha-D-glucan glucoamylase) (Clone PHV19) (Fragment).
 GN AMY1.3.
 OS Hordeum vulgare (Barley).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae; Triticeae; Hordeum.
 CC NCBI_TaxID=4513;
 RX MEDLINE=61338423; PubMed=6190808;
 RA Rogers J.C., Millman C.;
 RT "The effects of gibberellin acid and abscisic acid on alpha amylase mRNA levels in barley aleurone layers studies using an alpha amylase cDNA clone."
 RL Plant Mol. Biol. 3:407-418(1984).
 CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic linkages in oligosaccharides and polysaccharides.
 CC -1- COFACTOR: BINDS A CALCIUM ION REQUIRED FOR ITS ACTIVITY.
 CC -1- DEVELOPMENTAL STAGE: PRODUCTION OF ALPHA-AMYLASE IS HORMONALLY REGULATED. GERMINATING EMBRYOS PRODUCE THE HORMONE GIBBERELLIC ACID, WHICH WITHIN 10 HOURS STIMULATES THE ALEURONE CELLS COVERING THE ENDOSPERM OF THE SEED TO PRODUCE ALPHA-AMYLASE. THE ENZYME THEN DEGRADES THE STARCH WITHIN THE ENDOSPERM FOR USE BY THE DEVELOPING PLANT EMBRYO.
 CC -1- MISCELLANEOUS: THERE ARE AT LEAST 4 TYPES OF ALPHA-AMYLASE IN BARLEY.
 CC -1- MISCELLANEOUS: TYPE B ISOZYME mRNA IS UNDETECTABLE IN UNSTIMULATED CELLS AND INCREASES A HUNDRED-FOLD AFTER STIMULATION WITH GIBBERELLIC ACID.
 CC -1- SIMILARITY: BELONGS TO FAMILY 13 OF GLYCOSYL HYDROLASES, ALSO KNOWN AS THE ALPHA-AMYLASE FAMILY.
 CC -----
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 CC -----
 DR EMBL: K02638; AAA2933.1; -.
 DR HSSP: P04063; IAVA.
 DR InterPro: IPR006589; Alp_amy1_cat_sub.
 DR InterPro: IPR006047; Alpha_amy1_cat.
 DR Pfam: PF00128; alpha-amylase; 1.
 DR SMART: SM00642; Amy; 1.
 KW Hydrolyase; Glycosidase; Carbohydrate metabolism; Seed; Germination;
 KW Calcium; Multigene family; Signal.
 FT SIGNAL 1 24
 FT CHAIN 25 >368 ALPHA-AMYLASE TYPE B ISOZYME.
 FT ACT_SITE 203 203 BY SIMILARITY.
 FT ACT_SITE 228 228 BY SIMILARITY.
 FT ACT_SITE 313 313 BY SIMILARITY.
 FT NON_TER 368 368
 SO SEQUENCE 368 AA; 40787 MW; A237FE55793BA93B CRC64;

Query Match 83.9%; Score 47; DB 1; Length 368;
 Best Local Similarity 88.9%; Pred. No. 0.49;
 Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 1 VNMVKNVGG 9
 |||||:||||
 DB 253 VNMVKNVGG 261

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RESULT 5
ID AMY2_HORVU STANDARD; PRT; 427 AA.
AC P04063;
DT 01-NOV-1986 (Rel. 03, Created)
DT 15-JUN-1998 (Rel. 36, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Alpha-amylase type B isozyme precursor (EC 3.2.1.1) (1,4-alpha-D-
  glucan glucanohydrolase) (AMY2-2) (High pi alpha-amylase).
GN AMY1.2.
OS Hordeum vulgare (Barley).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
  Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
  OC Triticeae; Hordeum.
  OC NCBI_TaxID=4513;
  RN [1]
  RP SEQUENCE FROM N.A.
  RA Rahmatullah R.J., Huang J.K., Clark K.L., Reek G.R.,
  RA Chandra G.R., Muthukrishnan S.;
  RT "Nucleotide and predicted amino acid sequences of two different genes
  RT for high-pi alpha-amylases from barley.";
  RL Plant Mol. Biol. 12:119-121(1989).
  RN [2]
  RP SEQUENCE FROM N.A.
  RX MEDLINE=85131184; PubMed=3871776;
  RA Rogers J.C.;
  RT "Two barley alpha-amylase gene families are regulated differently in
  RT aleurone cells.";
  RL J. Biol. Chem. 260:3731-3738(1985).
  RN [3]
  RP X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS).
  RX MEDLINE=94234083; PubMed=8196040;
  RA Kadziola A., Abe J.-I., Svensson B., Haser R.;
  RT "Crystal and molecular structure of barley alpha-amylase.";
  RL J. Mol. Biol. 239:104-121(1994).
  RN [4]
  RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS) OF COMPLEX WITH BASI.
  RC STRAIN=cv. Mennet;
  RX MEDLINE=98298441; PubMed=9634702;
  RA Vallee F., Kadziola A., Bourne Y., Juy M., Rodenburg K.W.,
  RA Svensson B., Haser R.;
  RT "Barley alpha-amylase bound to its endogenous protein inhibitor BASI:
  RT crystal structure of the complex at 1.9-A resolution.";
  RL Structure 6:649-659(1998).
  CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic
  CC linkages in oligosaccharides and polysaccharides.
  CC -1- COFACTOR: BINDS A CALCIUM ION REQUIRED FOR ITS ACTIVITY.
  CC -1- DEVELOPMENTAL STAGE: PRODUCTION OF ALPHA-AMYLASE IS NORMALLY
  CC REGULATED. GERMINATING EMBRYOS PRODUCE THE HORMONE GIBBERELIC
  CC ACID, WHICH WITHIN 10 HOURS STIMULATES THE ALEURONE CELLS COVERING
  CC THE ENDOSPERM OF THE SEED TO PRODUCE ALPHA-AMYLASE. THE ENZYME
  CC THEN DEGRADES THE STARCH WITHIN THE ENDOSPERM FOR USE BY THE
  CC DEVELOPING PLANT EMBRYO.
  CC -1- INDUCTION: TYPE B ISOZYME MRNA IS UNDETECTABLE IN UNSTIMULATED
  CC CELLS AND INCREASES A HUNDRED-FOLD AFTER STIMULATION WITH
  CC GIBBERELIC ACID.
  CC -1- MISCELLANEOUS: THERE ARE AT LEAST 4 TYPES OF ALPHA-AMYLASE IN
  CC BARLEY.
  CC -1- SIMILARITY: BELONGS TO FAMILY 13 OF GLYCOSYL HYDROLASES, ALSO
  CC KNOWN AS THE ALPHA-AMYLASE FAMILY.
  CC -----
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  CC or send an email to license@isb-sib.ch).
  CC -----
  CC EMBL; X15226; CAA33298.1; -.
  CC EMBL; K02637; AAA98790.1; -.
  DR

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DR PIR; A31960; ALBHB.
DR PDB; LAMY; 13-MAY-95.
DR PDB; IAVA; 16-MAR-99.
DR PDB; IBG9; 15-JUN-99.
DR InterPro; IPR006589; Alp_amy1_cat_sub.
DR InterPro; IPR006047; Alpha_amy1_cat.
DR InterPro; IPR006046; Glyco_hydro_13.
DR Pfam; PF00128; alpha-amylase; 1.
DR PRINTS; PRO0110; ALPHAAMYLASE.
DR SMART; SM00642; Amy; 1.
KW Hydroxylase; Glycosidase; Carbohydrate metabolism; Seed; Germination;
KW Calcium; Multigene family; Signal; 3D-structure.
FT SIGNAL 1 24
FT CHAIN 25 427
FT ACT_SITE 203 203
FT ACT_SITE 228 228
FT ACT_SITE 313 313
FT CONFLICT 134 134
FT CONFLICT 195 197
FT CONFLICT 425 425
FT STRAND 27 29
FT STRAND 33 34
FT STRAND 35 37
FT STRAND 39 40
FT HELIX 42 47
FT HELIX 48 49
FT TURN 50 56
FT HELIX 57 57
FT TURN 60 63
FT STRAND 69 69
FT TURN 72 73
FT STRAND 77 77
FT TURN 80 81
FT TURN 84 85
FT TURN 87 88
FT TURN 91 104
FT TURN 105 105
FT STRAND 107 112
FT STRAND 116 116
FT STRAND 121 122
FT TURN 124 125
FT STRAND 128 130
FT TURN 139 140
FT STRAND 144 146
FT HELIX 147 147
FT TURN 149 150
FT TURN 152 154
FT STRAND 165 165
FT TURN 168 169
FT STRAND 172 173
FT TURN 175 176
FT HELIX 178 193
FT TURN 194 195
FT STRAND 199 202
FT TURN 203 204
FT HELIX 205 207
FT HELIX 210 220
FT STRAND 224 227
FT STRAND 235 235
FT STRAND 237 238
FT TURN 241 241
FT STRAND 246 260
FT HELIX 261 262
FT TURN 265 268
FT STRAND 270 279
FT HELIX 280 282
FT HELIX 284 287
FT TURN 290 291
FT HELIX 297 299
FT TURN 300 300
FT HELIX 302 304
FT STRAND 305 308
FT TURN 312 314

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FT TURN 316 318
FT HELIX 325 327
FT HELIX 328 327
FT STRAND 341 345
FT HELIX 346 350
FT TURN 351 351
FT HELIX 355 357
FT TURN 368 369
FT TURN 372 373
FT STRAND 376 382
FT TURN 383 384
FT STRAND 385 390
FT TURN 391 393
FT STRAND 394 398
FT HELIX 405 407
FT STRAND 412 418
FT TURN 419 420
FT STRAND 421 427
SQ SEQUENCE 427 AA; 47355 MW; 957C0B1621BF748 CRC64;

Query Match 83.9%; Score 47; DB 1; Length 427;
Best Local Similarity 88.9%; Pred. No. 0.56;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 VNMVNVKYG 9
Db 253 VNMVNVKYG 261

RESULT 6
AM3D_ORYSA STANDARD; PRT; 435 AA.
ID AM3D_ORYSA
AC P27933;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Alpha-amylase isozyme 3D precursor (EC 3.2.1.1) (1,4-alpha-D-glucan
glucanohydrolase).
GN AMY1.3 OR AMY3D.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Eriharoidae; Oryzaceae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Japonica M202; Tissue=Ettoled leaf;
RX MEDLINE=91088728; PubMed=2263460.
RA Huang N., Koiwumi N., Reini S., Rodriguez R.L.;
RT "Structural organization and differential expression of rice alpha-
amylase genes.";
RL Nucleic Acids Res. 18:7007-7014(1990).
RN [2]
RP SEQUENCE FROM N.A. (CLONE POS137).
RX MEDLINE=90318322; PubMed=2370848;
RA O'Neill S.D., Kumagai M.H., Majumdar A., Sutliff T.D.,
Rodriguez R.L.;
RT "The alpha-amylase genes in Oryza sativa: characterization of cDNA
clones and mRNA expression during seed germination.";
RL Mol. Genet. 221:235-244(1990).
CC -1- FUNCTION: IMPORTANT FOR BREAKDOWN OF ENDOSPERM STARCH DURING
GERMINATION.
CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic
linkages in oligosaccharides and polysaccharides.
CC -1- COFACTOR: BINDS A CALCIUM ION REQUIRED FOR ITS ACTIVITY.
CC -1- SUBUNIT: Monomer.
CC -1- TISSUE SPECIFICITY: IS EXPRESSED IN ALL TISSUES, EXCEPT IN
IMMATURE SEEDS. IS THE MOST ABUNDANT ALPHA-AMYLASE ISOZYME IN
CALLUS.
CC -1- DEVELOPMENTAL STAGE: EXPRESSED AT A HIGH LEVEL DURING GERMINATION
IN THE ALBURNONS CELLS UNDER THE CONTROL OF THE PLANT HORMONE
GIBBERELLIC ACID AND IN THE DEVELOPING GRAINS AT A LOW LEVEL.
CC -1- SIMILARITY: BELONGS TO FAMILY 13 OF GLYCOSYL HYDROLASES, ALSO

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CC -----
CC KNOWN AS THE ALPHA-AMYLASE FAMILY.
CC -----
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CC or send an email to license@sib-sib.ch).
CC -----
DR EMBL: M59351; AAA33895.1; -
DR EMBL: M24287; AAA33886.1; -
DR PIR: S12625; S12625.
DR HSP: P04063; IAVA.
DR Gramene: P27933; -
DR InterPro: IPR006589; Alp_aml1_cat_sub.
DR InterPro: IPR006047; Alp_aml1_cat.
DR Pfam: PF00128; alpha-amylase; 1.
DR SMART: SM00642; Amyy; 1.
KW Hydroxylase; Glycosidase; Carbohydrate metabolism; Calcium; Signal;
KW Multigene family.
FT SIGNAL 1..25
FT CHAIN 26..435
FT ACET SITE 203..203
FT ACET SITE 311..311
FT METAL 116..116
FT METAL 174..174
FT CONFLICT 73..74
FT CONFLICT 137..137
SQ SEQUENCE 435 AA; 47911 MW; 1BB06A195BA0D6 CRC64;

Query Match 82.1%; Score 46; DB 1; Length 435;
Best Local Similarity 88.9%; Pred. No. 0.85;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 VNMVNVKYG 9
Db 253 VNMVNVKYG 261

RESULT 7
AMYL_ORYSA STANDARD; PRT; 428 AA.
ID AMYL_ORYSA
AC P17654;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Alpha amylase precursor (EC 3.2.1.1) (1,4-alpha-D-glucan
glucanohydrolase) (Isozyme 1b).
GN AMY1.1 OR AMY1A.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Eriharoidae; Oryzaceae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Japonica M202;
RX MEDLINE=91346657; PubMed=2102847;
RA Huang N., Sutliff T.D., Lits J.C., Rodriguez R.L.;
RT "Classification and characterization of the rice alpha-amylase
multigene family.";
RL Plant Mol. Biol. 14:655-668(1990).
RN [2]
RP SEQUENCE FROM N.A. (CLONE POS103).
RC STRAIN=cv. Japonica M202;
RX MEDLINE=90318322; PubMed=2370848;
RA O'Neill S.D., Kumagai M.H., Majumdar A., Sutliff T.D.,
Rodriguez R.L.;
RT "The alpha-amylase genes in Oryza sativa: characterization of cDNA
clones and mRNA expression during seed germination.";
RL Mol. Genet. 221:235-244(1990).
CC -1- FUNCTION: IMPORTANT FOR BREAKDOWN OF ENDOSPERM STARCH DURING

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CC GERMINATION.
CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic
CC linkages in oligosaccharides and polysaccharides.
CC -1- COFACTOR: BINDS A CALCIUM ION REQUIRED FOR ITS ACTIVITY.
CC -1- SUBUNIT: Monomer.
CC -1- TISSUE SPECIFICITY: MORE ABUNDANT IN GERMINATING SEEDS, THAN IN
CC CALLUS, YOUNG ROOTS AND LEAVES.
CC -1- DEVELOPMENTAL STAGE: EXPRESSED AT A HIGH LEVEL DURING GERMINATION
CC IN THE ALEURONES CELLS UNDER THE CONTROL OF THE PLANT HORMONE
CC GIBBERELIC ACID AND IN THE DEVELOPING GRAINS AT A LOW LEVEL.
CC -1- PPM: ONLY CEREAL AMYLASE KNOWN TO BE GLYCOSYLATED.
CC -1- SIMILARITY: BELONGS TO FAMILY 13 OF GLYCOSYL HYDROLASES, ALSO
CC KNOWN AS THE ALPHA-AMYLASE FAMILY.
CC -----
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CC -----
DR EMBL: X16509; CAA34516.1; -.
DR PIR: S10013; S10013.
DR HSSP: P04063; IAVA.
DR Gramene; P17654; -.
DR InterPro: IPR006589; Alp_ami1_cat_sub.
DR InterPro: IPR006047; Alpha_ami1_cat.
DR InterPro: IPR006046; Glyco_hydro_13.
DR Pfam: PF00128; alpha-amyase; 1.
DR PRINTS: PR00110; ALPHAAMYLASE.
DR SMART: SM00642; Amy; 1.
DR KMW: Hydrolyase; Glycosidase; Carbohydrate metabolism; Calcium; Signal;
DR KMW: Glycoprotein; Multigene family.
FT SIGNAL 1 25 PROBABLE.
FT CHAIN 26 428 ALPHA-AMYLASE.
FT ACT_SITE 203 203 BY SIMILARITY.
FT ACT_SITE 314 314 BY SIMILARITY.
FT METAL 116 116 CALCIUM (BY SIMILARITY).
FT METAL 174 174 CALCIUM (BY SIMILARITY).
FT CARBOHND 265 275 N-LINKED (GLCNAC. . .) (PROBABLE).
SQ SEQUENCE 428 AA; 4775 MW; 3B71403AACF6C6A6 CRC64;

Query Match 80.4%; Score 45; DB 1; Length 428;
Best Local Similarity 70.0%; Pred. No. 1.3;
Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VNMVNRKVGGS 10
Db 253 VNMVDRVGA 262

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RT "Characterization of an alpha-amyase multigene cluster in rice.";
RL Plant Mol. Biol. 16:579-591(1991).
CC -1- FUNCTION: IMPORTANT FOR BREAKDOWN OF ENDOSPERM STARCH DURING
CC GERMINATION.
CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic
CC linkages in oligosaccharides and polysaccharides.
CC -1- COFACTOR: BINDS A CALCIUM ION REQUIRED FOR ITS ACTIVITY.
CC -1- SUBUNIT: Monomer.
CC -1- TISSUE SPECIFICITY: MOST ABUNDANT IN EMBRYO-DERIVED CALLUS TISSUE.
CC -1- DEVELOPMENTAL STAGE: EXPRESSED AT A HIGH LEVEL DURING GERMINATION
CC IN THE ALEURONES CELLS UNDER THE CONTROL OF THE PLANT HORMONE
CC GIBBERELIC ACID AND IN THE DEVELOPING GRAINS AT A LOW LEVEL.
CC -1- SIMILARITY: BELONGS TO FAMILY 13 OF GLYCOSYL HYDROLASES, ALSO
CC KNOWN AS THE ALPHA-AMYLASE FAMILY.
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CC -----
DR EMBL: X56336; CAA39776.1; -.
DR PIR: S14958; S14958.
DR HSSP: P04063; IAVA.
DR Gramene; P27932; -.
DR InterPro: IPR006589; Alp_ami1_cat_sub.
DR InterPro: IPR006047; Alpha_ami1_cat.
DR InterPro: IPR006046; Glyco_hydro_13.
DR Pfam: PF00128; alpha-amyase; 1.
DR PRINTS: PR00110; ALPHAAMYLASE.
DR SMART: SM00642; Amy; 1.
DR KMW: Hydrolyase; Glycosidase; Carbohydrate metabolism; Calcium; Signal;
DR KMW: Multigene family.
FT SIGNAL 1 26 POTENTIAL.
FT CHAIN 27 440 ALPHA-AMYLASE ISOZYME 3A.
FT ACT_SITE 207 207 BY SIMILARITY.
FT ACT_SITE 315 315 BY SIMILARITY.
FT METAL 119 119 CALCIUM (BY SIMILARITY).
FT METAL 178 178 CALCIUM (BY SIMILARITY).
SQ SEQUENCE 440 AA; 48872 MW; 5E9B78C29AA91C2B CRC64;

Query Match 75.0%; Score 42; DB 1; Length 440;
Best Local Similarity 77.8%; Pred. No. 4.4;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 VNMVNRKVG 9
Db 257 VNMVKQVGG 265

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RESULT 8
AM3A_ORYSA STANDARD; PRT; 440 AA.
ID AM3A_ORYSA
AC P27932;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Alpha-amyase isozyme 3A precursor (EC 3.2.1.1) (1,4-alpha-D-
DE glucan glucanohydrolase).
GN AM1.2 OR AM13A.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=4530;
[1]
SEQUENCE FROM N.A.
RP STRAIN=cv. Japonica M202; TISSUE=Etiolated leaf;
RX MEDLINE=91329692; PubMed=1714318;
RA Sutliff T.D., Huang N., Litts J.C., Rodriguez R.L.;

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RESULT 9
PTFA_MYCGE STANDARD; PRT; 680 AA.
ID PTFA_MYCGE
AC P47308;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Pts system, fructose-specific IIABC component (EIABC-Fru) (Fructose-
DE permease IIABC component) (Phosphotransferase enzyme II, ABC
DE component) (EC 2.7.1.69) (EII-Fru/EIII-Fru).
GN FRUA OR MG062.
OS Mycoplasma genitalium.
OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
OX NCBI_TaxID=2097;
[1]
SEQUENCE FROM N.A.
RP STRAIN=ATCC 33530 / G-37;
RX MEDLINE=96026346; PubMed=7569993;
RA Fraser C.M., Gocayne J.D., White O., Adams M.D., Clayton R.A.,
RA Fleischmann R.D., Bult C.J., Kerlavage A.R., Sutton G., Kelley J.M.,
RA Fitchman J.L., Weidman J.F., Small K.V., Sandusky M., Fuhrmann J.L.;

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RA Nguyen D.T., Utharack T.R., Saudek D.M., Phillips C.A., Merrick J.M.,
 RA Tomb J.-F., Dougherty B.A., Bolt K.F., Hu P.-C., Luchter T.S.,
 RA Peterson S.N., Smith H.O., Hutchison C.A. III, Venter J.C.;
 RT "The minimal gene complement of *Mycoplasma genitalium*,"
 RL Science 270:397-403(1995).
 RN [2]
 RN SEQUENCE OF 147-253 FROM N.A.
 RC STRAIN-ATCC 33530 / G-37;
 RX MEDLINE=94075230; PubMed=8253680;
 RA Peterson S.N., Hu P.-C., Bolt K.F., Hutchison C.A. III;
 RT "A survey of the *Mycoplasma genitalium* genome by using random
 RT sequencing,"
 RL J. Bacteriol. 175:7918-7930(1993).
 RN [3]
 RN DISCUSSION OF SEQUENCE.
 RP MEDLINE=98353635; PubMed=9689210;
 RA Reizer J., Paulsen I.T., Reizer A., Tligemeyer F., Sajer M.H. Jr.;
 RT "Novel phosphotransferase system genes revealed by bacterial genome
 RT analysis: the complete complement of pts genes in *Mycoplasma
 RT genitalium*,"
 RL Microb. Comp. Genomics 1:151-164(1996).
 CC -1- FUNCTION: THIS IS A COMPONENT OF THE PHOSPHOENOLPYRUVATE-DEPENDENT
 CC SUGAR PHOSPHOTRANSFERASE SYSTEM (PTS). A MAJOR CARBOHYDRATE ACTIVE
 CC -TRANSPORT SYSTEM. THE TCD DOMAIN CONTAIN THE SUGAR BINDING SITE
 CC AND THE TRANSMEMBRANE CHANNEL. THE IIA DOMAIN CONTAINS THE PRIMARY
 CC PHOSPHORYLATION SITE (THE DONOR IS PHOSPHO-ATP); IIA TRANSFERS ITS
 CC PHOSPHORYL GROUP TO THE IIB DOMAIN WHICH FINALLY TRANSFERS IT TO
 CC THE SUGAR.
 CC -1- CATALYTIC ACTIVITY: Protein N-phosphotransferase + sugar = protein
 CC histidine + sugar phosphate.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
 CC -1- SIMILARITY: Contains 1 PTS_EIIA domain.
 CC -1- SIMILARITY: Contains 1 PTS_EIIB domain.
 CC -----
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 CC -----
 DR EMBL: U09685; AAC71279.1; -
 DR EMBL: U02138; AAD12415.1; -
 DR PIR: H64206; H64206.
 DR TIGR: MG062; -
 DR InterPro: IPR002178; PTS_EIIA.2.
 DR InterPro: IPR003353; PTS_EIIC.
 DR InterPro: IPR003353; PTS_IIB-func.
 DR InterPro: IPR006327; PTS_EIIC-func.
 DR InterPro: IPR004715; PTS_IIA-func.
 DR Pfam: PF00359; PTS_EIIA.2; 1.
 DR Pfam: PF02378; PTS_EIIC; 1.
 DR Pfam: PF02379; PTS_IIB-func; 1.
 DR ProDom: PD001689; PTS_EIIA.2; 1.
 DR TIGRFAMs: TIGR00829; FRU; 1.
 DR TIGRFAMs: TIGR00848; frua; 1.
 DR TIGRFAMs: TIGR01427; PTS_IIC-functo; 1.
 DR TIGRFAMs: TIGR01427; PTS_IIC-functo; 1.
 KM Phosphotransferase system: Sugar transport; Transferase;
 KM Phosphorylation; Transmembrane; Complete proteome.
 FT DOMAIN 1 68
 FT DOMAIN ? 68
 FT MOD_RES ? 680
 FT MOD_RES 174 174
 FT MOD_RES 306 326
 FT TRANSMEM 352 372
 FT TRANSMEM 377 397
 FT TRANSMEM 410 430
 FT TRANSMEM 449 469
 FT TRANSMEM 488 508
 FT TRANSMEM 532 552
 FT TRANSMEM POTENTIAL.
 FT TRANSMEM POTENTIAL.

FT TRANSMEM 565 585 POTENTIAL.
 FT TRANSMEM 590 610 POTENTIAL.
 FT TRANSMEM 618 638 POTENTIAL.
 FT TRANSMEM 643 663 POTENTIAL.
 SQ SEQUENCE 680 AA; 74090 MW; AbACIBID7AA9D4A CRC64;
 Query Match 75.0%; Score 42; DB 1; Length 680;
 Best Local Similarity 75.0%; Pred. No. 6.6;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 Oy 2 MWVKNYGG 9
 Db 346 NWLNKILGG 353
 |||:|:
 |||:|:
 RESULT 10
 ID AROE_BUCAP STANDARD; PRT; 273 AA.
 AC P46240;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Shikimate 5-dehydrogenase (EC 1.1.1.25).
 GN AROE OR BUC6474
 OS Buchnera aphidicola (subsp. Schizaphis graminum).
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Buchnera.
 OX NCBI_TaxID=98794;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=95212914; PubMed=7535281;
 RA Roubaksh D., Baumann P.;
 RT "Characterization of a putative 23S-5S rRNA operon of *Buchnera
 RT aphidicola* (endosymbiont of aphids) unlinked to the 16S rRNA-encoding
 RT gene,"
 RL Gene 155:107-112(1995).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22084549; PubMed=12089438;
 RA Tams I., Klasson L., Canback B., Naeslund A.K., Eriksson A.-S.,
 RA Wernegreen J.J., Sandstrom J.P., Moran N.A., Andersson S.G.E.;
 RT "50 million years of genomic stasis in endosymbiotic bacteria,"
 RL Science 286:2376-2379(2002).
 CC -1- CATALYTIC ACTIVITY: Shikimate + NADP(+) = 5-dehydroshikimate +
 CC NADPH.
 CC -1- PATHWAY: Aromatic amino acids biosynthesis; shikimate pathway;
 CC fourth step
 CC -1- SIMILARITY: Belongs to the shikimate dehydrogenase family.
 CC -----
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 CC -----
 DR EMBL: U09230; AAD09433.1; -
 DR EMBL: AE014124; AAM68017.1; -
 DR HAMAP: MF_00222; ? 1.
 DR InterPro: IPR006152; Shikimate.
 DR InterPro: IPR006151; Shikimate_DH.
 DR Pfam: PF01488; Shikimate_DH; 1.
 DR TIGRFAMs: TIGR00507; aroe; 1.
 KM Aromatic amino acid biosynthesis; Oxidoreductase; NADP;
 KM Complete proteome.
 FT CONFLICT 203 204 LP -> T (IN REF. 1).
 FT CONFLICT 206 206 S -> I (IN REF. 1).
 FT CONFLICT 212 212 T -> R (IN REF. 1).
 SQ SEQUENCE 273 AA; 30885 MW; 50507AF854774A6 CRC64;
 Query Match 73.2%; Score 41; DB 1; Length 273;
 Best Local Similarity 60.0%; Pred. No. 4.3;

Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 NMVNVKVGGS 10
: || : |||
Db 227 INMCKRAGGS 236

RESULT 11
YOZ7_BPBP1 STANDARD; PRT; 689 AA.
ID YOZ7_BPBP1
AC P51731;
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical 72.8 kDa protein in Lys 3 region (ORF27).
OS Bacteriophage HP1.
CC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Myoviridae.
OX NCBI_TaxID=10690;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HP1C1;
RX MEDLINE=85128433; PubMed=6098523;
RA Benjamin R.C., Fitzmaurice W.P., Huang P.C., Scoocca J.J.;
RT "Nucleotide sequence of cloned DNA segments of the Haemophilus
RT Influenzae bacteriophage HP1C1."
RL Gene 31:173-185(1984).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=HP1C1;
RX MEDLINE=96279738; PubMed=8710508;
RA Esposito D., Fitzmaurice W.P., Benjamin R.C., Goodman S.D.,
RA Waldman A.S., Scoocca J.J.;
RT "The complete nucleotide sequence of bacteriophage HP1 DNA."
RL Nucleic Acids Res. 24:2360-2368(1996).
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CC -----
DR EMBL: U24159; AAB09214.1; -
DR PIR: S69535; S69535.
RW Hypothetical protein; Transmembrane.
FT TRANSMEM 385 405 POTENTIAL.
FT TRANSMEM 414 434 POTENTIAL.
SQ SEQUENCE 689 AA; 72837 MW; CGCD9BBA0CA17C22 CRC64;

Query Match 73.2%; Score 41; DB 1; Length 689;
Best Local Similarity 73.0%; Pred. No. 10;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 NMVNVKVGGS 9
: ||||| : |
Db 166 NMVNVKING 173

RESULT 12
VB17_VACCC STANDARD; PRT; 340 AA.
ID VB17_VACCC
AC P21075;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Protein B17.
GN B17L.
OS Vaccinia virus (strain Copenhagen).
CC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
CC Orthopoxvirus.
OX NCBI_TaxID=10249;
RN [1]

RP SEQUENCE FROM N.A.
RX MEDLINE=91021027; PubMed=2219722;
RA Goebel S.J., Johnson G.P., Perkins M.E., Davis S.W., Winslow J.P.,
RA Paoletti E.;
RT "The complete DNA sequence of vaccinia virus."
RL Virology 179:247-266(1990).
RN [2]
RP COMPLETE GENOME.
RA Goebel S.J., Johnson G.P., Perkins M.E., Davis S.W., Winslow J.P.,
RA Paoletti E.;
RT "Appendix to 'The complete DNA sequence of vaccinia virus'";
RL Virology 179:517-563(1990).
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CC -----
DR EMBL: M35027; AAA48216.1; -
DR PIR: G42527; G42527.
SQ SEQUENCE 340 AA; 39505 MW; 11B23AE072A4EF CRC64;

Query Match 71.4%; Score 40; DB 1; Length 340;
Best Local Similarity 77.8%; Pred. No. 7.9;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 NMVNVKVGGS 10
: ||||| : |
Db 96 NMVNVKVGDS 104

RESULT 13
VB17_VACCV STANDARD; PRT; 340 AA.
ID VB17_VACCV
AC 001221;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 01-APR-1993 (Rel. 25, Last annotation update)
DE Protein B17.
GN B17L OR B16L.
OS Vaccinia virus (strain WR).
CC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
CC Orthopoxvirus.
OX NCBI_TaxID=10254;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91259063; PubMed=2045793;
RA Smith G.L., Chan Y.S., Howard S.T.;
RT "Nucleotide sequence of 42 kbp of vaccinia virus strain WR from near
RT the right inverted terminal repeat."
RL J. Gen. Virol. 72:1349-1376(1991).
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CC -----
DR EMBL: D11079; BAA01846.1; -
DR PIR: J01810; J01810.
SQ SEQUENCE 340 AA; 39565 MW; 52680AA44C249AC9 CRC64;

Query Match 71.4%; Score 40; DB 1; Length 340;
Best Local Similarity 77.8%; Pred. No. 7.9;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 NMVNVKVGGS 10
: ||||| : |

Db 96 NMVSKVGS 104

RESULT 14

ID	VAR1	VAR2	STANDARD	PRT	340 AA
AC	P33876				
DT	01-FEB-1994 (Rel. 28, Created)				
DT	01-FEB-1994 (Rel. 28, Last sequence update)				
DT	01-FEB-1996 (Rel. 33, Last annotation update)				
DE	Protein B17				
GN	B17L OR B18L OR B15L				
OS	Varicella virus				
OC	Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;				
OC	Orthopoxvirus				
OX	NCBI_TaxID=10255;				
RA	SEQUENCE FROM N.A.				
RC	STRAIN-India-1967 / Isolate Ind3;				
RX	MEDLINE-92209372; PubMed-166548;				
RA	Shchelkunov S.N., Marennikova S.S., Tolmenin A.V., Blinov V.M.,				
RA	Chizhikova V.E., Gutorov V.V., Saifonov P.F., Pozdnyakov S.G.,				
RA	Shelukhina E.M., Gashnikov P.V., Anjaparidze O.G., Sandakchiev L.S.;				
RT	"Creation of a clone library of fragments from the natural variola				
RT	virus and study of the structural and functional organization of				
RT	viral genes from a circle of hosts"				
RL	Dokl. Akad. Nauk SSSR 321:402-406(1991).				
RN	[2]				
RP	COMPLETE GENOME				
RC	STRAIN-India-1967 / Isolate Ind3;				
RX	MEDLINE-93202281; PubMed-8384129;				
RA	Shchelkunov S.N., Blinov V.M., Sandakchiev L.S.;				
RT	Genes of variola and vaccinia viruses necessary to overcome the host				
RT	protective mechanisms"				
RL	FEBs Lett. 319:80-83(1993).				
RN	[3]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN-Bangladesh-1975;				
RX	MEDLINE-94088747; PubMed-8264798;				
RA	Maassig R.F., Esposito J.J., Liu L., Qi J., Uterback T.R.,				
RA	Knights J.C., Aubin L., Yuran T.E., Parsons J.M., Loparev V.N.,				
RA	Selivanov N.A., Cavallaro K.F., Kerlavac A.R., Mahy B.W.J.,				
RA	Venter C.J.;				
RT	"Potential virulence determinants in terminal regions of variola				
RT	smallpox virus genome."				
RL	Nature 366:748-751(1993).				
RN	[4]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN-Somalia-1977, and Garcia-1966;				
RA	Maassig R.F., Loparev V.N., Knights J.C., Chizhikov V.E., Parsons J.M.,				
RA	Tolmenin A.V., Shchelkunov S.N., Esposito J.J.;				
RL	Submitted (DEC-1994) to the EMBL/Genbank/DBJ databases.				
CC	-----				
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CC	-----				
DR	EMBL; X69198; CA449127.1; -				
DR	EMBL; X67117; CA447527.1; -				
DR	EMBL; X72086; CA50968.1; -				
DR	EMBL; L22579; AA60924.1; -				
DR	EMBL; U18339; AA69397.1; -				
DR	EMBL; U18341; AA69457.1; -				
DR	PIR; B72174; B72174.				
DR	PIR; I36856; I36856.				
DR	PIR; T28614; T28614.				
SO	SEQUENCE 340 AA; 39673 MW; CA0C18C9CE62448 CRC64;				

Query Match 71.4%; Score 40; DB 1; Length 340;

Best Local Similarity 77.8%; Pred. No. 7.9;

Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db 96 NMVSKVGS 104

RESULT 15

ID	VAR1	VAR2	STANDARD	PRT	443 AA
AC	P27935				
DT	01-AUG-1992 (Rel. 23, Created)				
DT	01-AUG-1992 (Rel. 23, Last sequence update)				
DT	15-SEP-2003 (Rel. 42, Last annotation update)				
DE	Alpha-amylase isozyme 2A precursor (EC 3.2.1.1) (1,4-alpha-D-glucan				
DE	glucanohydrolase)				
GN	AMY1.5 OR AMY2A.				
OS	Oryza sativa (Rice).				
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;				
OC	Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;				
OC	Erbartoideae; Oryzaceae; Oryza.				
OX	NCBI_TaxID=4530;				
RA	SEQUENCE FROM N.A.				
RC	STRAIN-cv Japonica M202.				
RX	MEDLINE-92175526; PubMed-1541400;				
RA	Huang N., Reini S.J., Rodriguez R.L.;				
RT	"Ramy2A: a novel alpha-amylase-encoding gene in rice."				
RL	Gene 111:223-228(1992).				
CC	-1- FUNCTION: IMPORTANT FOR BREAKDOWN OF ENDOSPERM STARCH DURING				
CC	GERMINATION.				
CC	-1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic				
CC	linkages in oligosaccharides and polysaccharides.				
CC	-1- COFACTOR: BINDS A CALCIUM ION REQUIRED FOR ITS ACTIVITY.				
CC	-1- SUBUNIT: Monomer.				
CC	-1- DEVELOPMENTAL STAGE: EXPRESSED AT A HIGH LEVEL DURING GERMINATION				
CC	IN THE ALEURONS CELLS UNDER THE CONTROL OF THE PLANT HORMONE				
CC	GIBBERELIC ACID AND IN THE DEVELOPING GRAINS AT A LOW LEVEL.				
CC	-1- SIMILARITY: BELONGS TO FAMILY 13 OF GLYCOSYL HYDROLASES, ALSO				
CC	KNOWN AS THE ALPHA-AMYLASE FAMILY.				
CC	-----				
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CC	-----				
DR	EMBL; M74177; AAA3894.1; -				
DR	PIR; J01527; J01527.				
DR	HSP; P04063; IAVA.				
DR	Gramene; P27935.				
DR	InterPro; IPR006047; Alpha-amyl-cat.				
DR	PIfam; PF00128; alpha-amylase; 1.				
KW	Hydrolase; Glycosidase; Carbohydrate metabolism; Calcium; Signal;				
KW	MultiGene family.				
FT	STGNL 1 21				
FT	CHAIN 22 443				
FT	ACT_SITE 202 202				
FT	ACT_SITE 314 314				
FT	METAL 113 113				
FT	METAL 172 172				
SO	SEQUENCE 443 AA; 48527 MW; 7B3F9264404F67F6 CRC64;				

Query Match 71.4%; Score 40; DB 1; Length 443;

Best Local Similarity 60.0%; Pred. No. 10;

Matches 6; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Db 96 NMVSKVGS 10

1 VNMVSKVGS 10

253 VDWVDRVGR 262

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RESULT 16
AMC2_ORYSA STANDARD; PRT; 445 AA.
ID 1
DT 01-AUG-1992 (Rel. 23, Created)
AC P27941
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Alpha-amylase isozyme C2 precursor (EC 3.2.1.1) (1,4-alpha-D-glucan
DE glucanohydrolase).
GN AMY1.8.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzeae; Oryza.
OC NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Indica-IR26; TISSUE=Seed;
RA Goldman S., Mawal Y., Wu R.;
RL Submitted (FEB-1992) to the EMBL/GenBank/DBJ databases.
CC -1 FUNCTION: IMPORTANT FOR BREAKDOWN OF ENDOSPERM STARCH DURING
CC GERMINATION.
CC -1 CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic
CC linkages in oligosaccharides and polysaccharides.
CC -1 COPACITOR: BINDS A CALCIUM ION REQUIRED FOR ITS ACTIVITY.
CC -1 SUBUNIT: Monomer.
CC -1 DEVELOPMENTAL STAGE: EXPRESSED AT A HIGH LEVEL DURING GERMINATION
CC IN THE ALEURONES CELLS UNDER THE CONTROL OF THE PLANT HORMONE
CC GIBBERELIC ACID AND IN THE DEVELOPING GRAINS AT A LOW LEVEL.
CC -1 SIMILARITY: BELONGS TO FAMILY 13 OF GLYCOSYL HYDROLASES, ALSO
CC KNOWN AS THE ALPHA-AMYLASE FAMILY.
CC -----
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CC -----
DR EMBL: X64619; CAA45903.1; -.
DR PIR: S19980; S19990.
DR HSSP: P04063; IAVA.
DR Gramene: P27941; -.
DR InterPro: IPR006047; Alpha_amyl_cat.
DR Pfam: PF00128; alpha-amylase; 1.
KW Hydrolyase; Glycosidase; Carbohydrate metabolism; Calcium; signal;
KW Multigene family.
FT SIGNAL 1 21 POTENTIAL.
FT CHAIN 22 445 ALPHA-AMYLASE ISOZYME C2.
FT ACT_SITE 202 202 BY SIMILARITY.
FT ACT_SITE 314 314 BY SIMILARITY.
FT METAL 113 113 CALCIUM (BY SIMILARITY).
FT METAL 172 172 CALCIUM (BY SIMILARITY).
SO SEQUENCE 445 AA; 49207 MW; DED23701E836ACDA CRC64;

Query Match 71.4%; Score 40; DB 1; Length 445;
Best Local Similarity 60.0%; Pred. No. 10;
Matches 6; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

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DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE ENV polyprotein precursor (coat polyprotein) [contains: Coat protein
DE GP62; Coat protein GP40].
ENV.
OS Bovine immunodeficiency virus (isolate 106) (BIV).
OC Viruses; Retroviruses; Retroviridae; Lentivirus.
OC NCBI_TaxID=11658;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90223985; PubMed=2183467;
RA Garvey K.J., Oberste M.S., Elser J.E., Braun M.J., Gonda M.A.;
RT "Nucleotide sequence and genome organization of biologically active
RT proviruses of the bovine immunodeficiency-like virus.";
RL Virology 175:391-409(1990).
RN [2]
RP SEQUENCE OF 1-99 FROM N.A.
RX MEDLINE=91251255; PubMed=1645801;
RA Oberste M.S., Greenwood J.D., Gonda M.A.;
RT "Analysis of the transcription pattern and mapping of the putative
RT rev and env splice junctions of bovine immunodeficiency-like virus.";
RL J. Virol. 65:3932-3937(1991).
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CC -----
DR EMBL: M32691; NOT ANNOTATED_CDS.
DR EMBL: M74711; AAA42762.1; -.
DR HIV: M32691; ENVBIV106.
KW Glycoprotein; Coat protein; Polypeptide; Transmembrane; signal.
FT SIGNAL 1 13
FT CHAIN 14 555
FT CHAIN 556 875
FT TRANSMEM 694 722
FT CARBOHYD 131 131
FT CARBOHYD 248 248
FT CARBOHYD 267 267
FT CARBOHYD 300 300
FT CARBOHYD 338 338
FT CARBOHYD 347 347
FT CARBOHYD 356 356
FT CARBOHYD 381 381
FT CARBOHYD 398 398
FT CARBOHYD 403 403
FT CARBOHYD 423 423
FT CARBOHYD 462 462
FT CARBOHYD 480 480
FT CARBOHYD 512 512
FT CARBOHYD 568 568
FT CARBOHYD 634 634
FT CARBOHYD 665 665
FT CARBOHYD 848 848
FT CONFLICT 24 24
FT CONFLICT 92 92
SO SEQUENCE 875 AA; 99166 MW; EBE6FCB32747EA6C CRC64;

Query Match 71.4%; Score 40; DB 1; Length 875;
Best Local Similarity 66.7%; Pred. No. 19;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

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AC p19557;
BT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DR 16-OCT-2001 (Rel. 40, Last annotation update)
DE ENV Polypeptide precursor (Coat polypeptide) [contains: Coat protein
DE gp62; Coat protein gp40].
GN ENV.
OS Bovine immunodeficiency virus (isolate 127) (BIV).
OC Viruses; Retroviridae; Retroviridae; Lentivirus.
OX NCBI_TaxID=11659;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90223985; PubMed=2183467;
RA Garvey K.J., Oberste M.S., Elser J.E., Braun M.J., Gonda M.A.;
RT "Nucleotide sequence and genome organization of biologically active
RT proviruses of the bovine immunodeficiency-like virus.";
RL Virology 175:391-409(1990).
CC -----
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CC -----
DR EMBL: M32690; AAA91274.1; -
DR PIR: E34742; VCLBVT.
DR HIV: M32690; ENV5BIV127.
KW Glycoprotein; Coat protein; Polypeptide; Transmembrane; Signal.
FT SIGNAL 1 13
FT CHAIN 14 555
FT CHAIN 904 904
FT TRANSMEM 723 751
FT CARBOHYD 131 131
FT CARBOHYD 255 255
FT CARBOHYD 277 277
FT CARBOHYD 296 296
FT CARBOHYD 329 329
FT CARBOHYD 367 367
FT CARBOHYD 376 376
FT CARBOHYD 385 385
FT CARBOHYD 410 410
FT CARBOHYD 427 427
FT CARBOHYD 432 432
FT CARBOHYD 452 452
FT CARBOHYD 491 491
FT CARBOHYD 509 509
FT CARBOHYD 541 541
FT CARBOHYD 597 597
FT CARBOHYD 653 653
FT CARBOHYD 694 694
FT CARBOHYD 877 877
FT SEQUENCE 904 AA: 102269 MW: F56100DC2AECDD66F CRC64;

Query Match 71.4%; Score 40; DB 1; Length 904;
Best Local Similarity 66.7%; Pred. No. 19;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 2 NNNVNVGGS 10
DB 788 NMLNKIGES 796
11:11:11

RESULT 19
ID NUP1_PENCI STANDARD; PRT: 270 AA.
AC P24289;
DT 01-MAR-1992 (Rel. 21, Created)
DT 01-MAR-1992 (Rel. 21, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Nuclease p1 (PC 3.1.30.1) (Endonuclease p1) (Deoxyribonuclease p1).
OS Penicillium citrinum.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiaceae; Trichocomaceae; mltosporic Trichocomaceae; Penicillium.
OX NCBI_TaxID=5077;
RN [1]
RP SEQUENCE.
RX MEDLINE=92007841; PubMed=1915339;
RA Maekawa K., Tsunawawa S., Dibo G., Sakiyama F.;
RT "Primary structure of nuclease p1 from Penicillium citrinum.";
RL Eur. J. Biochem. 200:651-661(1991).
RN [2]
RP X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS).
RX MEDLINE=91266887; PubMed=1710977;
RA Volbeda A., Lahm A., Sakiyama F., Suck D.;
RT "Crystal structure of Penicillium citrinum p1 nuclease at 2.8-A
RT resolution.";
RL EMBO J. 10:1607-1618(1991).
RN [3]
RP X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS);
RX MEDLINE=98393014; PubMed=9726413;
RA Komler G., Dominguez R., Lahm A., Dahl O., Suck D.;
RT "Recognition of single stranded DNA by nuclease p1: high resolution
RT crystal structures of complexes with substrate analogs.";
RL Protein 32:414-424(1998).
CC -1- FUNCTION: Hydrolyzes only single stranded DNA and RNA without
CC apparent specificity for bases.
CC -1- CATALYTIC ACTIVITY: Endonucleolytic cleavage to 5'-
CC -1- phosphomononucleotide and 5'-phosphooligonucleotide end-products.
CC -1- COFACTOR: BINDS 3 ZINC IONS.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: TO A.ORYZAE NUCLEASE S1, AND BARLEY NUCLEASE.
DR PIR: S17828; S17828.
DR PDB: 1AK0; 03-DEC-97.
DR InterPro: IPR003154; S1/P1nuclease.
DR Pfam: PF02265; Nuclease; 1.
KW Hydrolyase; Nuclease; Endonuclease; Glycoprotein; Zinc; 3D-structure.
FT DISULFID 72 217
FT CARBOHYD 80 85
FT CARBOHYD 92 92
FT CARBOHYD 138 138
FT CARBOHYD 184 184
FT CARBOHYD 197 197
FT METAL 1 1
FT METAL 6 6
FT METAL 45 45
FT METAL 60 60
FT METAL 116 116
FT METAL 120 120
FT METAL 126 126
FT METAL 149 149
FT METAL 153 153
FT METAL 270 270
FT HELIX 3 16
FT HELIX 19 29
FT HELIX 30 30
FT HELIX 34 37
FT HELIX 38 40
FT HELIX 41 42
FT HELIX 43 48
FT HELIX 49 49
FT HELIX 51 53
FT HELIX 54 60
FT STRAND 67 67
FT STRAND 68 70
FT STRAND 71 71
FT HELIX 76 79
FT HELIX 82 83
FT HELIX 86 97
FT HELIX 98 98
FT TURN 100 101
FT HELIX 104 120
FT TURN 121 122
FT HELIX 124 127

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FT HELIX 130 133
 FT TURN 134 136
 FT STRAND 138 141
 FT TURN 142 143
 FT STRAND 144 147
 FT HELIX 148 153
 FT TURN 154 154
 FT HELIX 155 161
 FT HELIX 166 182
 FT TURN 184 185
 FT HELIX 186 193
 FT TURN 194 195
 FT TURN 198 199
 FT HELIX 201 218
 FT TURN 219 220
 FT TURN 222 223
 FT HELIX 226 228
 FT STRAND 232 232
 FT TURN 234 235
 FT HELIX 236 263
 SQ SEQUENCE 270 AA; 29327 MM; FA9D25FE75A526EF CRC64;

Query Match 67.9%; Score 38; DB 1; Length 270;
 Best Local Similarity 55.6%; Pred. No. 14;
 Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 2 NMVKNVGS 10
 Db 258 NMINEHGS 266

RESULT 20
 NUP3_PENSO STANDARD; PRT; 270 AA.

AC P24504;
 DT 01-MAR-1992 (Rel. 21, Created)
 DT 01-MAR-1992 (Rel. 21, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Nuclease PA3 (EC 3.1.3.6) (Endonuclease PA3) (Deoxyribonuclease PA3).
 OS Penicillium sp.
 CC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
 CC Eurotiiales; Trichocomaceae; mitosporic Trichocomaceae; Penicillium.
 ON NCBI_TaxID=5081;
 RX [1]
 RP SEQUENCE.
 RP MEDLINE=91299282; PubMed=1369324;
 RA Tabata N., Kazama H., Ohgi K., Irie M.;
 RT "Primary structure of a nuclease (nuclease PA3) from a Penicillium
 sp.";
 RL Agric. Biol. Chem. 55:461-469(1991).
 RN [2]
 RP SEQUENCE OF 1-30 AND 268-270.
 RP MEDLINE=91199319; PubMed=1964878;
 RA Kazama H., Tabata N., Ohgi K., Irie M.;
 RT "Purification and characterization of a nuclease (3'-nucleotidase)
 from a Penicillium sp.";
 RL Chem. Pharm. Bull. 38:3081-3085(1990).
 CC -1- FUNCTION: Hydrolyzes only single stranded DNA and RNA without
 apparent specificity for bases.
 CC -1- CATALYTIC ACTIVITY: A 3'-ribonucleotide + H(2)O = a ribonucleoside
 + phosphate.
 CC -1- COFACTOR: BINDS 3 ZINC IONS.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: TO A.ORYZAE NUCLEASE SL, AND BARLEY NUCLEASE.
 DR PIR: J04048; J04048.
 DR HSSP: P24289; IAKO.
 DR InterPro: IPR003154; SI/Plnuclease.
 DR Pfam: PF02265; Nuclease; 1.
 KW Hydrolyase; Nuclease; Endonuclease; Glycoprotein; zinc.
 FT DISULFID 72 217
 FT BY SIMILARITY.
 FT RT 80 85
 FT BY SIMILARITY.
 FT CARBOHYD 92 92
 FT N-LINKED (GLCNAC. . .).
 FT CARBOHYD 138 138
 FT N-LINKED (GLCNAC. . .).

FT CARBOHYD 184 184 N-LINKED (GLCNAC. . .).
 FT CARBOHYD 197 197 N-LINKED (GLCNAC. . .).
 FT METAL 1 1 ZINC 3 (BY SIMILARITY).
 FT METAL 6 6 ZINC 3 (BY SIMILARITY).
 FT METAL 45 45 ZINC 1 (BY SIMILARITY).
 FT METAL 60 60 ZINC 1 (BY SIMILARITY).
 FT METAL 116 116 ZINC 1 (BY SIMILARITY).
 FT METAL 120 120 ZINC 1 AND 3 (BY SIMILARITY).
 FT METAL 126 126 ZINC 2 (BY SIMILARITY).
 FT METAL 149 149 ZINC 2 (BY SIMILARITY).
 FT METAL 153 153 ZINC 2 (BY SIMILARITY).
 SQ SEQUENCE 270 AA; 29215 MM; EF52CFDBBA4F16EF CRC64;

Query Match 67.9%; Score 38; DB 1; Length 270;
 Best Local Similarity 55.6%; Pred. No. 14;
 Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 2 NMVKNVGS 10
 Db 258 NMINEHGS 266

RESULT 21

HDFR_SALTY
 ID HDFR_SALTY STANDARD; PRT; 278 AA.

AC Q9L6T4; Q82336;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Transcriptional regulator hdtR (H-NS-dependent flhDC regulator).
 GN HDFR OR STM3897 OR STM01.99 OR STY3708 OR T3449.
 OS Salmonella typhimurium, and
 OS Salmonella typhi.
 CC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 CC Enterobacteriaceae; Salmonella.
 ON NCBI_TaxID=602, 601;
 RX [1]
 RP SEQUENCE FROM N.A.
 RP SPECIES=S.typhimurium; STRAIN=LT2 / SSGC1412 / ATCC 700720;
 RC MEDLINE=21534948; PubMed=11677609;
 RA McEllelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,
 RA Courtney L., Portwoll S., Ali J., Dantle M., Du F., Hou S., Layman D.,
 RA Leonard S., Nguyen C., Scott K., Holmes A., Grew N., Mulvaney E.,
 RA Ryan E., Sun H., Flores L., Miller W., Stoneking T., Nhan M.,
 RA Waterston R., Wilson R.K.;
 RT "Complete genome sequence of Salmonella enterica serovar Typhimurium
 LT2.";
 RL Nature 413:852-856(2001).
 RN [2]
 RP SEQUENCE FROM N.A.
 RP SPECIES=S.typhi; STRAIN=CT18;
 RC MEDLINE=21534947; PubMed=11677608;
 RA Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Main J.,
 RA Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebatina M.,
 RA Baker S., Basham D., Brooks K., Chillingworth T., Connor P.,
 RA Cronin A., Davis P., Davies R.M., Dowd L., White N., Barrer J.,
 RA Felwell T., Hamlin N., Haque A., Hien T.T., Holtroyd S., Jagels K.,
 RA Krogh A., Larsen T.S., Leather S., Moule S., O'Garra P., Parry C.,
 RA Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K.,
 RA Whitehead S., Barrall B.G.;
 RT "Complete genome sequence of a multiple drug resistant Salmonella
 enterica serovar Typhi CT18.";
 RL Nature 413:848-852(2001).
 RN [3]
 RP SEQUENCE FROM N.A.
 RP SPECIES=S.typhi; STRAIN=Ty2 / ATCC 700931;
 RC MEDLINE=22531367; PubMed=12644504;
 RA Deng W., Liou S.-R., Plunkett G., III, Mayhew G.F., Rose D.J.,
 RA Burland V., Kodoyanni V., Schwartz D.C., Blatter F.R.;
 RT "Comparative genomics of Salmonella enterica serovar Typhi strains Ty2
 and CT18.";
 RL J. Bacteriol. 185:2330-2337(2003).
 CC -1- FUNCTION: Negatively regulates the transcription of the flagellar


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RL Submitted (FEB-1995) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: DNA-DEPENDENT RNA POLYMERASE CATALYZES THE TRANSCRIPTION
CC OF DNA INTO RNA USING THE FOUR RIBONUCLEOSIDE TRIPHOSPHATES AS
CC SUBSTRATES.
CC -1- CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate +
CC (RNA)(N).
CC -1- SUBUNIT: In chloroplasts, the RNA polymerase is composed of four
CC subunits: alpha, beta, beta', and beta".
CC -1- SUBCELLULAR LOCATION: Chloroplast.
CC -1- SIMILARITY: Belongs to the RNA polymerase beta chain family.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: Y13690; CAA74024.1; ALT_INT.
DR EMBL: AP000423; BAA84377.1; -.
DR EMBL: X84159; CAA58965.1; -.
DR PIR: S52324; S52324.
DR HSSP: O9KWU7; IHOM.
DR InterPro: IPR001572; RNA_POL_B.
DR Pfam: PF04563; RNA_pol_Rpb2_1; 1.
DR Pfam: PF04561; RNA_pol_Rpb2_2; 1.
DR Pfam: PF04565; RNA_pol_Rpb2_3; 1.
DR Pfam: PF00562; RNA_pol_Rpb2_6; 2.
DR Pfam: PF04560; RNA_pol_Rpb2_7; 1.
DR PROSITE: PS01166; RNA_POL_BETA; 1.
DR Transferrase; DNA-directed RNA polymerase; Transcription; Chloroplast.
KM CONFLICT 286 286 I -> V (IN REF. 2).
FT CONFLICT 341 341 Y -> S (IN REF. 2).
FT CONFLICT 346 346 Y -> H (IN REF. 2).
FT CONFLICT 599 599 L -> F (IN REF. 2).
FT CONFLICT 927 927 T -> S (IN REF. 2).
FT CONFLICT 958 959 V I -> DK (IN REF. 2).
FT CONFLICT 1038 1038 Q -> P (IN REF. 2).
SQ SEQUENCE 1072 AA; 121049 MW; AE6DD28ED66FABA CRC64;

Query Match 67.9%; Score 38; DB 1; Length 1072;
Best Local Similarity 70.0%; Pred. No. 51;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 VNMVNVKGG 10
Db 790 VRWVQKGG 799

RESULT 24
PROB_SAPOF STANDARD; PRT; 1078 AA.
ID PROB_SAPOF
AC P46818; O9THV7;
DT 01-NOV-1995 (Rel. 32, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE DNA-directed RNA polymerase beta chain (EC 2.7.7.6).
GN RPOB.
OS Sinapis alba (White mustard) (Brassica hirta).
OC Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Sinapis.
OX NCBI_TaxID=3728;
[1]
RT SEQUENCE FROM N.A., AND SEQUENCE OF 1-8.
RP STRAIN=cv. Albatros; TISSUE=cotyledon;
RX MEDLINE=2006369; Pubmed=10601874;
RA Pianschmidt T., Ogrzewalla K., Baginsky S., Sickmann A., Meyer H.E.,
RA Link G.;
RT "The multisubunit chloroplast RNA polymerase A from mustard (Sinapis
RT alba L.). Integration of a prokaryotic core into a larger complex

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RT with organelle-specific functions.";
RL Eur. J. Biochem. 267:253-261(2000).
CC -1- FUNCTION: DNA-DEPENDENT RNA POLYMERASE CATALYZES THE TRANSCRIPTION
CC OF DNA INTO RNA USING THE FOUR RIBONUCLEOSIDE TRIPHOSPHATES AS
CC SUBSTRATES.
CC -1- CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate +
CC (RNA)(N).
CC -1- SUBUNIT: In chloroplasts, the RNA polymerase is composed of four
CC subunits: alpha, beta, beta', and beta".
CC -1- SUBCELLULAR LOCATION: Chloroplast.
CC -1- SIMILARITY: Belongs to the RNA polymerase beta chain family.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL Outstation-
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CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: X82417; CAA57814.1; -.
DR EMBL: AJ243754; CAB48411.1; -.
DR PIR: S48842; S48842.
DR HSSP: O9KWU7; IHOM.
DR InterPro: IPR001572; RNA_POL_B.
DR Pfam: PF04563; RNA_pol_Rpb2_1; 1.
DR Pfam: PF04561; RNA_pol_Rpb2_2; 1.
DR Pfam: PF04565; RNA_pol_Rpb2_3; 1.
DR Pfam: PF00562; RNA_pol_Rpb2_6; 2.
DR Pfam: PF04560; RNA_pol_Rpb2_7; 1.
DR PROSITE: PS01166; RNA_POL_BETA; 1.
DR Transferrase; DNA-directed RNA polymerase; Transcription; Chloroplast.
KM CONFLICT 4 4 A -> S (IN REF. 1; CAA57814).
SQ SEQUENCE 1078 AA; 121653 MW; BOCDF2367526DBF8 CRC64;

Query Match 67.9%; Score 38; DB 1; Length 1078;
Best Local Similarity 70.0%; Pred. No. 51;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 VNMVNVKGG 10
Db 796 VRWVQKGG 805

RESULT 25
PROB_SAPOF STANDARD; PRT; 417 AA.
ID PROB_SAPOF
AC P08036;
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-AUG-1988 (Rel. 08, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE DNA-directed RNA polymerase beta chain (EC 2.7.7.6) (Fragment).
GN RPOB.
OS Saponaria officinalis (Common soapwort).
OC Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Caryophyllales; Caryophyllaceae; Saponaria.
OX NCBI_TaxID=3572;
[1]
RT SEQUENCE FROM N.A.
RP TISSUE=leaf;
RX MEDLINE=88217525; Pubmed=3368320;
RA Benatti L., Lorenzetti R., Dani M., Martini D., Minganti C.,
RA Sasano M., Sidoli A., Sorla M.;
RT "A DNA sequence from Saponaria officinalis is similar to various RNA
RT polymerase genes.";
RL Nucleic Acids Res. 16:3103-3103(1988).
CC -1- FUNCTION: DNA-DEPENDENT RNA POLYMERASE CATALYZES THE TRANSCRIPTION
CC OF DNA INTO RNA USING THE FOUR RIBONUCLEOSIDE TRIPHOSPHATES AS
CC SUBSTRATES.
CC -1- CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate +
CC (RNA)(N).

```

-1- SUBUNIT: In chloroplasts, the RNA polymerase is composed of four subunits: alpha, beta, beta', and beta".

-1- SUBCELLULAR LOCATION: Chloroplast.

-1- SIMILARITY: Belongs to the RNA polymerase beta chain family.

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EMBL: X07026; CAA30075.1; -.

PIR: S00933; S00933.

HSSP: Q9KWU7; 1HQW.

InterPro: IPR001572; RNA_pol_B.

PIfam: PF00562; RNA_pol_Rpb2_6; 1.

PROSITE: PS01166; RNA_POL_BETA; 1.

Transferrase: DNA-directed RNA polymerase; Transcription; Chloroplast.

NON_TER 1 1

FT NON_TER 417 417

SEQUENCE 417 AA; 46637 MW; 2AF853B23B35A8 CRC64;

Query Match 66.1%; Score 37; DB 1; Length 417;

Best Local Similarity 60.0%; Pred. No. 32;

Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 1 VNMWVKVGS 10

DB 230 VNMWVKVGS 239

RESULT 26

R114_SACPA STANDARD; PRT; 432 AA.

AC P/8956;

DT 01-NOV-1997 (Rel. 35, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 30-MAY-2000 (Rel. 39, Last annotation update)

DE Meiotic recombination protein REC114.

GN REC114.

OS Saccharomyces paradoxus (Yeast).

OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Saccharomyces.

OX NCBI_TaxID=27291;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=DBGV 6466 / CBS 5829;

RC MEDLINE=97412794; PubMed=9267437;

RA Malone R.E., Pittman D.L., Nau J.J.;

RA "Examination of the Intron in the meiosis-specific recombination gene REC114 in Saccharomyces";

RT Mol. Gen. Genet. 255:410-419(1997).

RL -1- FUNCTION: REQUIRED FOR MEIOTIC RECOMBINATION EVENTS; NOT REQUIRED FOR MIOSIS.

CC -1- DEVELOPMENTAL STAGE: MEIOSIS-SPECIFIC.

CC -----

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EMBL: Y08767; CAA70020.1; -.

InterPro: IPR004354; Meiotic_rec114.

PIfam: PF03525; Meiotic_rec114; 1.

PROSITE: PS01548; MEIOTICR114.

Transferrase: DNA-directed RNA polymerase; Transcription; Chloroplast.

NON_TER 1 1

FT NON_TER 432 AA; 48921 MW; C53AF897B943075D CRC64;

SEQUENCE 432 AA; 48921 MW; C53AF897B943075D CRC64;

Query Match 66.1%; Score 37; DB 1; Length 432;

Best Local Similarity 85.7%; Pred. No. 33;

Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 VNMWVKV 7

DB 416 MNWVKV 422

RESULT 27

RPOB_SPTOL STANDARD; PRT; 1070 AA.

AC P11703;

DT 01-OCT-1989 (Rel. 12, Created)

DT 01-OCT-1989 (Rel. 12, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE DNA-directed RNA polymerase beta chain (EC 2.7.7.6).

GN RPOB.

OS Spinacia oleracea (Spinach).

OC Chloroplast.

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; OC Caryophyllidae; Caryophyllales; Chenopodiaceae; Spinacia.

OX NCBI_TaxID=3562;

RN [1]

RP SEQUENCE FROM N.A.

RC MEDLINE=88316931; PubMed=3045324;

RA Hudson G.S., Holton T.A., Whitfield P.R., Bottomley W.;

RA "Spinach chloroplast rpoBc genes encode three subunits of the chloroplast RNA polymerase";

RT J. Mol. Biol. 200:639-654(1988).

RL [2]

RP SEQUENCE FROM N.A.

RC STRAIN=cv. Giant d'hiver, and cv. Monatoli;

RC MEDLINE=21187424; PubMed=11292076;

RA Schmitz-Lineweber C., Maier R.M., Alcaraz J.-P., Cottet A., Herrmann R.G., Mache R.;

RA "The plastid chromosome of spinach (Spinacia oleracea): complete nucleotide sequence and gene organization";

RT Plant Mol. Biol. 45:307-315(2001).

RL -1- FUNCTION: DNA-DEPENDENT RNA POLYMERASE CATALYZES THE TRANSCRIPTION OF DNA INTO RNA USING THE FOUR RIBONUCLEOSIDE TRIPHOSPHATES AS SUBSTRATES.

CC -1- CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate + {RNA}(N).

CC -1- SUBUNIT: In chloroplasts, the RNA polymerase is composed of four subunits: alpha, beta, beta', and beta".

CC -1- SUBCELLULAR LOCATION: Chloroplast.

CC -1- SIMILARITY: Belongs to the RNA polymerase beta chain family.

CC -----

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EMBL: A0400848; CAB88717.1; -.

PIR: C28959; C28959.

HSSP: Q9KWU7; 1HQW.

InterPro: IPR001572; RNA_pol_B.

PIfam: PF04563; RNA_pol_Rpb2_1; 1.

PIfam: PF04561; RNA_pol_Rpb2_2; 1.

PIfam: PF04565; RNA_pol_Rpb2_3; 1.

PIfam: PF00562; RNA_pol_Rpb2_6; 2.

PIfam: PF04560; RNA_pol_Rpb2_7; 1.

PROSITE: PS01166; RNA_POL_BETA; 1.

Transferrase: DNA-directed RNA polymerase; Transcription; Chloroplast.

NON_TER 1 1

FT NON_TER 1070 AA; 120899 MW; 8BA809389BA421F9 CRC64;

SEQUENCE 1070 AA; 120899 MW; 8BA809389BA421F9 CRC64;

Query Match 66.1%; Score 37; DB 1; Length 1070;


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DR 15-SEP-2003 (rel. 42, last annotation update)
DE Alpha-amylase isozyme 3b precursor (EC 3.2.1.1) (1,4-alpha-D-glucan
GN glucanohydrolase).
OS AM1.6 OR AM13B.
OC Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxId=4530;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Japonica M202; TISSUE=Etioolated leaf;
RX MEDLINE=91329692; PubMed=1714318;
RA Sutcliffe T.D., Huang N., Litts J.C., Rodriguez R.L.;
RT "Characterization of an alpha-amylase multigene cluster in rice.";
RL Plant Mol. Biol. 16:579-591(1991).
RN [2]
RP SEQUENCE FROM N.A.
RA Sutcliffe T.D., Huang N., Rodriguez R.L.;
RL Submitted (MAY-1989) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: IMPORTANT FOR BREAKDOWN OF ENDOSPERM STARCH DURING
CC GERMINATION.
CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic
CC linkages in oligosaccharides and polysaccharides.
CC -1- COFACTOR: BINDS A CALCIUM ION REQUIRED FOR ITS ACTIVITY.
CC -1- SUBUNIT: Monomer.
CC -1- TISSUE SPECIFICITY: GERMINATING SEEDS.
CC -1- DEVELOPMENTAL STAGE: EXPRESSED AT A HIGH LEVEL DURING GERMINATION
CC IN THE ALBURNONS CELLS UNDER THE CONTROL OF THE PLANT HORMONE
CC GIBBERELIC ACID AND IN THE DEVELOPING GRAINS AT A LOW LEVEL.
CC -1- SIMILARITY: BELONGS TO FAMILY 13 OF GLYCOSYL HYDROLASES, ALSO
CC KNOWN AS THE ALPHA-AMYLASE FAMILY.
CC -----
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CC or send an email to license@sib-sib.ch).
CC -----
DR EMBL: X56337; CAA39777.1; -
DR EMBL: M24941; AAA3897.1; -
DR PIR: S14957; S14957.
DR HSSP: P04063; IAVA.
DR Gramene: P27937; -.
DR InterPro: IPR006589; Alp_ami1_cat_sub.
DR InterPro: IPR006047; Alpha_ami1_cat.
DR Pfam: PF00128; alpha-amylase; 1.
DR SMART: SM00642; Amy; 1.
DR SMART: SM00642; Amy; 1.
KW Hydrolyase; Glycosidase; Carbohydrate metabolism; Calcium; Signal;
KW Multigene family.
FT SIGNAL 1 26 POTENTIAL.
FT CHAIN 27 438 ALPHA-AMYLASE ISOZYME 3B.
FT ACT_SITE 205 205 BY SIMILARITY.
FT ACT_SITE 313 313 BY SIMILARITY.
FT METAL 117 117 CALCIUM (BY SIMILARITY).
FT METAL 176 176 CALCIUM (BY SIMILARITY).
SQ SEQUENCE 438 AA; 48591 MW; B9DE0DB5ABC63F9C CRC64;
Query Match 64.3%; Score 36; DB 1; Length 438;
Best Local Similarity 66.7%; Pred. NO. 51;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 VNMVKNKVG 9
DB 255 VNMVAQVGG 263

```

Search completed: August 29, 2003, 18:45:14
 Job time : 8.57143 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 29, 2003, 18:40:26 ; Search time 24.5714 Seconds

(without alignments)
105.021 Million cell updates/sec

Title: US-09-830-876-3

Perfect score: 56

Sequence: 1 VNMWVKVGS 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

830525

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database :

Listing first 100 summaries

```

SPRMBL_23:*
1: sp-archaea:*
2: sp-bacteria:*
3: sp-fungi:*
4: sp-human:*
5: sp-invertebrate:*
6: sp-mammal:*
7: sp-mhc:*
8: sp-organelle:*
9: sp-phage:*
10: sp-plant:*
11: sp-rodent:*
12: sp-virus:*
13: sp-vertebrate:*
14: sp-unclassified:*
15: sp-virus:*
16: sp-bacteriap:*
17: sp-archaeap:*

```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	56	100.0	28	10 Q42364	Q42364 triticum ae
2	56	100.0	427	10 Q03651	Q03651 hordeum vul
3	56	100.0	429	10 Q40016	Q40016 hordeum vul
4	50	89.3	424	10 Q94DK9	Q94DK9 oryza sativ
5	48	85.7	29	10 Q42365	Q42365 triticum ae
6	48	85.7	421	10 Q42504	Q42504 hordeum vul
7	48	85.7	437	10 Q04964	Q04964 hordeum vul
8	48	85.7	437	10 Q04965	Q04965 hordeum vul
9	48	85.7	438	10 Q40017	Q40017 hordeum vul
10	47	83.9	427	10 Q40018	Q40018 hordeum vul
11	47	83.9	437	10 Q40019	Q40019 hordeum vul
12	47	83.9	437	10 Q40020	Q40020 hordeum vul
13	42	75.0	416	10 Q8LJ06	Q8LJ06 musa acumin
14	42	75.0	434	10 Q8GUR0	Q8GUR0 musa acumin
15	41	73.2	437	10 Q8L700	Q8L700 avena fatua
16	41	73.2	709	9 Q94MY4	Q94MY4 haemophilus

17	40	71.4	136	12 Q8V211	Q8V211 camelipox vi
18	40	71.4	139	15 Q04144	Q04144 bovine immu
19	40	71.4	340	12 Q57262	Q57262 vaccinia vi
20	40	71.4	340	12 Q8QNM7	Q8QNM7 cowpox viru
21	40	71.4	340	12 Q72752	Q72752 cowpox viru
22	40	71.4	340	12 Q9JF57	Q9JF57 ectromelia
23	40	71.4	340	12 Q9JF36	Q9JF36 vaccinia vi
24	40	71.4	875	15 Q65597	Q65597 bovine immu
25	39	69.6	157	16 Q92AAS	Q92AAS listeria in
26	39	69.6	157	16 Q8Y600	Q8Y600 listeria mo
27	39	69.6	397	17 Q9YD25	Q9YD25 aeropyrum p
28	39	69.6	472	17 Q8ZX92	Q8ZX92 pyrobaculum
29	39	69.6	492	2 Q8GCK3	Q8GCK3 mycoplasma
30	39	69.6	548	16 Q8Y7M0	Q8Y7M0 listeria mo
31	39	69.6	937	2 Q8GCN3	Q8GCN3 mycoplasma
32	39	69.6	937	2 Q8GCK4	Q8GCK4 mycoplasma
33	38	67.9	420	10 Q9ZP43	Q9ZP43 phaseolus v
34	38	67.9	555	16 Q8XMX6	Q8XMX6 clostridium
35	38	67.9	627	16 Q8YR83	Q8YR83 arabidopsis
36	37	66.1	132	17 Q30054	Q30054 archaeoglob
37	37	66.1	149	2 Q93OM0	Q93OM0 erythra tra
38	37	66.1	149	2 Q93OM4	Q93OM4 erythra tra
39	37	66.1	238	17 Q27733	Q27733 methanobact
40	37	66.1	252	17 Q9YTA0	Q9YTA0 thetoplast
41	37	66.1	278	10 Q9AKJ3	Q9AKJ3 arabidopsis
42	37	66.1	346	10 Q9S0Z8	Q9S0Z8 arabidopsis
43	37	66.1	346	16 Q8EWS5	Q8EWS5 mycoplasma
44	37	66.1	439	16 Q9HW58	Q9HW58 pseudomonas
45	37	66.1	455	16 Q8ESL2	Q8ESL2 oceanobacill
46	37	66.1	516	5 Q18198	Q18198 caenorhabdi
47	37	66.1	527	16 Q9CJ47	Q9CJ47 lactococcus
48	37	66.1	574	16 Q9KFR82	Q9KFR82 bacillus ha
49	37	66.1	952	3 Q9UVV5	Q9UVV5 gibberella
50	37	66.1	952	3 Q9V290	Q9V290 gibberella
51	37	66.1	1070	8 Q8HVS5	Q8HVS5 glycine max
52	37	66.1	1273	12 Q9GSK2	Q9GSK2 chilo iride
53	37	66.1	1280	5 Q22554	Q22554 caenorhabdi
54	36	64.3	149	16 Q05904	Q05904 mycobacteri
55	36	64.3	160	16 Q8RAS4	Q8RAS4 thermoaer
56	36	64.3	207	16 Q8EFL7	Q8EFL7 shewanella
57	36	64.3	226	8 Q94O59	Q94O59 odontoterm
58	36	64.3	281	10 Q94JG6	Q94JG6 oryza sativ
59	36	64.3	321	16 Q9CNT5	Q9CNT5 pasteurella
60	36	64.3	341	2 Q8RJS8	Q8RJS8 haemophilus
61	36	64.3	344	2 Q8RML9	Q8RML9 haemophilus
62	36	64.3	344	2 Q8RML0	Q8RML0 haemophilus
63	36	64.3	344	2 Q8RML1	Q8RML1 haemophilus
64	36	64.3	344	2 Q8RML2	Q8RML2 haemophilus
65	36	64.3	344	2 Q8RML3	Q8RML3 haemophilus
66	36	64.3	344	2 Q8RML4	Q8RML4 haemophilus
67	36	64.3	344	2 Q8RML5	Q8RML5 haemophilus
68	36	64.3	344	2 Q8RML6	Q8RML6 haemophilus
69	36	64.3	344	2 Q8RML7	Q8RML7 haemophilus
70	36	64.3	344	2 Q8RML8	Q8RML8 haemophilus
71	36	64.3	344	2 Q8RML9	Q8RML9 haemophilus
72	36	64.3	344	2 Q8RML0	Q8RML0 haemophilus
73	36	64.3	344	2 Q8RML1	Q8RML1 haemophilus
74	36	64.3	344	2 Q8RML2	Q8RML2 haemophilus
75	36	64.3	344	2 Q8RML3	Q8RML3 haemophilus
76	36	64.3	344	2 Q8RML4	Q8RML4 haemophilus
77	36	64.3	344	2 Q8RML5	Q8RML5 haemophilus
78	36	64.3	344	2 Q8RML6	Q8RML6 haemophilus
79	36	64.3	344	2 Q8RML7	Q8RML7 haemophilus
80	36	64.3	344	2 Q8RML8	Q8RML8 haemophilus
81	36	64.3	344	2 Q8RML9	Q8RML9 haemophilus
82	36	64.3	344	2 Q8RML0	Q8RML0 haemophilus
83	36	64.3	344	2 Q8RML1	Q8RML1 haemophilus
84	36	64.3	344	2 Q8RML2	Q8RML2 haemophilus
85	36	64.3	344	2 Q8RML3	Q8RML3 haemophilus
86	36	64.3	344	2 Q8RML4	Q8RML4 haemophilus
87	36	64.3	344	2 Q8RML5	Q8RML5 haemophilus
88	36	64.3	344	2 Q8RML6	Q8RML6 haemophilus
89	36	64.3	344	2 Q8RML7	Q8RML7 haemophilus

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90      36      64.3      589      10      004091
91      36      64.3      589      10      094060
92      36      64.3      602      16      08E215
93      36      64.3      664      16      092EG8
94      36      64.3      664      16      08Y9N6
95      36      64.3      702      17      08ZU82
96      36      64.3      1070      10      08S8X9
97      35      62.5      96      5      096106
98      35      62.5      98      6      09TS95
99      35      62.5      101      2      08RLX1
100     35      62.5      137      16      08E6T4
004091 arabidopsis
094060 arabidopsis
08E215 lespopita
092EG8 listeria in
08Y9N6 listeria mo
08ZU82 pyrobaculum
08S8X9 atropa bell
096106 reticuliter
09TS95 oryctolagus
08RLX1 chlorobium
08E6T4 streptococc

```

ALIGNMENTS

```

RESULT 1
042364      PRELIMINARY;      PRT;      28 AA.

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```

AC      042364;
DT      01-NOV-1996 (TREMblrel. 01, Created)
DT      01-NOV-1996 (TREMblrel. 01, Last sequence update)
DT      01-OCT-2000 (TREMblrel. 15, Last annotation update)
DE      Alpha-amylase subfamily Amyl protein (Fragment).
OS      Triticum aestivum (wheat).
OC      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC      Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
OC      Triticeae; Triticum.
OX      NCBI_TaxID=4565;
RN      [1]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=92366494; PubMed=1502164;
RA      Huang N., Stebbins G.L., Rodriguez R.L.;
RT      "Classification and evolution of alpha-amylase genes in plants.";
RL      Proc. Natl. Acad. Sci. U.S.A. 89:7526-7530(1992).
DR      EMBL: S42213; AAD13822.1; -
DR      HSSP: P04063; JAVa. 1
FT      NON_TER
SQ      SEQUENCE      28 AA: 3022 MW; 69EB0A4138FA3A1 CRC64;

```

```

Query Match      100.0%; Score 56; DB 10; Length 28;
Best Local Similarity 100.0%; Pred. No. 0.0054;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      1 VNMVNVKVGGS 10
      |||||
DB      5 VNMVNVKVGGS 14

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RESULT 2
003651      PRELIMINARY;      PRT;      427 AA.
AC      003651;
DT      01-NOV-1996 (TREMblrel. 01, Created)
DT      01-NOV-1996 (TREMblrel. 01, Last sequence update)
DT      01-MAR-2003 (TREMblrel. 23, Last annotation update)
DE      Alpha-amylase precursor (EC 3.2.1.1).
GN      AMY46.
OS      Hordeum vulgare (Barley).
OC      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC      Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
OC      Triticeae; Hordeum.
OX      NCBI_TaxID=4513;
RN      [1]
RP      SEQUENCE FROM N.A.
RX      STRAIN=Himalaya;
RC      MEDLINE=89066691; PubMed=3264283;
RA      Khurshid B., Rogers J.C.;
RT      "Barley alpha-amylase genes. Quantitative comparison of steady-state
RT      mRNA levels from individual members of the two different families
RT      expressed in aleurone cells.";
RL      J. Biol. Chem. 263:18953-18960(1988).
DR      EMBL: J04202; AA98615.1; -

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DR      HSSP: P04063; JAVa.
DR      InterPro: IPR006047; Alpha-amyl_cat.
DR      InterPro: IPR006589; Alp_amyl_cat_sub.
DR      InterPro: IPR006046; Glyco_hydro_13.
DR      Pfam: PF00128; alpha-amylase; 1.
DR      PRINTS: PR00110; ALPHAAMYLASE.
DR      SMART: SM00642; Amy; 1.
KW      Glycosidase; Hydrolase; Signal.
FT      SIGNAL      1
FT      CHAIN      26
SQ      SEQUENCE      427 AA: 47456 MW; 5A7496B9E6643824 CRC64;

```

```

Query Match      100.0%; Score 56; DB 10; Length 427;
Best Local Similarity 100.0%; Pred. No. 0.091;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      1 VNMVNVKVGGS 10
      |||||
DB      253 VNMVNVKVGGS 262

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```

RESULT 3
040016      PRELIMINARY;      PRT;      429 AA.
ID      040016;
AC      040016;
DT      01-NOV-1996 (TREMblrel. 01, Created)
DT      01-NOV-1996 (TREMblrel. 01, Last sequence update)
DT      01-MAR-2003 (TREMblrel. 23, Last annotation update)
DE      Barley (H.vulgare) alpha-amylase 1.
OS      Hordeum vulgare (Barley).
OC      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC      Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
OC      Triticeae; Hordeum.
OX      NCBI_TaxID=4513;
RN      [1]
RP      SEQUENCE FROM N.A.
RA      Knox C.A.P., Sonthayanon B., Chandra G.R., Muthukrishnan S.;
RT      "Structure and organization of two divergent alpha-amylase genes from
RT      barley";
RL      Plant Mol. Biol. 9:3-17(1987).
RN      [2]
RP      SEQUENCE FROM N.A.
RA      Muthukrishnan S.;
RL      Submitted (JUL-1988) to the EMBL/GenBank/DBJ databases.
DR      EMBL: M17125; AAA32926.1; -
DR      HSSP: P04063; JAVa.
DR      InterPro: IPR006047; Alpha-amyl_cat.
DR      InterPro: IPR006589; Alp_amyl_cat_sub.
DR      Pfam: PF00128; alpha-amylase; 1.
DR      SMART: SM00642; Amy; 1.
SQ      SEQUENCE      429 AA: 47970 MW; 4E7B8B741C944095 CRC64;

```

```

Query Match      100.0%; Score 56; DB 10; Length 429;
Best Local Similarity 100.0%; Pred. No. 0.092;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

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QY      1 VNMVNVKVGGS 10
      |||||
DB      255 VNMVNVKVGGS 264

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```

RESULT 4
094DK9      PRELIMINARY;      PRT;      424 AA.
AC      094DK9;
DT      01-DEC-2001 (TREMblrel. 19, Created)
DT      01-DEC-2001 (TREMblrel. 19, Last sequence update)
DT      01-OCT-2002 (TREMblrel. 22, Last annotation update)
DE      Putative alpha-amylase.
GN      P0514H03.1 OR P0025H06.12.
OS      Oryza sativa (Rice), and
OS      Oryza sativa (Japonica cultivar-group).
OC      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

```



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OC  Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC  Ehrhartoideae; Oryzaceae; Oryza.
OX  NCBI_TaxID=4530, 39947;
RN  [1]
RP  SEQUENCE FROM N.A.
RC  SPECIES-O.saliva; STRAIN-cv. Nipponbare;
RA  Sasaki T., Matsumoto T., Yamamoto K.;
RT  "Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, PAC
RT  clone:P0514H03."
RL  Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
RN  [2]
RP  SEQUENCE FROM N.A.
RC  SPECIES-O.saliva (japonica cultivar-group); STRAIN-cv. Nipponbare;
RA  Sasaki T., Matsumoto T., Yamamoto K.;
RT  "Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, PAC
RT  clone:P0025H06."
RL  Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR  EMBL; AP003125; BAB63640.1; -
DR  EMBL; AP003112; BAC10723.1; -
DR  Gramene; G94DK9; -
DR  InterPro; IPR006047; Alpha-amyl_cat.
DR  Pfam; PF00128; alpha-amylase; 1.
SQ  SEQUENCE 424 AA; 45862 MW; 228582D57B271692 CRC64;

Query Match      89.3%; Score 50; DB 10; Length 424;
Best Local Similarity 80.0%; Pred. No. 1.1;
Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY  1 VNMVNRKVGGS 10
    |||||:||||
DB  130 VNMVNRVGGA 139

RESULT 5
OQ 042365      PRELIMINARY;      PRT;      29 AA.
ID 042365;
DT 01-NOV-1996 (TRENBLREL. 01, Created)
DT 01-NOV-1996 (TRENBLREL. 01, Last sequence update)
DT 01-OCT-2000 (TRENBLREL. 15, Last annotation update)
DE Alpha-amylase subfamily Amy2 protein (Fragment).
OS Triticum aestivum (Wheat).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
OC Triticaceae; Triticum.
OX NCBI_TaxID=4565;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92366494; PubMed=1502164;
RA Huang N., Stebbins G.L., Rodriguez R.L.;
RT "Classification and evolution of alpha-amylase genes in plants."
RT Proc. Natl. Acad. Sci. U.S.A. 89:7526-7530(1992).
DR EMBL; S42217; AAD13823.1; -
DR HSSP; P04063; IAVA.
DR NON_TER 1
SQ SEQUENCE 29 AA; 3082 MW; 71FB73013D584A8 CRC64;

Query Match      85.7%; Score 48; DB 10; Length 29;
Best Local Similarity 80.0%; Pred. No. 0.15;
Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY  1 VNMVNRKVGGS 10
    |||||:||||
DB  5 VNMVNRVGGA 14

RESULT 6
OQ 042504      PRELIMINARY;      PRT;      421 AA.
ID 042504;
DT 01-NOV-1996 (TRENBLREL. 01, Created)
DT 01-NOV-1996 (TRENBLREL. 01, Last sequence update)
DT 01-MAR-2003 (TRENBLREL. 23, Last annotation update)
SQ SEQUENCE 437 AA; 47776 MW; E163524C8BCB2480 CRC64;

DE Alpha-amylase type A.
GN AMY1 OR AMY32B.
OS Hordeum vulgare (Barley).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
OC Triticaceae; Hordeum.
OX NCBI_TaxID=4513;
RN [1]
RP SEQUENCE FROM N.A.
RA Whittier R.F., Dean D.A., Rogers J.C.;
RT Nucleic Acids Res. 13:0-0(1987).
RN [2]
RP SEQUENCE OF 146 FROM N.A.
RX MEDLINE=85006965; PubMed=6090459;
RA Rogers J.C., Millman C.;
RT "Coordinate increase in major transcripts from the high pi alpha-
RT amylase multigene family in barley aleurone cells stimulated with
RT gibberellic acid."
RT J. Biol. Chem. 259:12234-12240(1984).
RN [3]
RP SEQUENCE FROM N.A.
RA Whittier R.F., Dean D.A., Rogers J.C.;
RT Submitted (FEB-1991) to the EMBL/GenBank/DBJ databases.
DR EMBL; X05166; CAA28803.1; -
DR EMBL; M15208; AAA32935.1; -
DR HSSP; P04063; IAVA.
DR InterPro; IPR006047; Alpha-amyl_cat.
DR InterPro; IPR006589; Alp_amyl_cat_sub.
DR InterPro; IPR006046; Glyco_hydro_13.
DR Pfam; PF00128; alpha-amylase; 1.
DR PRINTS; PR00110; ALPHAMYLASE.
DR SMART; SM00642; Amy; 1.
DR Glycosidase; Hydrolase.
SQ SEQUENCE 421 AA; 46102 MW; 7E43D13A75ACBC56 CRC64;

Query Match      85.7%; Score 48; DB 10; Length 421;
Best Local Similarity 80.0%; Pred. No. 2.4;
Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY  1 VNMVNRKVGGS 10
    |||||:||||
DB  253 VNMVNRVGGA 262

RESULT 7
OQ 004964      PRELIMINARY;      PRT;      437 AA.
ID 004964;
AC 004964;
DT 01-JUL-1997 (TRENBLREL. 04, Created)
DT 01-JUL-1997 (TRENBLREL. 04, Last sequence update)
DT 01-MAR-2003 (TRENBLREL. 23, Last annotation update)
DE Alpha-amylase (EC 3.2.1.1).
OS Hordeum vulgare (Barley).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
OC Triticaceae; Hordeum.
OX NCBI_TaxID=4513;
RN [1]
RP SEQUENCE FROM N.A.
RA Matthews P.R., Gubler F., Jacobsen J.V.;
RT "A plant-based expression system for matching cDNA clones and
RT isozyms."
RT Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; Y11276; CAA72143.1; -
DR HSSP; P04063; IAVA.
DR InterPro; IPR006047; Alpha-amyl_cat.
DR InterPro; IPR006589; Alp_amyl_cat_sub.
DR InterPro; IPR006046; Glyco_hydro_13.
DR Pfam; PF00128; alpha-amylase; 1.
DR PRINTS; PR00110; ALPHAMYLASE.
DR SMART; SM00642; Amy; 1.
DR Glycosidase; Hydrolase.
SQ SEQUENCE 437 AA; 47776 MW; E163524C8BCB2480 CRC64;

```

Query Match 85.7%; Score 48; DB 10; Length 437;
 Best Local Similarity 80.0%; Pred. No. 2.5;
 Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VNMVNRVGS 10
 |||||
 Db 253 VNMVDRVGA 262

RESULT 8

004965 ID 004965 PRELIMINARY; PRT; 437 AA.
 AC 004965;
 DT 01-JUL-1997 (TREMBlrel. 04, Created)
 DT 01-JUL-1997 (TREMBlrel. 04, Last sequence update)
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
 DE Alpha-amylase (EC 3.2.1.1).
 GN AMT.
 OS Hordeum vulgare (Barley).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
 OC Triticeae; Hordeum.
 OC NCBI_TaxId=4513;
 RX [1]
 RP SEQUENCE FROM N.A.
 RA Matthews P.R., Gubler F., Jacobsen J.V.;
 RT "A plant-based expression system for matching cDNA clones and
 RT isozymes."
 RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL: Y11277; CAA72144.1; -.
 DR HSSP: P04063; IAVA.
 DR InterPro: IPR006047; Alpha_amyl_cat.
 DR InterPro: IPR006589; Alp_amyl_cat_sub.
 DR Pfam: PF00128; alpha-amylase; 1.
 DR SMART: SM00642; Amy; 1.
 KW Glycosidase; Hydrolase.
 SQ SEQUENCE 437 AA; 47770 MW; 67E910E7CB7769F4 CRC64;
 Query Match 85.7%; Score 48; DB 10; Length 437;
 Best Local Similarity 80.0%; Pred. No. 2.5;
 Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 VNMVNRVGS 10
 |||||
 Db 253 VNMVDRVGA 262

RESULT 9

040017 ID 040017 PRELIMINARY; PRT; 438 AA.
 AC 040017;
 DT 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
 DE Barley (H.vulgare) alpha-amylase 2.
 OS Hordeum vulgare (Barley).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
 OC Triticeae; Hordeum.
 OC NCBI_TaxId=4513;
 RX [1]
 RP SEQUENCE FROM N.A.
 RA Knox C.A.P., Sonthayanon B., Chandra G.R., Muthukrishnan S.;
 RT "Structure and organization of two divergent alpha-amylase genes from
 RT barley."
 RL Plant Mol. Biol. 9:3-17(1987).
 DR EMBL: M17128; AAA32927.1; -.
 DR HSSP: P04063; IAVA.
 DR InterPro: IPR006047; Alpha_amyl_cat.
 DR InterPro: IPR006589; Alp_amyl_cat_sub.
 DR Pfam: PF00128; alpha-amylase; 1.
 DR SMART: SM00642; Amy; 1.

SQ SEQUENCE 438 AA; 47824 MW; 38945AF6DBA2309 CRC64;

Query Match 85.7%; Score 48; DB 10; Length 438;
 Best Local Similarity 80.0%; Pred. No. 2.5;
 Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VNMVNRVGS 10
 |||||
 Db 254 VNMVDRVGA 263

RESULT 10

040015 ID 040015 PRELIMINARY; PRT; 427 AA.
 AC 040015;
 DT 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
 DE Barley (H.vulgare) alpha-amylase 1.
 OS Hordeum vulgare (Barley).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
 OC Triticeae; Hordeum.
 OC NCBI_TaxId=4513;
 RX [1]
 RP SEQUENCE FROM N.A.
 RA Knox C.A.P., Sonthayanon B., Chandra G.R., Muthukrishnan S.;
 RT "Structure and organization of two divergent alpha-amylase genes from
 RT barley."
 RL Plant Mol. Biol. 9:3-17(1987).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Muthukrishnan S.;
 RL Submitted (JUL-1988) to the EMBL/GenBank/DBJ databases.
 DR EMBL: M17126; AAA32925.1; -.
 DR HSSP: P04063; IAVA.
 DR InterPro: IPR006047; Alpha_amyl_cat.
 DR InterPro: IPR006046; Glyco_hydro_13.
 DR Pfam: PF00128; alpha-amylase; 1.
 DR PRINTS: PR00110; ALPHAMYLASE.
 SQ SEQUENCE 427 AA; 47402 MW; D21BA12EAE5F3534 CRC64;
 Query Match 83.9%; Score 47; DB 10; Length 427;
 Best Local Similarity 88.9%; Pred. No. 3.7;
 Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VNMVNRVGS 9
 |||||
 Db 253 VNMVDRVGA 261

RESULT 11

040018 ID 040018 PRELIMINARY; PRT; 437 AA.
 AC 040018;
 DT 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
 DE Barley (H.vulgare) alpha-amylase 2.
 OS Hordeum vulgare (Barley).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
 OC Triticeae; Hordeum.
 OC NCBI_TaxId=4513;
 RX [1]
 RP SEQUENCE FROM N.A.
 RA Knox C.A.P., Sonthayanon B., Chandra G.R., Muthukrishnan S.;
 RT "Structure and organization of two divergent alpha-amylase genes from
 RT barley."
 RL Plant Mol. Biol. 9:3-17(1987).
 DR EMBL: M17127; AAA32928.1; -.
 DR HSSP: P04063; IAVA.
 DR InterPro: IPR006047; Alpha_amyl_cat.

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DR InterPro: IPR006589: Alp_aryl_cat_sub.
DR InterPro: IPR006046: Glyco_hydro_13.
DR Pfam: PR00128: alpha-amy1ase. 1.
DR PRINTS: PR00110: ALPHAMYLASE.
DR SMART: SM00642; Amy; 1.
SO SEQUENCE 437 AA; 4781 MW; 6886B0A1A650656 CRC64;

Query Match
Best Local Similarity 83.9%; Score 47; DB 10; Length 437;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 VNMVKNKVG 9
DB 253 VNMVQVGVG 261

RESULT 12
OBLJ06 PRELIMINARY; PRT; 416 AA.
AC OBLJ06;
DT 01-OCT-2003 (TREMBlrel. 22, Created)
DT 01-OCT-2003 (TREMBlrel. 22, Last sequence update)
DE 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Alpha-amy1ase precursor (EC 3.2.1.1).
OS Musa acuminata (Banana).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Zingiberales; Musaceae;
OC Musa.
OX NCBI_TaxID=4641;
RN SEQUENCE FROM N.A.
RC STRAIN=cv. Nanicao; TISSUE=Fruit;
RA Vieira A. Jr.; Nascimento J.R.O., Lajolo F.M.;
RT "Sequence and molecular characterization of the alpha-amy1ase cDNA
RT expressed during maturation of the banana (Musa spp.).";
RL Thesis (2001), Universidade de Sao Paulo, Sao Paulo, Brasil.
RN SEQUENCE FROM N.A.
RC STRAIN=cv. Nanicao; TISSUE=Fruit;
RA Vieira A. Jr.; Nascimento J.R.O., Lajolo F.M.;
RT "Sequencing and molecular characterization of a banana alpha-amy1ase
RT cDNA clone related to the fruit ripening";
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF533648; AN01149.1; -.
DR InterPro: IPR006047: Alpha_aryl_cat.
DR InterPro: IPR006589: Alp_aryl_cat_sub.
DR Pfam: PR00128; alpha-amy1ase. 1.
DR PRINTS: PR00110; ALPHAMYLASE.
DR SMART: SM00642; Amy; 1.
KW Signal; Hydrolase; Glycosidase.
FT SIGNAL 1 15 POTENTIAL.
FT CHAIN 16 416 ALPHA-AMY1ASE.
SO SEQUENCE 416 AA; 46798 MW; 590CFA3A92EEDC45 CRC64;

Query Match
Best Local Similarity 75.0%; Score 42; DB 10; Length 416;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 VNMVKNKVG 9
DB 244 VNMVQVGVG 252

RESULT 13
OBLJ06 PRELIMINARY; PRT; 416 AA.
AC OBLJ06;
DT 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DE 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Alpha-amy1ase precursor (EC 3.2.1.1).
OS Musa acuminata (Banana).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Zingiberales; Musaceae;
OC Musa.
OX NCBI_TaxID=4641;
RN SEQUENCE FROM N.A.
RC STRAIN=cv. Nanicao; TISSUE=Leaf;
RA Vieira A. Jr.; Nascimento J.R.O., Lajolo F.M.;
RT "Sequencing and molecular characterization of a banana alpha-amy1ase
RT gene.";
RL Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: AY171068; AA011776.1; -.
KW Signal; Hydrolase; Glycosidase.
FT SIGNAL 1 15 POTENTIAL.
FT CHAIN 16 416 ALPHA-AMY1ASE.
SO SEQUENCE 416 AA; 46558 MW; 7D5EC630F221915 CRC64;

Query Match
Best Local Similarity 75.0%; Score 42; DB 10; Length 416;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 VNMVKNKVG 9
DB 244 VNMVQVGVG 252

RESULT 14
OBLJ06 PRELIMINARY; PRT; 434 AA.
AC OBLJ06;
DT 01-NOV-1998 (TREMBlrel. 08, Created)
DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)
DE 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Alpha amy1ase precursor (EC 3.2.1.1).
GN ALPHA-AMY2A.
OS Avena fatua.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Avenae; Avena.
OX NCBI_TaxID=4499;
RN SEQUENCE FROM N.A.
RA Willmott R.L.; University of Bristol.
RL Thesis (1994).
RN SEQUENCE FROM N.A.
RX MEDLINE=99077315; PubMed=9862499.
RA Willmott R.L.; Rushion F.J.; Hooley R.; Lazarus C.M.;
RT "Dnae1 footprints suggest the involvement of at least three types of
RT transcription factors in the regulation of alpha-Amy2/A by
RT gibberellin";
RL Plant Mol. Biol. 38:817-825 (1998).
DR EMBL: AJ010728; CA09323.1; -.
DR HSSP: P04063; IAVA.
DR InterPro: IPR006047: Alpha_aryl_cat.
DR InterPro: IPR006589: Alp_aryl_cat_sub.
DR Pfam: PF00128; alpha-amy1ase. 1.
DR PRINTS: PR00110; ALPHAMYLASE.
DR SMART: SM00642; Amy; 1.
KW Glycosidase; Hydrolase; Signal.
FT SIGNAL 1 23 POTENTIAL.
FT CHAIN 24 434 ALPHA-AMY1ASE.
SO SEQUENCE 434 AA; 47642 MW; 499FC3E9767C1E1 CRC64;

Query Match
Best Local Similarity 73.2%; Score 41; DB 10; Length 434;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 VNMVKNKVG 10
DB 253 VNMVQVGVG 262

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RESULT 15
O81700
ID 081700 PRELIMINARY; PRT: 437 AA.
AC 081700:
DT 01-NOV-1998 (TReMBLrel. 08, Created)
DT 01-NOV-1998 (TReMBLrel. 08, Last sequence update)
DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
DE Alpha-amylose precursor (EC 3.2.1.1).
GN ALPHA-AMY2D.
OS
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
OC Avenae; Avena.
OX NCBL_TaxID=4499;
RN [1]
RP SEQUENCE FROM N.A.
RL Willmott R.L.; University of Bristol.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=99077315; PubMed=9862499;
RA Willmott R.L., Rushton P.J., Hookey R., Lazarus C.M.;
RT "Dnasel footprints suggest the involvement of at least three types of
RT transcription factors in the regulation of alpha-Amy2/A by
RT gldberellin."
RL Plant Mol. Biol. 38:817-825(1998).
DR EMBL: AJ010729; CAA09324.1; -.
DR HSSP: P04063; IAVA.
DR InterPro: IPR006047; Alpha_amyL_cat.
DR InterPro: IPR006589; Alp_amyL_cat_sub.
DR InterPro: IPR006046; Glyco_hydro_13.
DR Pfam: PF00128; alpha-amylose; 1.
DR PRINTS: PR00110; ALPHAAMYDASE.
DR SMART: SM00642; Amy; 1.
KW Glycosidase; Hydrolase; Signal.
FT SIGNAL 1 26
FT CHAIN 27 437 POTENTIAL.
FT SEQUENCE 437 AA; 48103 MW; 88CFE3095737585A CRC64;
SQ
Query Match 73.2%; Score 41; DB 10; Length 437;
Best local similarity 70.0%; Pred. No. 44;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 VNVNKKVGS 10
DB 256 VNVWGVGGA 265

RESULT 16
O94MY4
ID 094MY4 PRELIMINARY; PRT: 709 AA.
AC 094MY4:
DT 01-DEC-2001 (TReMBLrel. 19, Created)
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
DE Orl27.
GN ORF27.
OS
OC Haemophilus phage HP2.
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Myoviridae.
OX NCBL_TaxID=157239;
RN [1]
RP SEQUENCE FROM N.A.
RA Williams B.J., Golomb M., Olson M.V., Smith A.L.;
RT "The HP2 genome of Haemophilus influenzae."
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AY027935; AAK37811.1; -.
DR InterPro: IPR006126; Staph/Strept_tox.
DR PROSITE: PS00277; STAPH_STREPT_TOXIN_1; 1.
SQ SEQUENCE 709 AA; 75730 MW; A00DB1DCF68802A9 CRC64;

Query Match 73.2%; Score 41; DB 9; Length 709;
Best local similarity 73.0%; Pred. No. 73;

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Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 NMVNVKVG 9
DB 166 NMVNVKTAG 173

RESULT 17
O8V211
ID 08V211 PRELIMINARY; PRT: 136 AA.
AC 08V211:
DT 01-MAR-2002 (TReMBLrel. 20, Created)
DT 01-MAR-2002 (TReMBLrel. 20, Last sequence update)
DT 01-OCT-2002 (TReMBLrel. 22, Last annotation update)
DE Hypothetical 16.3 kDa protein (CMP193L).
GN CMP193L.
OS
OC Camel痘 virus (strain CP-1).
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Orthopoxvirus.
OX NCBL_TaxID=203174;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=M-96;
RA Afonso C.L., Tulman E.R., Lu Z., Zsak L., Zaitsev V.L.,
RT "The genome of camel痘 virus."
RT The genome of camel痘 virus shows it is most closely related to
RT "The sequence of camel痘 virus shows it is most closely related to
RT J. Gen. Virol. 83:855-872(2002).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=CMS;
RA Gubser C., Smith G.L.;
RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF438165; AAL73905.1; -.
DR EMBL: AY009089; AAG37702.1; -.
KW Hypothetical protein
SQ SEQUENCE 136 AA; 16302 MW; CF62496C588D54CF CRC64;

Query Match 71.4%; Score 40; DB 12; Length 136;
Best local similarity 77.8%; Pred. No. 20;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 NMVNVKVG 10
DB 96 NMVSKVGDS 104

RESULT 18
O04144
ID 004144 PRELIMINARY; PRT: 159 AA.
AC 004144:
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
DE Rev protein 2.
GN REV2.
OS
OC Bovine immunodeficiency-like virus.
OC Viruses; Retrod viruses; Retroviridae; Lentivirus.
OX NCBL_TaxID=11647;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91251255; PubMed=1645801;
RA Oberste M.S., Greenwood J.D., Gonda M.A.;
RT "Analysis of the transcription pattern and mapping of the putative rev
RT and env splice junctions of bovine immunodeficiency-like virus."
RL J. Virol. 65:3932-3937(1991).

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DR EMBL: M74712: AAA42773.1: -
 SQ SEQUENCE 159 AA: 18002 MW: 4DDA6ECE94626C2E CRC64;
 Query Match 71.4%; Score 40; DB 15; Length 159;
 Best Local Similarity 66.7%; Pred. No. 23;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 2 MNVNRVGS 10
 DB 43 MNLNKIGES 51
 ||:|||||
 ||:|||||

RESULT 19
 ID 057262 PRELIMINARY; PRT: 340 AA.
 AC 057262;
 DT 01-JUN-1998 (TREMBLrel. 06, Created)
 DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE Putative 39.6k protein.
 GN MVA195L.
 OS Vaccinia virus (strain Ankara).
 OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
 OC Orthopoxvirus.
 OX NCBI_TaxID=126794;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-Ankara;
 RA Antoine G., Scheiflinger F., Falkner F.G., Dörner F.;
 RT "The complete genomic sequence of the Modified Vaccinia Ankara (MVA)
 strain.";
 RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL: U94848; AAB96481.1: -
 SQ SEQUENCE 340 AA: 39566 MW: DA944A21A712FFB7 CRC64;

Query Match 71.4%; Score 40; DB 12; Length 340;
 Best Local Similarity 77.8%; Pred. No. 51;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 2 MNVNRVGS 10
 DB 96 MNVSKVGS 104
 ||:|||||
 ||:|||||

RESULT 20
 ID 080M7 PRELIMINARY; PRT: 340 AA.
 AC 080M7;
 DT 01-JUN-2002 (TREMBLrel. 21, Created)
 DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE V201.
 OS Cowpox virus (CPV).
 OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
 OC Orthopoxvirus.
 OX NCBI_TaxID=10243;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-Brighton Red;
 RA MEDLINE=83117629; PubMed=6961398;
 RA Pickup D.J., Bastia D., Stone H.O., Joklik W.K.;
 RT "Sequence of terminal regions of cowpox virus DNA: arrangement of
 RT repeated and unique sequence elements.";
 RT Proc. Natl. Acad. Sci. U.S.A. 79:7112-7116(1982).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-Brighton Red;
 RA MEDLINE=90177240; PubMed=2309453;
 RA Parsons B.L., Pickup D.J.;
 RT "Transcription of orthopoxvirus telomeres at late times during
 RT infection.";
 RL Virology 175:69-80(1990).
 RN [3]

RP SEQUENCE FROM N.A.
 RC STRAIN-Brighton Red;
 RX MEDLINE=91196263; PubMed=2014645;
 RA Hu F.Q., Pickup D.J.;
 RT "Transcription of the terminal loop region of vaccinia virus DNA is
 RT initiated from the telomere sequences directing DNA resolution.";
 RL Virology 181:716-720(1991).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN-Brighton Red;
 RX MEDLINE=94378510; PubMed=8091665;
 RA Hu F.Q., Smith C.A., Pickup D.J.;
 RT "Cowpox virus contains two copies of an early gene encoding a soluble
 RT secreted form of the type II TNF receptor.";
 RL Virology 204:343-356(1994).
 RN [5]
 RP SEQUENCE FROM N.A.
 RC STRAIN-Brighton Red;
 RA Pickup D.J.;
 RL Submitted (AUG-1993) to the EMBL/GenBank/DBJ databases.
 RN [6]
 RP SEQUENCE FROM N.A.
 RC STRAIN-Brighton Red;
 RA Dietrich F.S., Ray C.A., Sharma A.D., Allen A., Pickup D.J.;
 RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF482758; AAM13649.1: -
 SQ SEQUENCE 340 AA: 39662 MW: A13ACEFF851CF662 CRC64;

Query Match 71.4%; Score 40; DB 12; Length 340;
 Best Local Similarity 77.8%; Pred. No. 51;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 2 MNVNRVGS 10
 DB 96 MNVSKVGS 104
 ||:|||||
 ||:|||||

RESULT 21
 ID 072752 PRELIMINARY; PRT: 340 AA.
 AC 072752;
 DT 01-AUG-1998 (TREMBLrel. 07, Created)
 DT 01-AUG-1998 (TREMBLrel. 07, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE B15L protein.
 GN B15L.
 OS Cowpox virus (CPV).
 OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
 OC Orthopoxvirus.
 OX NCBI_TaxID=10243;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-GRI-90;
 RX MEDLINE=98229462; PubMed=9568042;
 RX Shchelkunov S.N., Saitonov P.F., Totmenin A.V., Petrov N.A.,
 RA Ryzantkina O.I., Gutorov V.V., Kotwal G.J.;
 RT "Species-specific differences in genome organization of cowpox,
 RT smallpox and vaccinia viruses.";
 RL Virology 243:432-460(1998).
 DR EMBL: Y15035; CA875291.1: -
 SQ SEQUENCE 340 AA: 39409 MW: CA8BE1F3089627D3 CRC64;

Query Match 71.4%; Score 40; DB 12; Length 340;
 Best Local Similarity 77.8%; Pred. No. 51;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 2 MNVNRVGS 10
 DB 96 MNVSKVGS 104
 ||:|||||
 ||:|||||

RESULT 22
 ID 09JF57

ID 09JES7 PRELIMINARY; PRT: 340 AA.
 AC 09JFS7;
 DT 01-OCT-2000 (TREMBlrel. 15, Created)
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
 DE 101.
 GN C10L.
 OS Ectromelia virus.
 OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
 OC Orthopoxvirus.
 OX NCBI_TaxID=12643;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MOSCOW;
 RC MEDLINE=20192152; PubMed=10725549;
 RA Chen N., Buller R.M.L., Wall E.M., Upton C.;
 RT "Analysis of host response modifier ORFs of ectromelia virus, the
 RT causative agent of mousepox.";
 RL Virus Res. 66:155-173(2000).
 DR EMBL: AF012825; AAC95569.1;
 SQ SEQUENCE 340 AA; 39636 MW; 29414769AA1EAC49 CRC64;

Query Match 71.4%; Score 40; DB 12; Length 340;
 Best Local Similarity 77.8%; Pred. No. 51;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 2 NMVNVKVGGS 10
 Db 96 NMVSKVGS 104

RESULT 23
 ID 09JF36 PRELIMINARY; PRT: 340 AA.
 AC 09JF36;
 DT 01-OCT-2000 (TREMBlrel. 15, Created)
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
 DE 101.
 GN TBI17.
 OS Vaccinia virus (strain Tian Tan).
 OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
 OC Orthopoxvirus.
 OX NCBI_TaxID=10253;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Tian Tan;
 RA Jin Q., Hou Y.D., Cheng N.H., Yao E.M., Cheng S.X., Yang X.K.,
 RA Jing D.Y., Yu W.H., Yuan J.S., Ma X.J.;
 RT "Complete genomic sequence of vaccinia virus (Tian Tan strain).";
 RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF095689; AAF34088.1;
 SQ SEQUENCE 340 AA; 39481 MW; CEALC9CBDF3462AC CRC64;

Query Match 71.4%; Score 40; DB 12; Length 340;
 Best Local Similarity 77.8%; Pred. No. 51;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 2 NMVNVKVGGS 10
 Db 96 NMVSKVGS 104

RESULT 24
 ID 065597 PRELIMINARY; PRT: 875 AA.
 AC 065597;
 DT 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DE 101.
 GN Envelope glycoprotein.
 OS Bovine immunodeficiency-like virus.
 OC Viruses; Retroviridae; Lentivirus.

OX NCBI_TaxID=11647;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=29;
 RA Nadin-Davis S.A., Chang S.C., Roth J.A., Carpenter S.;
 RT "Isolation and characterization of cDNAs encoding rev and tat of
 RT bovine immunodeficiency-like virus.";
 RL Submitted (OCT-1992) to the EMBL/GenBank/DBJ databases.
 DR EMBL: L04972; AAA42771.1;
 DR InterPro: IPR001064; Crystal1in.
 DR InterPro: IPR002114; HEP_Serp_site.
 DR PROSITE: PS00225; CRYSTALIN_BETAGAMMA; 1.
 DR PROSITE: PS00589; PTS_HPR_SER; 1.
 SQ SEQUENCE 875 AA; 99108 MW; 0FA8D362A7FD7EF3 CRC64;

Query Match 71.4%; Score 40; DB 15; Length 875;
 Best Local Similarity 66.7%; Pred. No. 1.4e+02;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 2 NMVNVKVGGS 10
 Db 759 NMVNVKVGGS 767

RESULT 25
 ID 092AA5 PRELIMINARY; PRT: 157 AA.
 AC 092AA5;
 DT 01-DEC-2001 (TREMBlrel. 19, Created)
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
 DE 101.
 GN Hypothetical protein lin2017.
 GN LIN2017.
 OS Listeria innocua.
 OC Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.
 OX NCBI_TaxID=1642;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CLIP 11262 / Serovar 6a;
 RX PubMed=11679669;
 RA Glaser P., Franjeul L., Buchrieser C., Rusniok C., Amend A.,
 RA Baquero F., Berche P., Bloeker H., Brandt P., Chakraborty T.,
 RA Charbit A., Chetouani F., Couve E., de Daruvar A., Deloux P.,
 RA Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Dussutget O.,
 RA Ertan K.-D., Esli H., Garcia-del Portillo F., Garrido P.,
 RA Gautier L., Goebel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D.,
 RA Jones L.-M., Kaerst U., Kreft J., Kuhn M., Kunst F., Kurupkat G.,
 RA Madueno E., Maitournam A., Mata Vicente J., Ng E., Nedjati H.,
 RA Nordiek G., Novella S., de Pablos B., Perez-Diaz J.-C., Purrell R.,
 RA Remmel B., Rose M., Schlueter T., Simoes N., Tierrez A.,
 RA Vazquez-Boland J.-A., Voss H., Wehlund J., Cossart P.;
 RT "Comparative genomics of Listeria species.";
 RL Science 294:849-852(2001).
 DR EMBL: AL596170; CAC97247.1;
 DR Listlist: LIN2017;
 DR InterPro: IPR006663; ThioRedox_dom2.
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 157 AA; 17707 MW; C0F858787c36E65 CRC64;

Query Match 69.6%; Score 39; DB 16; Length 157;
 Best Local Similarity 75.0%; Pred. No. 34;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 2 NMVNVKVGGS 9
 Db 146 NMVNVKVGGS 153

RESULT 26
 ID 081600 PRELIMINARY; PRT: 157 AA.
 AC 081600;
 DT 01-MAR-2002 (TREMBlrel. 20, Created)

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DT 01-MAR-2002 (TReMBLrel. 20, last sequence update)
DE 01-MAR-2003 (TReMBLrel. 23, last annotation update)
GN Hypothetical protein lmo1903.
OS Listeria monocytogenes.
OC Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.
OX NCBI_TaxID=1639;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=EGD-e / Serovar 1/2a;
RX MEDLINE=21537279; PubMed=11679669;
RA Glaser P., Frangeul L., Buchrieser C., Rusnok C., Amend A.,
RA Baguer F., Brangeul P., Blocher H., Brandt P., Chakraborty T.,
RA Charit A., Chetouani F., Couve E., de Daruvar A., Dehoux P.,
RA Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Dussuguet O.,
RA Entlin K.-D., Fajth H., Garcia-del Portillo F., Garrido P.,
RA Gautier L., Goebel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D.,
RA Jones L.-M., Kaerst U., Kreft J., Kunz M., Kung F., Kurapat G.,
RA Madueno E., Maicouran A., Mata Vicente J., Ng E., Nedjari H.,
RA Nordstedt G., Novella S., de Pablos B., Perez-Diaz J.-C., Furell R.,
RA Remmel B., Rose M., Schlueter T., Simoes N., Tietzer A.,
RA Vazquez-Boland J.-A., Voss H., Weiland J., Cossart P.;
RT Comparative genomics of Listeria species.";
RI Science 294:849-852(2001).
DR EMBL: AL591981; CAC9981.1; -.
DR Listlist; LMO01903; -.
DR InterPro: IPR006663; ThioRedox_dom2.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 157 AA; 17618 MW; BA34208FD8C9DE2 CRC64;

Query Match
Best Local Similarity 69.6%; Score 39; DB 16; Length 157;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 2 VMVNVKVG 9
DB 146 NMANKVSG 153

RESULT 27
OYD5 PRELIMINARY; PRT; 397 AA.
ID OYD5;
AC OYD5;
DT 01-NOV-1999 (TReMBLrel. 12, Created)
DT 01-NOV-1999 (TReMBLrel. 12, last sequence update)
DE 01-MAR-2003 (TReMBLrel. 23, last annotation update)
DE Hypothetical protein APE0774.
GN APE0774.
OS Aeropyrum pernix.
OC Archaea; Crenarchaeota; Thermoprotei; Desulfurococcaceae;
OC Desulfurococcaceae; Aeropyrum.
OX NCBI_TaxID=56636;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=K1;
RX MEDLINE=99310339; PubMed=10382966;
RA Kawarabayashi Y., Hino Y., Horikawa H., Yamazaki S., Halkawa Y.,
RA Jin-no K., Takahashi M., Sekine M., Baba S.-I., Akai A., Kosugi H.,
RA Hosogawa K., Fukui S., Nagai Y., Nishijima K., Nakazawa H.,
RA Takahata K., Masuda S., Funahashi T., Tanaka T., Kudoh Y.,
RA Nakamura Y., Kushiida N., Oguchi A., Aoki K.-I., Kubota K.,
RA Nakamura Y., Nomura N., Sako Y., Kikuchi H.;
RT "Complete genome sequence of an aerobic hyper-thermophilic
RT crenarchaeon, Aeropyrum pernix K1.";
RL DNA Res. 6:83-101(1999).
DR EMBL: AP000060; BAA79752.1; -.
DR InterPro: IPR002052; N6_Mtase.
DR PROSITE: PS00092; N6_MTASE; 1.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 397 AA; 41172 MW; 6E2862EBCF406C61 CRC64;

Query Match
Best Local Similarity 69.6%; Score 39; DB 17; Length 397;
Matches 55.6%; Pred. No. 90;

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Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 1 VMVNVKVG 9
DB 167 LMNVRRIG 175

RESULT 28
O82X92 PRELIMINARY; PRT; 472 AA.
ID O82X92;
AC O82X92;
DT 01-MAR-2002 (TReMBLrel. 20, Created)
DT 01-MAR-2002 (TReMBLrel. 23, last sequence update)
DE 01-MAR-2003 (TReMBLrel. 23, last annotation update)
DE Branched-chain amino acid binding protein.
GN PAB3392.
OS Pyrobaculum aerophilum.
OC Archaea; Crenarchaeota; Thermoprotei; Thermoproteales;
OC Thermoproteales; Pyrobaculum.
OX NCBI_TaxID=13773;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=IM2 / ATCC 51768 / DSM 7523;
RX PubMed=11792869;
RA Fitz-Gibbon S.T., Ladner H., Kim U.-J., Stettler K.O., Simon M.I.,
RA Miller J.H.;
RT "Genome sequence of the hyperthermophilic crenarchaeon Pyrobaculum
RT aerophilum.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:984-989(2002).
DR EMBL: AE009819; AAL63457.1; -.
DR InterPro: IPR002965; P_fich_extensn.
DR PRINTS: PRO1217; PRICEXTENSN.
KW Complete proteome.
SQ SEQUENCE 472 AA; 51167 MW; 041175B8AA05E70F CRC64;

Query Match
Best Local Similarity 66.7%; Score 39; DB 17; Length 472;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 VMVNVKVG 9
DB 102 VMWINDGG 110

RESULT 29
O8GCK3 PRELIMINARY; PRT; 492 AA.
ID O8GCK3;
AC O8GCK3;
DT 01-MAR-2003 (TReMBLrel. 23, Created)
DT 01-MAR-2003 (TReMBLrel. 23, last sequence update)
DE 01-MAR-2003 (TReMBLrel. 23, last annotation update)
DE ICEF-II ORE17 (Fragment).
OS Mycoplasma fermentans.
OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
OX NCBI_TaxID=2115;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PC18;
RX MEDLINE=22336318; PubMed=12446643;
RA Calcutt M.J., Lewis M.S., Wise K.S.;
RT "Molecular Genetic Analysis of ICEF, an Integrative Conjugal Element
RT That is Present as a Repetitive Sequence in the Chromosome of
RT Mycoplasma fermentans PC18.";
RL J. Bacteriol. 184:6929-6941(2002).
DR EMBL: AY168965; AAN85277.1; -.
FT NON_TER
SQ SEQUENCE 492 AA; 55875 MW; B37487ADF79F3783 CRC64;

Query Match
Best Local Similarity 69.6%; Score 39; DB 2; Length 492;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

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DB 124 VKMANMGG 132

RESULT 30

08Y7M0 PRELIMINARY; PRT; 548 AA.
 AC 08Y7M0;
 DT 01-MAR-2002 (TREMBLrel. 20, Created)
 DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
 DE Hypothetical protein lmo1254.
 GN lmo1254.
 OS Listeria monocytogenes.
 OC Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.
 OX NCBI_TaxID=1639;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=EGD-e / Serovar 1/2a;
 RX MEDLINE=21537279; PubMed=11679669;
 RA Glaser P., Frangoul L., Buchrieser C., Rusniok C., Amend A.,
 Baquero F., Berche P., Bloeker H., Brandt P., Chakraborty T.,
 Charbit A., Cherouani F., Couve E., de Daruvar A., Dehoux P.,
 Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Dussurget O.,
 Ertian K.-D., Pshi H., Garcia-del Portillo F., Garrido P.,
 Gautier L., Goebel W., Gomez-Lopez N., Hain T., Haut J., Jackson D.,
 Jones L.-M., Kaerst U., Kreft U., Kuhn M., Kunst F., Kurapkai G.,
 Madueno E., Maitounam A., Mata Vicente J., Ng E., Nedjari H.,
 Nordsiek G., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell R.,
 Remmel B., Rose M., Schlueter T., Simoes N., Tierrez A.,
 Vazquez-Boland J.-A., Voss H., Wehland J., Cossart P.,
 "Comparative genomics of Listeria species."
 RT Science 294:849-852(2001).
 RL EMBL; AL591978; CAC9332.1; -
 DR L1stLibist; LMO01254; -
 DR InterPro: IPR006047; Alpha-amyl_cat.
 DR InterPro: IPR006589; Alp_amyl_cat_sub.
 DR Pfam; PF00128; alpha-amylase; 1.
 DR SMART; SM00642; Amy; 1.
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 548 AA; 63194 MW; D010A588529197D3 CRC64;

Query Match 69.6%; Score 39; DB 16; Length 548;
 Best Local Similarity 66.7%; Pred. NO. 1.3e+02;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 NWYMKVGS 10
 |||:| ||:
 DB 137 NWVSKFSGN 145

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 Job time : 27.5714 secs